



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 133719

To: Jeffrey Parkin
Location: rem/3d39/3c18
Art Unit: 1648
Wednesday, September 29, 2004

Case Serial Number: 10/084813

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:00:23 ; Search time 16.2 Seconds
(without alignments)
57.362 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96

Sequence: 1 SQYQFWNFQTLKIVILG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	54	4	US-08-833-752-11
2	96	100.0	352	3	US-08-466-343D-2
3	96	100.0	352	3	US-09-087-232A-13
4	96	100.0	352	3	US-08-861-105-14
5	96	100.0	352	3	US-08-575-967A-2
6	96	100.0	352	3	US-09-045-583-52
7	96	100.0	352	4	US-09-517-605-5
8	96	100.0	352	4	US-09-534-185-52
9	96	100.0	352	4	US-08-833-752-5
10	96	100.0	352	4	US-09-502-783A-2
11	96	100.0	352	4	US-09-796-202-1
12	82	85.4	21	3	US-08-907-468-11
13	74	77.1	354	4	US-08-724-984A-2
14	47	49.0	355	4	US-09-886-319A-13
15	45	46.9	355	3	US-09-045-583-53
16	45	46.9	355	4	US-09-534-185-53
17	43.5	45.3	352	4	US-09-489-039A-13500
18	43	44.8	172	4	US-09-621-976-4131
19	43	44.8	344	3	US-08-681-192-2
20	42	43.8	460	3	US-08-935-283-4
21	42	43.8	460	4	US-09-594-185-4
22	42	43.8	727	4	US-09-540-236-3023
23	41	42.7	160	4	US-09-328-352-6593
24	41	42.7	255	4	US-09-491-577-2
25	41	42.7	363	4	US-09-252-991A-25052
26	40	41.7	254	4	US-09-134-001C-4582
27	40	41.7	311	4	US-09-134-001C-5171

28	40	41.7	316	4	US-09-489-039A-8904	Sequence 8904, Ap
29	40	41.7	355	1	US-08-012-988A-2	Sequence 2, Appli
30	40	41.7	355	1	US-08-450-393A-5	Sequence 5, Appli
31	40	41.7	355	3	US-08-446-669-5	Sequence 5, Appli
32	40	41.7	355	4	US-09-239-938-1	Sequence 1, Appli
33	40	41.7	355	4	US-08-833-752-9	Sequence 9, Appli
34	40	41.7	355	4	US-09-886-319A-14	Sequence 14, Appli
35	40	41.7	355	5	PCT-US95-00476-5	Sequence 5, Appli
36	40	41.7	371	3	US/08/622	INFORMATION FOR
37	40	41.7	371	4	US-09-165-922A-10	Sequence 10, Appli
38	40	41.7	659	4	US-09-252-991A-26013	Sequence 26013, A
39	40	41.7	2037	4	US-09-543-681A-5538	Sequence 5538, Ap
40	39	40.6	92	4	US-09-328-352-5171	Sequence 5171, Ap
41	39	40.6	448	4	US-09-134-000C-3794	Sequence 3794, Ap
42	39	40.6	452	4	US-09-530-836-6	Sequence 6, Appli
43	39	40.6	485	4	US-09-134-000C-6031	Sequence 6031, Ap
44	39	40.6	598	2	US-08-853-659A-53	Sequence 53, Appli
45	39	40.6	564	4	US-09-377-497-70	Sequence 70, Appli

ALIGNMENTS

RESULT 1
US-08-833-752-11
; Sequence 11, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-833-752-11

Query Match 100.0%; Score 96; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWNFQTLKIVILG 18

Db 9 SQYQFWNFQTLKIVILG 26

RESULT 2

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US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGMR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-2
Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNFTLKIVILG 18
|||||
Db 185 SOYQFWKFNFTLKIVILG 202

RESULT 3
US-08-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435

US-08-466-343D-2
Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNFTLKIVILG 18
|||||
Db 185 SOYQFWKFNFTLKIVILG 202

RESULT 3
US-08-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE: US/08/861,105
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:

US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; FILING DATE: 19-JUN-1996
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:

US-08-087-232A-13
Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNFTLKIVILG 18
|||||
Db 185 SOYQFWKFNFTLKIVILG 202

RESULT 4
US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-861-105-14

Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 5
US-08-575-967A-2
; Sequence 2, Application US/08575967A
; Patent No. 6265184
; GENERAL INFORMATION:
; APPLICANT: Gray et al.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,967A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy R.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-52

Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 7
US-09-517-605-5
; Sequence 5, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-605-5

Query Match 100.0%; Score 96; DB 4; Length 352;
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Patent No. 6548636
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796.202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVLG 18
Db 185 SQYQFWKNFQTLKIVLG 202

RESULT 12
US-08-907-468-11
Sequence 11, Application US/08907468
Patent No. 6057102
GENERAL INFORMATION:
APPLICANT: Landau, Nathaniel R.
APPLICANT: Koup, Richard A.
APPLICANT: Liu, Rong
APPLICANT: Paxton, William
TITLE OF INVENTION: HIV CORECEPTOR MUTANTS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/907,468
APPLICATION NUMBER: US/08/907,468
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-005 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1694
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-907-468-11

Query Match 85.4%; Score 82; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQYQFWKNFQTLKIV 15
Db 7 SQYQFWKNFQTLKIV 21

RESULT 13
US-08-724-984A-2
Sequence 2, Application US/08724984A
Patent No. 6388055
GENERAL INFORMATION:
APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-
TITLE OF INVENTION: CCR5 Receptor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSES: Smithkline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,984A
FILING DATE: October 3, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEFAX: 610 270 5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 354
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-724-984A-2

Query Match 77.1%; Score 74; DB 4; Length 354;
Best Local Similarity 76.5%; Pred. No. 0.00017;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVIL 17
Db 187 QYHFWSFQILKMWIL 203

RESULT 14
US-09-886-319A-13
Sequence 13, Application US/09886319A
Patent No. 6586185
GENERAL INFORMATION:
APPLICANT: Wolf, Eckard
APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014002

US-09-886-319A-13
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 355
TYPE: PPT
ORGANISM: Mus musculus

Query Match 49.0%; Score 47; DB 4; Length 355;
Best Local Similarity 61.5%; Pred. No. 5;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18
DB 195 WKRFQALKNLIFG 207

RESULT 15
US-09-045-583-53
Sequence 53, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNT-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal

US-09-045-583-53
Query Match 46.9%; Score 45; DB 3; Length 355;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 YQFWKNFQTLKIVILG 18
DB 192 FQWKLFOALKNLIFG 207

RESULT 16
US-09-534-185-53
Sequence 53, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNT-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-534-185-53

Query Match 46.9%; Score 45; DB 4; Length 355;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 YQFWKNFQTLKIVILG 18
DB 192 FQWKLFOALKNLIFG 207

RESULT 17
US-09-489-039A-13500
Sequence 13500, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13500
LENGTH: 352

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; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13500

Query Match      45.3%; Score 43.5; DB 4; Length 352;
Best Local Similarity 43.5%; Pred. No. 19;
Matches 10; Conservative 3; Mismatches 3; Indels 7; Gaps 1;

QY  2 QYQFW-----KNFQTLKIVIL 17
    ||| : ||| ||| ||| : |||
Db  196 QLRFWQAGSLDIRTQTLKIVIL 218

RESULT 18
US-09-621-976-4131
; Sequence 4131, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4131
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -30...-1
US-09-621-976-4131

Query Match      44.8%; Score 43; DB 4; Length 172;
Best Local Similarity 57.1%; Pred. No. 11;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY  4 QFWKNFQTLKIVIL 17
    : ||| ||| ||| : |||
Db  74 EFRKNFELRLDVL 87

RESULT 19
US-08-681-192-2
; Sequence 2, Application US/08681192
; Patent No. 6287801
; GENERAL INFORMATION:
; APPLICANT: BERGSMÄ, DERK
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: SARAU, HENRY
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNPD578
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681.192
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATG50014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-681-192-2

Query Match      44.8%; Score 43; DB 3; Length 344;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  5 FWKNFQTLKIVI 16
    ||| : ||| : |||
Db  195 FWKHFLLKQNI 206

RESULT 20
US-08-935-263-4
; Sequence 4, Application US/08935263A
; Patent No. 6117669
; GENERAL INFORMATION:
; APPLICANT: Furuichi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
; APPLICANT: Kiyasu, Tatsuya
; APPLICANT: Nagahashi, Yoshie
; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
; FILE REFERENCE: Biotin Genes
; CURRENT APPLICATION NUMBER: US/08/935.263A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: EP 96115540.5
; EARLIER FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Kurthia sp.
US-08-935-263-4

Query Match      43.8%; Score 42; DB 3; Length 460;
Best Local Similarity 54.5%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  3 YQFWKNFQTLK 13
    ||| : ||| : |||
Db  127 YQYWKNDPVK 137

RESULT 21
US-09-594-185-4
; Sequence 4, Application US/09594185
; Patent No. 6365388
; GENERAL INFORMATION:
; APPLICANT: Furuichi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
```

; APPLICANT: Kiyasu, Tateuya
 ; APPLICANT: Nagahashi, Yoshie
 ; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
 ; FILE REFERENCE: Biotin Genes
 ; CURRENT APPLICATION NUMBER: US/09/594,185
 ; CURRENT FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: 08/935,263
 ; PRIOR FILING DATE: 1997-09-22
 ; PRIOR APPLICATION NUMBER: EP 96115540.5
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 460
 ; TYPE: PRT
 ; ORGANISM: Kurthia sp.
 US-09-594-185-4

Query Match 43.8%; Score 42; DB 4; Length 460;
 Best Local Similarity 54.5%; Pred. No. 45;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 3 YQFWKNFQTLK 13
 Db 127 YQWKNIDPVK 137
 RESULT 22
 US-09-540-236-3023
 ; Sequence 3023, Application US/09540236
 ; Patent No. 6673910
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
 ; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
 ; CURRENT APPLICATION NUMBER: US/09/540,236
 ; CURRENT FILING DATE: 2000-04-04
 ; NUMBER OF SEQ ID NOS: 3840
 ; SEQ ID NO 3023
 ; LENGTH: 727
 ; TYPE: PRT
 ; ORGANISM: M. catarrhalis
 US-09-540-236-3023

Query Match 43.8%; Score 42; DB 4; Length 727;
 Best Local Similarity 37.5%; Pred. No. 74;
 Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 YQFWKNFQTLK 17
 Db 167 YQWKNQTLK 182

RESULT 23
 US-09-328-352-6593
 ; Sequence 6593, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 6593
 ; LENGTH: 160
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-6593

Query Match 42.7%; Score 41; DB 4; Length 160;

Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 YQFWKNFQ 10
 Db 146 YVFWKNYQ 153

RESULT 24
 US-09-491-577-2
 ; Sequence 2, Application US/09491577
 ; Patent No. 6610511
 ; GENERAL INFORMATION:
 ; APPLICANT: Yale University
 ; APPLICANT: Carlson, John R.
 ; APPLICANT: Kim, Hunhyong
 ; APPLICANT: Clyne, Peter J.
 ; APPLICANT: Marr, Coral G.
 ; TITLE OF INVENTION: No. 6610511el Family of Odorant Receptor Genes in Drosophila
 ; FILE REFERENCE: 44574-5061-US
 ; CURRENT APPLICATION NUMBER: US/09/491,577
 ; CURRENT FILING DATE: 2000-01-25
 ; EARLIER APPLICATION NUMBER: US 60/117,132
 ; EARLIER FILING DATE: 1999-01-25
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 255
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-491-577-2

Query Match 42.7%; Score 41; DB 4; Length 255;
 Best Local Similarity 53.3%; Pred. No. 35;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 YQFWKNFQTLK 17
 Db 48 YKLWSTFVTLFIL 62

RESULT 25
 US-09-252-991A-25052
 ; Sequence 25052, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25052
 ; LENGTH: 363
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25052

Query Match 42.7%; Score 41; DB 4; Length 363;
 Best Local Similarity 60.0%; Pred. No. 51;
 Matches 9; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 4 QFWKNFQTLK 18
 Db 237 KFWKHQFQ---VILG 247

RESULT 26

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US-09-134-001C-4582
; Sequence 4582, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4582
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4582
Query Match 41.7%; Score 40; DB 4; Length 254;
Best Local Similarity 53.8%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 SOYQWKNFQTLK 13
Db 9 SOYPLNQLNLTUK 21
RESULT 27
US-09-134-001C-5171
; Sequence 5171, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5171
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5171
Query Match 41.7%; Score 40; DB 4; Length 311;
Best Local Similarity 38.5%; Pred. No. 63;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 6 WKNFQTLKIVILG 18
Db 271 WPNFATILWVVG 283
RESULT 28
US-09-489-039A-8904
; Sequence 8904, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
```

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US-09-489-039A-8904
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8904
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8904
Query Match 41.7%; Score 40; DB 4; Length 316;
Best Local Similarity 61.5%; Pred. No. 64;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 6 WKNFQTLKIVILG 18
Db 226 WINVQGLKVEILG 238
RESULT 29
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; FILE REFERENCE: Macrophage Inflammatory Protein-1 alpha (MIP-1)
; TITLE OF INVENTION: alpha/BANTES Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,988A
; FILING DATE: 19930128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-012-988A-2
Query Match 41.7%; Score 40; DB 1; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 6 WKNFQTLKIVILG 18
Db 195 WKLFCALKLNLF 207
RESULT 30
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
```

APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cseerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-450-393A-5

Query Match 41.7%; Score 40; DB 1; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18
||| ||| : :
Db 195 WKLFQALKNLFG 207

RESULT 31
US-08-446-669-5
Sequence 5, Application US/08446669
Patent No. 6132987
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-446-669-5

Query Match 41.7%; Score 40; DB 3; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18
||| ||| : :
Db 195 WKLFQALKNLFG 207

RESULT 32
US-09-239-938-1
Sequence 1, Application US/09239938
Patent No. 6329510
GENERAL INFORMATION:
APPLICANT: Qin, Shixin
APPLICANT: Newman, Walter
APPLICANT: Kassam, Nasim
APPLICANT: LeukoSite, Inc.
TITLE OF INVENTION: ANTI-CCR1 ANTIBODIES AND METHODS OF USE
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: LKS97-13
CURRENT APPLICATION NUMBER: US/09/239,938
CURRENT FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 355
TYPE: PRP
ORGANISM: Homo sapien
US-09-239-938-1

Query Match 41.7%; Score 40; DB 4; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18
||| ||| : :
Db 195 WKLFQALKNLFG 207

RESULT 33
US-08-833-752-9
Sequence 9, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kocbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6448375e
US-08-833-752-9

Query Match 41.7%; Score 40; DB 4; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVLG 18
||| ||| : :
Db 195 WKLFQALKNLFG 207

RESULT 34
US-09-886-319A-14
Sequence 14, Application US/09886319A
Patent No. 6586185
GENERAL INFORMATION:
APPLICANT: Wolf, Eckard
APPLICANT: Werner, Sabine
APPLICANT: Halle, Jorn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
the Diagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 355
TYPE: PRT
ORGANISM: Homo sapiens
US-09-886-319A-14

Query Match 41.7%; Score 40; DB 4; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVLG 18
||| ||| : :
Db 195 WKLFQALKNLFG 207

RESULT 35
PCT-US95-00476-5
Sequence 5, Application PC/TUS9500476
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-00476-5

Query Match 41.7%; Score 40; DB 5; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVLG 18
||| ||| : :
Db 195 WKLFQALKNLFG 207

RESULT 36
US/08/622
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: <unknown>
DESCRIPTION: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US/08/622,679D-10

Query Match 41.7%; Score 40; DB 3; Length 371;
Best Local Similarity 40.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIV 15
||| ||| : :
Db 319 NQYFWDDFHPSEV 333

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2004, 08:51:21 ; Search time 52.525 seconds
(without alignments)
118.345 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFGNTMCQLLTGLYFIGFPPS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq 29Jan04: *
1: geneseqp1980a: *
2: geneseqp1990a: *
3: geneseqp2000a: *
4: geneseqp2001a: *
5: geneseqp2002a: *
6: geneseqp2003a: *
7: geneseqp2003bs: *
8: geneseqp2004a: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126	100.0	22	AAB88994	AAB88994 HIV gp120
2	126	100.0	184	AAW27406	AAW27406 Inactive
3	126	100.0	215	AAW27408	AAW27408 Inactive
4	126	100.0	215	AAW88238	AAW88238 HIV-1 co-
5	126	100.0	268	ADC10142	ADC10142 Human NOV
6	126	100.0	268	ADC10144	ADC10144 Human NOV
7	126	100.0	332	AAW26766	AAW26766 Human che
8	126	100.0	352	AAW27407	AAW27407 Human CCR
9	126	100.0	352	AAW27123	AAW27123 Human che
10	126	100.0	352	AAW27125	AAW27125 Macaque c
11	126	100.0	352	AAW07602	AAW07602 Human G-P
12	126	100.0	352	AAW23835	AAW23835 Human CC
13	126	100.0	352	AAW88232	AAW88232 HIV-1 co-
14	126	100.0	352	AAW880128	AAW880128 Human G-P
15	126	100.0	352	AAW79089	AAW79089 Amino aci
16	126	100.0	352	AAW07046	AAW07046 Human G-P
17	126	100.0	352	AAW07048	AAW07048 Human G-P
18	126	100.0	352	AAW80111	AAW80111 Human CCR
19	126	100.0	352	AAW04321	AAW04321 Human che
20	126	100.0	352	AAW07037	AAW07037 Human G-P
21	126	100.0	352	AAW07039	AAW07039 Human G-P
22	126	100.0	352	AAW46858	AAW46858 Human HDG
23	126	100.0	352	AAW56342	AAW56342 Non-endog
24	126	100.0	352	AAW83354	AAW83354 Human CCR
25	126	100.0	352	AAW82948	AAW82948 Human HIV

ALIGNMENTS

RESULT 1

AAB88994

ID AAB88994 standard; peptide; 22 AA.

XX AAB88994;

XX 23-MAY-2001 (first entry)

DE HIV gp120 protein binding peptide #87.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;

KW replication; CCR5; CXCR4; CD4; STRL33.

XX Homo sapiens.

XX WC200116182-R2.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-US023505.

XX 27-AUG-1999; 99US-0151270P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions.

XX Claim 21; Page 38; 114pp; English.

XX The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4, and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention

XX Sequence 22 AA;

Query Match 100.0%; Score 126; DB 4; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.2e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFPPS 22

26 126 100.0 352 5 AAU97150 Aau97150 Human G-P
27 126 100.0 352 5 AAU97152 Aau97152 Human G-P
28 126 100.0 352 5 AAM52829 Aam52829 Human CCR
29 126 100.0 352 5 AAM52828 Aam52828 Human CC
30 126 100.0 352 5 ABG70597 Abg70597 Human G-P
31 126 100.0 352 5 ABG92883 Abg92883 Human imm
32 126 100.0 352 5 ABG92880 Abg92880 Human G-P
33 126 100.0 352 5 AAE35808 Aae35808 Human G-P
34 126 100.0 352 5 AAE35811 Aae35811 Human G-P
35 126 100.0 352 5 ABB81054 Aab81054 G-protein
36 126 100.0 352 5 ABB08343 Abb08343 Human che
37 126 100.0 352 6 ABG75540 Abg75540 Human G-P
38 126 100.0 352 6 ABR58602 Abr58602 Human can
39 126 100.0 352 6 AAO39514 Aao39514 Human C-C
40 126 100.0 352 6 ABU61654 Abu61654 Human G-P
41 126 100.0 352 6 ABP97728 Abp97728 Amino aci
42 126 100.0 352 6 ABP81933 Abp81933 Human C-C
43 126 100.0 352 7 ADC03341 Adc03341 Human che
44 126 100.0 352 7 ADC03359 Adc03359 Macaque c
45 126 100.0 371 2 AAW23834 Aaw23834 Human CC

Db 1 QWDFGNTMCLLTGLYFIGFPS 22

RESULT 2

AAW27406

ID AAW27406 standard; protein; 184 AA.

XX AC AAW27406;

XX DT 14-APR-1998 (first entry)

XX DE Inactive human CCR5.

XX KW Inactive; human Cys-Cys chemokine receptor-5; CCR5;

XX KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;

XX KW predisposition; resistance; diagnosis; treatment; prevention;

XX KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;

XX KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;

XX KW atherosclerosis; autoimmune disorder.

XX OS Homo sapiens.

XX FN WO9732019-A2.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-BE000023.

XX PR 01-MAR-1996; 96EP-00870021.

XX PR 06-AUG-1996; 96EP-00870102.

XX FA (EURO-) EUROSREEN SA.

XX PI Samson M, Parmentier M, Vassart G, Libert F;

XX DR WPI; 1997-479829/44.

XX DR N-PSDB; AAT90116.

XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful

XX PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune

XX PT disease and viral infection.

XX PS Claim 1; Fig 1a; 94pp; English.

XX CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor

XX CC 5 (CCRS), which is not a receptor of human immunodeficiency virus type 1

XX CC or type 2 (Hiv-1 or Hiv-2). CCR5 or its cDNA can be used to diagnose, treat

XX CC and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,

XX CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,

XX CC viral infections, especially HIV-1 or HIV-2 infection, cancer,

XX CC atherosclerosis and autoimmune disorders. Subjects that express the

XX CC inactive receptor have a predisposition, or resistance to HIV-1 and/or

XX CC HIV-2

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 126; DB 2; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.2e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCLLTGLYFIGFPS 22

Db 93 QWDFGNTMCLLTGLYFIGFPS 114

RESULT 3

AAW27408

ID AAW27408 standard; protein; 215 AA.

XX AC AAW27408;

XX DT 14-APR-1998 (first entry)

XX DE Inactive human CCR5.

XX KW Inactive; human Cys-Cys chemokine receptor 5; CCR5;

XX KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;

XX KW predisposition; resistance; diagnosis; treatment; prevention;

XX KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;

XX KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;

XX KW atherosclerosis; autoimmune disorder.

XX OS Homo sapiens.

XX FN WO9732019-A2.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-BE000023.

XX PR 01-MAR-1996; 96EP-00870021.

XX PR 06-AUG-1996; 96EP-00870102.

XX FA (EURO-) EUROSREEN SA.

XX PI Samson M, Parmentier M, Vassart G, Libert F;

XX DR WPI; 1997-479829/44.

XX DR N-PSDB; AAT90116.

XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful

XX PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune

XX PT disease and viral infection.

XX PS Claim 1; Fig 1a; 94pp; English.

XX CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor

XX CC 5 (CCRS), which is not a receptor of human immunodeficiency virus type 1

XX CC or type 2 (Hiv-1 or Hiv-2). CCR5 or its cDNA can be used to diagnose, treat

XX CC and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,

XX CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,

XX CC viral infections, especially HIV-1 or HIV-2 infection, cancer,

XX CC atherosclerosis and autoimmune disorders. Subjects that express the

XX CC inactive receptor have a predisposition, or resistance to HIV-1 and/or

XX CC HIV-2

XX SQ Sequence 215 AA;

Query Match 100.0%; Score 126; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.5e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCLLTGLYFIGFPS 22

Db 93 QWDFGNTMCLLTGLYFIGFPS 114

XX DE

XX KW

XX KW

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FT Domain 67..87
 FT /note= "transmembrane domain 2"
 FT Domain 103..124
 FT /note= "transmembrane domain 3"
 FT Domain 142..167
 FT /note= "transmembrane domain 4"

FN WO9854317-A1.

XX 03-DEC-1998.

PD 29-MAY-1998; 98WO-EP003437.

XX 30-MAY-1997; 97US-0048057P.

XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.

XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;

PI WPI; 1999-059835/05.

XX N-PSDB; AAV84159.

DR New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 resistance of CCR5-expressing cells to HIV-1 infection.

XX Disclosure; Page 38-39; 55pp; English.

XX This is the amino acid sequence of a CCR5 variant protein, designated
 CC CCR5-delta32, that includes the first 4 transmembrane domains of wild-
 CC type CCR5 (see AAW88232), but lacks transmembrane domains 5-7. CCR5
 CC serves as a co-receptor for infection by macrophage-tropic (M-tropic)
 CC strains of HIV-1. Individuals homozygous for the CCR5-delta32 mutation
 CC are resistant to HIV-1 infection, but heterozygous individuals are
 CC susceptible. The invention additionally relates to the identification of
 CC variant CCR5s (see AAW88231), which lacks transmembrane domains 3-7 of
 CC CCR5. The detection of CCR5 variants may be used to identify individuals
 CC at lower risk of infection relative to the general population who, if
 CC infected, may exhibit slower progression to AIDS. Probes and primers (see
 CC AAW84127-36) are provided for use in diagnostic methods for detecting the
 CC presence of such variants. A method is provided for inhibiting HIV-1
 CC infection of a cell expressing the CCR5 receptor. This involves
 CC introducing a nucleic acid encoding a CCR5 variant into the cell, thereby
 CC reducing the number of functional CCR5 molecules present on the cell
 CC surface

XX Sequence 215 AA;

Query Match 100.0%; Score 126; DB 2; Length 215;

Best Local Similarity 100.0%; Pred.No.1.5e-11; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy

1 QWDFGNTMCQLLGLYFIIGFFS 22

Db 93 QWDFGNTMCQLLGLYFIIGFFS 114

RESULT 5

ADCL0142

ID ADCL0142 standard; protein; 268 AA.

XX AC ADCL0142;

XX 18-DEC-2003 (first entry)

XX Human NOVX polypeptide SEQ ID NO: 162.

XX cytostatic; anidiabetic; anorectic; cerebroprotective; neuroprotective;
 KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
 KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
 KW inflammatory disorder; chromosome mapping; tissue typing;
 KW predictive medicine.

XX Homo sapiens.

OS

XX WO2003000842-A2.
 FN 03-JAN-2003.
 XX 04-JUN-2002; 2002WO-US017443.
 XX 04-JUN-2001; 2001US-0295607P.
 PR 04-JUN-2001; 2001US-0295661P.
 PR 06-JUN-2001; 2001US-0296404P.
 PR 06-JUN-2001; 2001US-0296418P.
 PR 07-JUN-2001; 2001US-0296575P.
 PR 11-JUN-2001; 2001US-0297414P.
 PR 12-JUN-2001; 2001US-0295573P.
 PR 12-JUN-2001; 2001US-0297567P.
 PR 14-JUN-2001; 2001US-0298285P.
 PR 15-JUN-2001; 2001US-0298528P.
 PR 18-JUN-2001; 2001US-0299133P.
 PR 19-JUN-2001; 2001US-0299230P.
 PR 21-JUN-2001; 2001US-0299949P.
 PR 22-JUN-2001; 2001US-0300177P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 28-JUN-2001; 2001US-0301530P.
 PR 28-JUN-2001; 2001US-0301550P.
 PR 03-JUL-2001; 2001US-0302951P.
 PR 31-JUL-2001; 2001US-0308890P.
 PR 14-SEP-2001; 2001US-0322297P.
 PR 25-SEP-2001; 2001US-0324659P.
 PR 03-DEC-2001; 2001US-0337477P.
 PR 14-DEC-2001; 2001US-0341562P.
 PR 21-FEB-2002; 2002US-0358656P.
 PR 21-FEB-2002; 2002US-0359123P.
 PR 22-FEB-2002; 2002US-0358978P.
 PR 22-FEB-2002; 2002US-0359034P.
 PR 22-FEB-2002; 2002US-0359035P.
 PR 27-FEB-2002; 2002US-0359121P.
 PR 27-FEB-2002; 2002US-0359964P.
 PR 01-MAR-2002; 2002US-0360858P.
 PR 12-MAR-2002; 2002US-0363430P.
 PR 12-MAR-2002; 2002US-0363676P.
 PR 10-APR-2002; 2002US-0371346P.
 PR 10-MAY-2002; 2002US-0379444P.
 PR 04-JUN-2002; 2002US-00379444.

(CURA-) CURAGEN CORP.

Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
 Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
 Gerlach VL, Gorman L, Guo X, Herrmann JM, Hjalte T, Ji W, Kekuda R;
 Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
 Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
 Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
 Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
 Burgess CE, Lepley DM;

WPI: 2003-210149/20.

N-PSDB; ADCL0141.

New isolated NOVX polypeptides and nucleic acid molecules useful for
 treating, preventing and diagnosing pathological conditions with NOVX-
 associated disorders, such as cancer, obesity, diabetes and inflammatory
 or CNS diseases.

Claim 1; SEQ ID NO 162; 772pp; English.

The invention relates to novel isolated polypeptides, mature form of the
 polypeptide, a sequence that is 95% identical to the polypeptide or the
 polypeptide comprising one or more conservative substitutions. The NOVX
 polypeptide is useful for treating or preventing a pathology associated
 with the polypeptide e.g. disorders associated with aberrant expression
 or activity of the polypeptide, such as cancer, diabetes, obesity, and
 endocrine, CNS and inflammatory disorders. They can also be used in
 various detection and screening assays, chromosome mapping, tissue typing

CC and predictive medicine. This sequence corresponds to one of the
 CC polypeptides of the invention.

SQ Sequence 268 AA;

Query Match 100.0%; Score 126; DB 7; Length 268;

Best Local Similarity 100.0%; Pred. No. 1.9e-11; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22

Db 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 6

ADCI0144

ID ADCI0144 standard; protein; 268 AA.

AC ADCI0144;

DT 18-DEC-2003 (first entry)

DE Human NOVX polypeptide SEQ ID NO: 164.

XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
 KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
 KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
 KW inflammatory disorder; chromosome mapping; tissue typing;
 KW predictive medicine.

XX Homo sapiens.

XX WO2003000842-A2.

XX 03-JAN-2003.

XX 04-JUN-2002; 2002WO-US017443.

XX 04-JUN-2001; 2001US-0295607P.

XX 04-JUN-2001; 2001US-0295661P.

XX 06-JUN-2001; 2001US-0286404P.

XX 06-JUN-2001; 2001US-0286418P.

XX 07-JUN-2001; 2001US-0296575P.

XX 11-JUN-2001; 2001US-0297414P.

XX 12-JUN-2001; 2001US-0295573P.

XX 12-JUN-2001; 2001US-0297567P.

XX 14-JUN-2001; 2001US-0298285P.

XX 15-JUN-2001; 2001US-0298528P.

XX 18-JUN-2001; 2001US-0299133P.

XX 19-JUN-2001; 2001US-0299230P.

XX 21-JUN-2001; 2001US-0299949P.

XX 22-JUN-2001; 2001US-0300177P.

XX 26-JUN-2001; 2001US-0300883P.

XX 28-JUN-2001; 2001US-0301530P.

XX 28-JUN-2001; 2001US-0301550P.

XX 03-JUL-2001; 2001US-0302951P.

XX 31-JUL-2001; 2001US-0308890P.

XX 14-SEP-2001; 2001US-0322297P.

XX 25-SEP-2001; 2001US-0324669P.

XX 03-DEC-2001; 2001US-0337477P.

XX 14-DEC-2001; 2001US-0341562P.

XX 21-FEB-2002; 2002US-0358656P.

XX 21-FEB-2002; 2002US-0359122P.

XX 22-FEB-2002; 2002US-0358978P.

XX 22-FEB-2002; 2002US-0359034P.

XX 22-FEB-2002; 2002US-0359035P.

XX 22-FEB-2002; 2002US-0359121P.

XX 27-FEB-2002; 2002US-0359949P.

XX 01-MAR-2002; 2002US-0360858P.

XX 12-MAR-2002; 2002US-0363430P.

XX 12-MAR-2002; 2002US-0363676P.

XX 10-APR-2002; 2002US-0371346P.

XX 10-MAY-2002; 2002US-0379444P.

PR 04-JUN-2002; 2002US-00379444.

XX (CURA-) CURAGEN CORP.

XX Aggee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;

PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;

PI Gerlach VL, German L, Guo X, Herrmann JM, Hjalte T, Ji W, Kekuda R;

PI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;

PI Ort T, Padigaru M, Patturajan M, Pena CA, Rastelli L, Rieger DK;

PI Rotherberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;

PI Sytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;

PI Burgess CE, Lepley DM;

XX WPI; 2003-210149/20.

DR N-PSDB; ADCI0143.

XX New isolated NOVX polypeptides and nucleic acid molecules useful for

PT treating, preventing and diagnosing pathological conditions with NOVX-

PT associated disorders, such as cancer, obesity, diabetes and inflammatory

PT or CNS diseases.

XX Claim 1; SEQ ID NO 164; 772pp; English.

XX The invention relates to novel isolated polypeptides, mature form of the

CC polypeptide, a sequence that is 95% identical to the polypeptide or the

CC polypeptide comprising one or more conservative substitutions. The NOVX

CC polypeptide is useful for treating or preventing a pathology associated

CC with the polypeptide e.g. disorders associated with aberrant expression

CC or activity of the polypeptide, such as cancer, diabetes, obesity, and

CC endocrine, CNS and inflammatory disorders. They can also be used in

CC various detection and screening assays, chromosome mapping, tissue typing

CC and predictive medicine. This sequence corresponds to one of the

CC polypeptides of the invention.

XX SQ Sequence 268 AA;

Query Match 100.0%; Score 126; DB 7; Length 268;

Best Local Similarity 100.0%; Pred. No. 1.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22

Db 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 7

AAW26766

ID AAW26766 standard; protein; 332 AA.

XX AAW26766;

XX 21-MAY-1998 (first entry)

XX Human chemokine receptor MMLR-CCR.

XX Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human;

XX monocyte; macrophage; chemotaxis; haematopoiesis; infection;

XX inflammation; proliferative disease; cardiovascular disease; tumour;

XX rheumatoid arthritis; alveolitis; atherosclerosis; diabetes;

XX chronic granulomatous disease; asthma; myasthenia gravis; shock;

XX inflammatory bowel disease; toxic shock syndrome; septic shock;

XX Chediak-Higashi syndrome; therapy; diagnosis.

XX Homo sapiens.

XX Key

XX Peptide

XX Location/Qualifiers

XX 107..128

XX /note="conserved peptide"

XX Misc-difference 121

XX /note="a claimed polypeptide has isoleucine at residue

XX 121"

XX WO9741225-A2.

```

XX PD 06-NOV-1997.
XX PF 25-APR-1997; 97WO-US006993.
XX PR 26-APR-1996; 96US-00639081.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Au-Young J, Bandman O, Coleman R, Wilde CG;
XX WPI; 1997-549729/50.
XX DR N-PSDB; AAT99542.
XX PT Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful
XX to study, diagnose and treat, e.g. infection, inflammation, solid tumour
XX and proliferative and cardiovascular disease.
XX PS Claim 8; Page 37-38; 59pp; English.
XX CC This protein comprises human MMLR-CCR, a novel C-C chemokine receptor
XX associated with monocyte/macrophage infiltration and chemotaxis and
XX haematopoiesis. The amino acid sequence was deduced from a cDNA clone
XX (see AAT99542) obtained from a cDNA library made from mononuclear cells
XX collected on day 2 of a mixed lymphocyte culture, i.e. cells associated
XX with inflammation and immunomodulation. Another novel chemokine receptor,
XX MPHG-CCR (see AAT936767), is also claimed. MMLR-CCR contains 7
XX transmembrane spanning segments connected by a series of intracellular
XX and extracellular loops. MMLR-CCR and MPHG-CCR can be used to study,
XX diagnose and treat disease states in which normal leukocyte function is
XX perturbed by normal leukopoiesis or inappropriate activation via
XX chemokine agonists or antagonists, such as infection, inflammation,
XX proliferative disease, tumorigenesis, autoimmune disease, abnormal cell
XX proliferation, solid tumours, cardiovascular disease, rheumatoid
XX arthritis, alveolitis, atherosclerosis, chronic granulomatous disease,
XX asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic
XX shock syndrome, septic shock and Chediak-Higashi syndrome
XX SQ Sequence 332 AA;

Query Match 100.0%; Score 126; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 84 QWDFGNTMCQLLTGLYFIFGFFS 105

RESULT 8
AAW27407
ID AAW27407 standard; protein; 352 AA.
XX AC AAW27407;
XX DT 14-APR-1998 (first entry)
XX DE Human CCR5.
XX KW Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
XX type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
XX inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
XX idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
XX atherosclerosis; autoimmune disorder.
XX OS Homo sapiens.
XX PN WO9732019-A2.
XX PR 04-SEP-1997.
XX PF 28-FEB-1997; 97WO-BE000023.
XX XX

PR 01-MAR-1996; 96EP-00870021.
PR 06-AUG-1996; 96EP-00870102.
XX XX
XX PA (EURO-) EUROSREEN SA.
XX PI Samson M, Parmentier M, Vassart G, Libert F;
XX WPI; 1997-479829/44.
XX DR N-PSDB; AAT90117.
XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune
XX disease and viral infection.
XX PS Claim 4; Fig 1b-c; 94pp; English.
XX CC The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
XX which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but
XX not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,
XX interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
XX chemokines. Active CCR-5 is also a receptor of human immunodeficiency
XX virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to
XX diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
XX arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
XX psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
XX atherosclerosis and autoimmune disorders
XX SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 9
AAW27123
ID AAW27123 standard; protein; 352 AA.
XX AC AAW27123;
XX DT 14-DEC-1997 (first entry)
XX DE Human chemokine receptor 89C.
XX KW Chemokine receptor 89C; atherosclerosis; rheumatoid arthritis; tumour;
XX asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
XX diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX modulator; antibody; human.
XX OS Homo sapiens.
XX FH Key
XX FT Domain Location/Qualifiers
XX FT Domain 1..32 /label= Extracellular_domain
XX FT Domain 56..67 /label= Intracellular_domain
XX FT Domain 89..112 /label= Extracellular_domain
XX FT Domain 125..145 /label= Extracellular_domain
XX FT Domain 166..191 /label= Intracellular_domain
XX FT Domain 213..235 /label= Extracellular_domain
XX FT Domain 259..280 /label= Intracellular_domain
XX FT Domain 301..352 /label= Extracellular_domain
XX FT Domain /label= Intracellular_domain
XX XX

```

PN WO9722698-A2.
 PD 26-JUN-1997.
 XX
 PF 20-DEC-1996; 96WO-US020759.
 XX
 PR 20-DEC-1995; 95US-00575967.
 PR 07-JUN-1996; 96US-00661393.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 XX Gray PW, Schweickart VL, Raport CU;
 PI WPI; 1997-341689/31.
 XX N-PSDB; AAT85161.
 DR
 XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
 PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
 PT tumours, viral infections, auto-immune diseases, etc.
 XX
 PS Claim 16; Page 47-48; 65pp; English.
 XX
 CC This polypeptide sequence comprises novel human chemokine receptor 88C, a
 CC G protein coupled receptor that is involved in leukocyte trafficking. Its
 CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
 CC macrophage library. It shows 62% identity to CCR1. Chemokine receptor
 CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
 CC and their polypeptide fragments can be produced in transformed host
 CC cells. The receptors, peptides comprising one or more of the
 CC extracellular or intracellular domains, and anti-receptor antibodies can
 CC be used to modulate receptor activities, particularly ligand and G
 CC protein binding, and are potentially useful in the treatment
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune response,
 CC abnormal haematopoietic processes etc
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLTGLYFIGFSS 22
 DB 93 QWDFGNTWCQLLTGLYFIGFSS 114
 RESULT 10
 ID AAW27125 standard; protein; 352 AA.
 XX
 AC AAW27125;
 XX
 DT 14-DEC-1997 (first entry)
 XX
 DE Macaque chemokine receptor 88C.
 KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
 KW asthma; viral infection; AIDS; inflammation; auto-immune disease; therapy;
 KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
 KW modulator; antibody.
 XX
 OS Macaca sp.
 XX
 PN WO9722698-A2.
 XX
 PD 26-JUN-1997.
 XX
 PF 20-DEC-1996; 96WO-US020759.
 XX
 PR 20-DEC-1995; 95US-00575967.
 PR 07-JUN-1996; 96US-00661393.
 XX

PA (ICOS-) ICOS CORP.
 XX
 PI Gray PW, Schweickart VL, Raport CU;
 XX
 DR WPI; 1997-341689/31.
 DR N-PSDB; AAT85161.
 XX
 PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
 PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
 PT tumours, viral infections, auto-immune diseases, etc.
 XX
 PS Claim 36; Page 57-58; 65pp; English.
 XX
 CC This polypeptide sequence comprises macaque chemokine receptor 88C, a G
 CC protein coupled receptor that is involved in leukocyte trafficking. Its
 CC amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
 CC amplification. It shows 97% identity to human 88C (AAW27123). 88C
 CC receptors and their polypeptide fragments can be produced in transformed
 CC host cells. The receptors, peptides comprising one or more of the
 CC extracellular or intracellular domains, and anti-receptor antibodies can
 CC be used to modulate receptor activities, particularly ligand and G
 CC protein binding, and are potentially useful in the treatment
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune response,
 CC abnormal haematopoietic processes etc. A hybridoma that produces an
 CC antibody that specifically binds to macaque 88C is claimed
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLTGLYFIGFSS 22
 DB 93 QWDFGNTWCQLLTGLYFIGFSS 114
 RESULT 11
 ID AAW07602 standard; protein; 352 AA.
 XX
 AC AAW07602;
 XX
 DT 26-FEB-1997 (first entry)
 XX
 DE Human G-protein chemokine receptor HDGMR10.
 KW G-protein chemokine receptor; HDGMR10; signal transduction;
 KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9639437-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 06-JUN-1995; 95WO-US007173.
 PR 06-JUN-1995; 95WO-US007173.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Li Y, Ruben SM;
 XX
 DR WPI; 1997-043072/04.
 DR N-PSDB; AAT44042.
 XX
 PT Human G-protein chemokine receptor, HDGMR10 - useful to identify
 PT (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and
 PT acute inflammation, rheumatoid arthritis, etc.
 XX

PS Claim 1; Page 44-46; 61pp; English.

XX Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7

CC -transmembrane protein involved in signal transduction. Its amino acid

CC sequence was deduced from a cDNA clone (AA744042) isolated from a human

CC monocyte library. Isolation of the cDNA allows prodn. of recombinant

CC HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant

CC receptor can be used to identify agonists or antagonists of the receptor;

CC such cpds. can be used to treat conditions related to the under- and over

XX -expression of G-protein chemokine receptors

XX

SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTWCQLLTGLYFIQGFPS 22

Db 93 QWDFGNTWCQLLTGLYFIQGFPS 114

RESULT 12

AAW23835

ID AAW23835 standard; protein; 352 AA.

AC AAW23835;

XX

DT 08-JUN-1998 (first entry)

XX

XX Human CC chemokine receptor 5 (CCR5).

XX

CC chemokine receptor 5; CCR5; G-protein coupled receptor;

KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 29..55

FT /label= I

FT /note= "transmembrane domain"

FT 104..126

FT /label= III

FT /note= "transmembrane domain"

FT 109..120

FT /note= "extracellular loop-1 (Claim 19)"

FT 143..171

FT /label= IV

FT /note= "transmembrane domain"

FT 187..210

FT /note= "extracellular loop-2 (Claim 19)"

FT 194..219

FT /label= V

FT /note= "transmembrane domain"

FT 238..258

FT /label= VI

FT /note= "transmembrane domain"

FT 261..276

FT /note= "extracellular loop-3 (Claim 19)"

FT 277..300

FT /label= VII

FT /note= "transmembrane domain"

XX

PN WO9745543-A2.

XX

PD 04-DEC-1997.

XX

XX 28-MAY-1997; 97WO-US009586.

XX

XX 28-MAY-1996; 96US-0018508P.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;

PI Broder CC, Kennedy PE;

XX

DR WPI; 1998-032650/03.

DR N-PSDB; AAT76920.

XX

CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion

PT between HIV and a target cell.

XX

PS Claim 68; Fig 1C; 70pp; English.

XX

CC This protein sequence comprises of a novel human macrophage-selective CC

CC chemokine receptor that has been designated CCR5. The sequence was

CC deduced from an isolated cDNA clone (see AAT76920). An Alai27Leu variant

CC (see W238340 of CCR5 was also identified. The susceptibility of human

CC macrophages to HIV infection depends on cell surface expression of CD4

CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-

CC protein coupled cell surface molecules. It plays an essential role in the

CC membrane fusion step of infection by some HIV isolates. The establishment

CC of stable, non-human cell lines and transgenic mammals having cells that

CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV

CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding

CC agents capable of blocking membrane fusion between HIV and target cells

CC represent potential anti-HIV therapeutics for macrophage tropic strains

CC of HIV

XX

SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTWCQLLTGLYFIQGFPS 22

Db 93 QWDFGNTWCQLLTGLYFIQGFPS 114

RESULT 13

AAW88232

ID AAW88232 standard; protein; 352 AA.

XX

AC AAW88232;

XX

DT 15-MAR-1999 (first entry)

XX

DE HIV-1 co-receptor CCR5.

XX

KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;

KW Gene therapy; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 32..56

FT /note= "transmembrane domain 1"

FT 67..87

FT /note= "transmembrane domain 2"

FT Misc-difference 101

FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA

FT (Stop) in CCR5m303"

FT 103..124

FT /note= "transmembrane domain 3"

FT 142..167

FT /note= "transmembrane domain 4"

FT 200..223

FT /note= "transmembrane domain 5"

FT 236..260

FT /note= "transmembrane domain 6"

FT 275..301

FT /note= "transmembrane domain 7"

XX

PN WO9854317-A1.

XX

PD 03-DEC-1998.
 XX 29-MAY-1998; 98WO-EP003437.
 XX 30-MAY-1997; 97US-0048057P.
 XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;

XX WPI; 1999-059835/05.
 XX N-PSDB; AAV84126.

XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 PT resistance of CCR5-expressing cells to HIV-1 infection.
 PT Disclosure; Page 34-35; 55pp; English.

XX This is the amino acid sequence of wild-type human CCR5, which serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see
 CC AAV8231), designated CCR5m303, comprising the first two transmembrane
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
 CC presence of the CCR5m303 variant with the wild-type CCR5 allele shows a
 CC positive correlation with resistance to infection with M-tropic HIV-1
 CC strains, and may indicate slower progression of the disease. The
 CC detection of CCR5 variants may be used to identify individuals at lower
 CC risk of infection relative to the general population who, if infected,
 CC may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
 CC 36) are provided for use in diagnostic methods for detecting the presence
 CC of such variants. A method is provided for inhibiting HIV-1 infection of
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number
 CC of functional CCR5 molecules present on the cell surface

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFES 22
 DB 93 QWDFGNTWCQLLTGLYFIGFES 114

RESULT 14
 AAY80128
 ID AAY80128 standard; protein; 352 AA.
 XX AC AAY80128;

DT 19-MAY-2000 (first entry)

DE Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.

XX Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
 KW diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
 KW tumor; infection; leukaemia; psoriasis; allergy;
 KW T-cell mediated autoimmune disease; atherogenesis; anaphylaxis;
 KW inflammation; allergic reaction; silicosis; sarcoidosis;
 KW rheumatoid arthritis; hyper-eosinophilia syndrome.

OS Homo sapiens.

XX US6025154-A.

PN 15-FEB-2000.

PD 06-JUN-1995; 95US-00466343.

XX 06-JUN-1995; 95US-00466343.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX Li Y, Ruben SM;

XX WPI; 2000-181807/16.

DR N-PSDB; AAZ51481.

XX Isolated nucleic acid encoding human G-protein chemokine receptor useful
 PT for diagnostic assays, scientific research and screening for compounds
 PT which bind to and activate or inhibit activation of the receptor
 PT polypeptides.

PS Claim 1; Fig 1; 22pp; English.

XX The present sequence represents a human G-protein chemokine receptor
 CC designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
 CC screening for compounds which bind to and either: (1) activate the
 CC HDGNR10 polypeptides causing stimulation of haematopoiesis, wound
 CC healing, coagulation, and angiogenesis; treatment of solid tumours,
 CC chronic infections, leukaemia, T-cell mediated autoimmune diseases,
 CC parasitic infections, psoriasis, and to stimulate growth factor activity;
 CC or (2) inhibit activation of the HDGNR10 polypeptides which is useful for
 CC preventing and/or treating allergy, atherogenesis, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 CC E-mediated allergic reactions, prostaglandin-independent fever, bone
 CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
 CC hyper-eosinophilia syndrome. The polynucleotides are also useful for
 CC diagnostic assays for detecting diseases related to mutations in the
 CC nucleic acid sequences encoding the polypeptides and for detecting an
 CC altered level of the soluble form of the receptor polypeptides. The
 CC polynucleotides are also useful for in vitro purposes related to
 CC scientific research, synthesis of DNA and manufacture of DNA vectors

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFES 22
 DB 93 QWDFGNTWCQLLTGLYFIGFES 114

RESULT 15
 AAG79089
 ID AAG79089 standard; protein; 352 AA.
 XX AC AAG79089;

DT 10-DEC-2001 (first entry)

DE Amino acid sequence of human CCR5 protein.

XX Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
 KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
 KW Homo sapiens.

XX WO200164752-A2.

PN 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006322.

XX 02-MAR-2000; 2000US-00517605.

PA (UYNY) UNIV NEW YORK STATE.

XX (UYNI-) UNIV NIJMEGEN.

XX Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;

XX WPI; 2001-602565/68.

XX An antibody for the treatment or prevention of HIV-infection comprises a
 PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
 FT DC-SIGN due to concomitant conformational change.
 XX
 PS Disclosure; Page 118-119; 131pp; English.
 XX
 CC The specification describes an antibody which is specific for an
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
 CC is exposed upon gp120 binding of DC-SIGN due to concomitant
 CC conformational change. DC-SIGN is a receptor that is specifically
 CC expressed on dendritic cells and facilitates infection of T lymphocytes
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
 CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 CC with high affinity. The antibody of the invention inhibits the trans
 CC enhancement of HIV entry into a T cell or macrophage facilitated by
 CC dendritic cells. The antibody is useful to treat or prevent HIV
 CC infection. The present sequence represents a human CCR5 protein, which is
 CC a translocation promoting agent that interacts with CD4. This receptor
 CC functions in HIV-1 entry into cells
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFS 22
 Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 16

AAE07046
 ID AAE07046 standard; protein; 352 AA.

AC AAE07046;

XX 16-OCT-2001 (first entry)

DE Human G-protein chemokine receptor (CCRS) HDGNR10 protein #1.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

Key	Location/Qualifiers
Domain	1..36
FT	/label= Extracellular_domain
FT	37..305
FT	/label= Transmembrane_domain
FT	37..58
FT	/label= Transmembrane_domain
FT	/note= "Segment 1"
Domain	59..67
FT	/label= Intracellular_loop_1
FT	68..88
FT	/label= Transmembrane_domain
FT	/note= "Segment 2"
FT	89..102
FT	/label= Extracellular_loop_1
FT	103..124
FT	/label= Transmembrane_domain
FT	/note= "Segment 3"
Domain	125..141

Domain	Location/Qualifiers
FT	/label= Intracellular_loop_2
FT	142..166
FT	/label= Transmembrane_domain
FT	/note= "Segment 4"
Domain	167..195
FT	/label= Extracellular_loop_2
FT	196..223
FT	/label= Transmembrane_domain
FT	/note= "Segment 5"
Domain	224..235
FT	/label= Intracellular_loop_3
FT	236..260
FT	/label= Transmembrane_domain
FT	/note= "Segment 6"
Domain	261..274
FT	/label= Extracellular_loop_3
FT	287..305
FT	/label= Transmembrane_domain
FT	/note= "Segment 7"
Domain	306..352
FT	/label= Intracellular_domain

WO200158916-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US004153.

09-FEB-2000; 2000US-0181258P.

09-MAR-2000; 2000US-0187999P.

22-SEP-2000; 2000US-0234336P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Roschke V, Li Y, Ruben SM;

WPI; 2001-488966/53.

N-PSDB; AAD13282.

Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

Claim 102; Fig 1; 518pp; English.

The invention relates to human G-protein chemokine receptor (CCRS) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemia) and wound healing. The present sequence is human CCR5 HDGNR10 protein

Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
|||||
DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 17
AAE07048
ID AAE07048 standard; protein; 352 AA.

AC AAE07048;

DT 16-OCT-2001 (first entry)

DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
KW cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;
KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX WO200158916-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004153.

XX 09-FEB-2000; 2000US-0181258P.

PR 09-MAR-2000; 2000US-0187999P.

PR 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488966/53.

XX N-PSDB; AAD13299.

PT Isolated nucleic acid encoding a human G-protein chemokine receptor
(CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
PT neurodegenerative disorders.

XX Example 40; Page 504-505; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)
CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
CC useful for treating, preventing or ameliorating a disease or disorder
CC associated with inflammation, defective or aberrant chemotaxis of immune
CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
CC sarcoma) or defective or aberrant T-cell antigen presenting cell
CC interaction. The disease or disorder may also be an infectious disease
CC (e.g. a viral infection such as an early stage HIV infection, a
CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
CC disease or disorder may be associated with aberrant CCR5 expression, lack
CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
CC function. CCR5 HDGNR10 protein is used as a food additive or preservative
CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
CC protein, antibodies, agonists and antagonists are also useful in the
CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
CC urogenital); immune disorders (Addison's disease, allergies, autoimmune

CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The
CC present sequence is human CCR5 HDGNR10 protein

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
|||||

DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 18

AAAG80111

ID AAG80111 standard; protein; 352 AA.

XX AAG80111;

DT 17-JAN-2002 (first entry)

DE Human CCR5 protein.

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.

XX Homo sapiens.

XX WO200172830-A2.

XX 04-OCT-2001.

XX 02-APR-2001; 2001WO-EP003708.

XX 31-MAR-2000; 2000DE-01016013.

XX (IPPP-) IPF PHARM GMBH.

XX (FORS/) FORSMANN U.

XX Forssmann W, Adermann K, Heitland A, Spodberg N;

XX WPI; 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands, useful
PT for detecting tumors, inflammation etc., also therapeutic use of ligand
PT inhibitors.

XX Disclosure; Page 10; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiasthmatic,
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC proliferation of chemokine receptors (CR), which control migration and
CC consolidation of these cells. AAG8045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 19

AAE04321
 ID AAE04321 standard; protein; 352 AA.

XX AC AAE04321;
 XX DT 04-SEP-2001 (first entry)

XX DE Human chemokine receptor (CKR), CC-CKR-5 related protein #2.

XX KW Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CKR-5; envelope glycoprotein; anti-HIV.

XX OS Homo sapiens.

XX PN US6258527-B1.

XX PD 10-JUL-2001.

XX PF 21-MAY-1997; 97US-00861105.

XX PR 26-MAY-1996; 96US-0017157P.

XX PR 19-JUN-1996; 96US-0020043P.

XX PR 19-MAY-1997; 97US-00858660.

XX PA (AARO-) AARON DIAMOND AIDS RES CENT.

XX PA (UJNY) UNIV NEW YORK STATE.

XX PI Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;

XX DR WPI; 2001-417127/44.

XX DR N-PSDB; AAD08577.

XX PT Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
 and HIV LTR for identification of drugs and antibodies for treatment of
 HIV.

XX PS Disclosure; Col 47-50; 37pp; English.

XX CC The present invention relates to a transformed mammalian cell that
 contains a gene encoding CD4, a construct encoding a reporter gene under
 the regulation of an human immuno deficiency virus (HIV) long terminal
 repeat (LTR) and that has been transduced with a vector encoding a human
 chemokine receptor (CKR) where the CD4 and the CKR are present on the
 cell surface of transformed mammalian cell. The invention is useful for
 identifying drugs or antibodies that interfere with the translocation of
 HIV into transformed mammalian cell or for identifying a human chemokine
 receptor that facilitates the infection of a particular HIV strain into
 the transformed mammalian cell. Compounds identified can be used to treat
 cellular dysfunction and to prevent or combat HIV infection. The present
 sequence is a human chemokine receptor (CKR), CC-CKR-5 related protein.
 CC-CKR-5 is the principal cofactor for entry mediated by the envelope
 glycoproteins of primary macrophage-tropic strains of HIV-1

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22

DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 20

AAE07037

ID AAE07037 standard; protein; 352 AA.

XX AC AAE07037;

XX DT 16-OCT-2001 (first entry)

XX DE Human G-protein chemokine receptor (CKR5) HDGNR10 protein #1.

XX KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; neutrotic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 1..36
 /label= Extracellular_domain
 FT Domain 37..305
 /label= Transmembrane_domain
 FT Domain 37..58
 /label= Transmembrane_domain
 FT Domain /note= "Segment 1"
 FT Domain 59..67
 /label= Intracellular_loop_1
 FT Domain 68..88
 /label= Transmembrane_domain
 FT Domain /note= "Segment 2"
 FT Domain 89..102
 /label= Extracellular_loop_1
 FT Domain 103..124
 /label= Transmembrane_domain
 FT Domain /note= "Segment 3"
 FT Domain 125..141
 /label= Intracellular_loop_2
 FT Domain 142..166
 /label= Transmembrane_domain
 FT Domain /note= "Segment 4"
 FT Domain 167..195
 /label= Extracellular_loop_2
 FT Domain 196..223
 /label= Transmembrane_domain
 FT Domain /note= "Segment 5"
 FT Domain 224..235
 /label= Intracellular_loop_3
 FT Domain 236..260
 /label= Transmembrane_domain
 FT Domain /note= "Segment 6"
 FT Domain 261..274
 /label= Extracellular_loop_3
 FT Domain 287..305
 /label= Transmembrane_domain
 FT Domain /note= "Segment 7"
 FT Domain 306..352
 /label= Intracellular_domain

XX WO200158915-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US004152.

PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2001-488965/53.
 DR N-PSDB; AAD13181.
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX Claim 102; Fig 1; 495pp; English.
 CC The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No. 97183. CCR5
 CC HDGNR10 antibodies are useful for treating, preventing or ameliorating a
 CC disease or disorder associated with inflammation, defective or aberrant
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen
 CC presenting cell interaction. The disease or disorder may also be an
 CC infectious disease (e.g. a viral infection such as an early stage HIV
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative
 CC disorder. The disease or disorder may be associated with aberrant CCR5
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or
 CC lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene
 CC therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists
 CC are also useful in the diagnosis, treatment and prevention of cancer
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis); cardiovascular disorders (myocardial ischaemias) and wound
 CC healing
 XX Sequence 352 AA;
 SQ Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2,6e-11; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0;
 QY 1 QWDFGNTWCQLLTGLTYFGFSS 22
 DB 93 QWDFGNTWCQLLTGLTYFGFSS 114
 RESULT 21
 AAE07039
 ID AAE07039 standard; protein; 352 AA.
 XX AAE07039;
 AC AAE07039;
 XX 16-OCT-2001 (first entry)
 DT Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
 DE Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 XX human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; neotropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

OS Homo sapiens.
 XX WC2000158915-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004152.
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2001-488965/53.
 DR N-PSDB; AAD13198.
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX Example 40; Page 486-487; 495pp; English.
 CC The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
 CC ameliorating a disease or disorder associated with inflammation,
 CC defective or aberrant chemotaxis of immune cells, HIV infection (such as
 CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
 CC aberrant T-cell antigen presenting cell interaction. The disease or
 CC disorder may also be an infectious disease (e.g. a viral infection such
 CC as an early stage HIV infection, a cytomegalovirus infection, or a
 CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
 CC a neurodegenerative disorder. The disease or disorder may be associated
 CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
 CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
 CC is used as a food additive or preservative to increase or decrease
 CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
 CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
 CC antibodies, agonists and antagonists are also useful in the diagnosis,
 CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
 CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
 CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
 CC disorders (myocardial ischaemias) and wound healing
 XX Sequence 352 AA;
 SQ Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2,6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLTGLTYFGFSS 22
 DB 93 QWDFGNTWCQLLTGLTYFGFSS 114
 RESULT 22
 AAB46858
 ID AAB46858 standard; protein; 352 AA.
 XX AAB46858;
 AC AAB46858;
 XX 16-AUG-2001 (revised)
 DT 02-AUG-2001 (revised)
 DT 04-MAY-2001 (first entry)
 XX Human HDGNR10 protein.
 DE Human HDGNR10 protein.
 XX HDGNR10; human; G-protein chemokine receptor; antiinflammatory;

immunomodulatory; anticoagulant; anti-allergic; immunosuppressive; cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic; vasopressor; gene therapy; haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour; infection; leukemia; growth factor activity; T-cell mediated autoimmune disease; psoriasis; allergy; atherosclerosis; anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock; immunoglobulin E-mediated allergic reaction; rheumatoid arthritis; prostaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnery.

OS Homo sapiens.
XX WO200177172-A2.
XX XX
XX 18-OCT-2001.
XX XX
XX 05-APR-2001; 2001WO-US011098.
XX PF
XX 07-APR-2000; 2000US-0195747P.
XX PR
XX (AREN-) ARENA PHARM INC.
XX PA
XX Lehmann-Bruinsma K, Liaw CW, Lin I;
XX PI
XX WPI; 2001-648759/74.
XX DR N-PSDB; ABI97978.
XX DR
XX PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
XX PT disease treatment, comprises contacting candidate compounds with versions
XX PT of GPCRs.
XX PS
XX Claim 1; Page 277-278; 394pp; English.
XX CC The invention relates to G protein-coupled receptors (GPCRs) for which
XX CC the endogenous ligand has been identified. Non-endogenous constitutively
XX CC activated versions of known GPCRs are used in the invention for the
XX CC direct identification of candidate compounds as receptor agonists,
XX CC inverse agonists or partial agonists. Such agonists are useful as
XX CC therapeutic agents for diseases or disorders associated with GPCRs. The
XX CC present sequence is a non-endogenous version of a known human GPCR
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;
QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114
RESULT 24
AAB83354
ID AAB83354 standard; protein; 352 AA.
XX AC AAB83354;
XX DT 09-OCT-2001 (first entry)
XX DE Human CCR5 protein sequence.
XX KW Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
XX KW human immunodeficiency virus; anti-inflammatory disease; human.
XX OS Homo sapiens.
XX PN EP1118858-A2.
XX PD 25-JUL-2001.
XX PF 03-JAN-2001; 2001EP-00300020.
XX PR 12-JAN-2000; 2000GB-00000659.
XX PR 12-JAN-2000; 2000GB-00000661.

immunomodulatory; anticoagulant; anti-allergic; immunosuppressive; cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic; vasopressor; gene therapy; haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour; infection; leukemia; growth factor activity; T-cell mediated autoimmune disease; psoriasis; allergy; atherosclerosis; anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock; immunoglobulin E-mediated allergic reaction; rheumatoid arthritis; prostaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnery.

OS Homo sapiens.
XX US2001000241-A1.
XX PD
XX 12-APR-2001.
XX PF
XX 29-NOV-2000; 2000US-00725285.
XX PR
XX 06-JUN-1995; 95US-00466343.
XX PR 18-NOV-1998; 98US-00195662.
XX PR 25-JUN-1999; 99US-00339912.
XX XX
XX (LIYY/) LI Y.
XX PA (RUBE/) RUBEN S M.
XX PI
XX Li Y, Ruben SM;
XX XX
XX WPI; 2001-226317/23.
XX DR N-PSDB; AAF26390.
XX XX
XX New human G-protein chemokine receptor polypeptides and polynucleotides,
XX PT useful for identifying (ant)agonists to the G-protein chemokine receptor.
XX PS
XX Claim 1a; Page 15; 22pp; English.
XX CC This invention describes a novel receptor polypeptide (I) selected from
XX CC (i) a fully defined 329 amino acid sequence (ii) fully disclosed in the
XX CC specification; and (iii) a polypeptide encoded by the cDNA contained in a
XX CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
XX CC products of the invention have anti-inflammatory, immunomodulatory,
XX CC anticoagulant, anti-allergic, immunosuppressive, vulnery, cytostatic,
XX CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic
XX CC activity and can be used for gene therapy. The G-protein chemokine
XX CC receptors, HDGMR10, (I) are useful for screening for compounds which
XX CC activate or inhibit activation of (I). The products of the invention can
XX CC also be used for stimulating haematopoiesis, wound healing, coagulation,
XX CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-
XX CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and
XX CC stimulating growth factor activity. HDGMR10 is useful for treating
XX CC allergy, atherosclerosis, anaphylaxis, malignancy, chronic and acute
XX CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
XX CC reactions, prostaglandin-independent fever, bone marrow failure,
XX CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
XX CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
XX CC errors in the keyword formatting)
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114
RESULT 23
ABB56342
ID ABB56342 standard; protein; 352 AA.
XX AC ABB56342;
XX XX

18-FEB-2002 (first entry)
XX Non-endogenous human GPCR protein, SEQ ID NO: 477.
XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
XX constitutively activated GPCR; agonist; disease.
XX OS Homo sapiens.
XX Synthetic.
XX WO200177172-A2.
XX XX
XX 18-OCT-2001.
XX XX
XX 05-APR-2001; 2001WO-US011098.
XX PF
XX 07-APR-2000; 2000US-0195747P.
XX PR
XX (AREN-) ARENA PHARM INC.
XX PA
XX Lehmann-Bruinsma K, Liaw CW, Lin I;
XX PI
XX WPI; 2001-648759/74.
XX DR N-PSDB; ABI97978.
XX DR
XX PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
XX PT disease treatment, comprises contacting candidate compounds with versions
XX PT of GPCRs.
XX PS
XX Claim 1; Page 277-278; 394pp; English.
XX CC The invention relates to G protein-coupled receptors (GPCRs) for which
XX CC the endogenous ligand has been identified. Non-endogenous constitutively
XX CC activated versions of known GPCRs are used in the invention for the
XX CC direct identification of candidate compounds as receptor agonists,
XX CC inverse agonists or partial agonists. Such agonists are useful as
XX CC therapeutic agents for diseases or disorders associated with GPCRs. The
XX CC present sequence is a non-endogenous version of a known human GPCR
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;
QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114
RESULT 24
AAB83354
ID AAB83354 standard; protein; 352 AA.
XX AC AAB83354;
XX DT 09-OCT-2001 (first entry)
XX DE Human CCR5 protein sequence.
XX KW Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
XX KW human immunodeficiency virus; anti-inflammatory disease; human.
XX OS Homo sapiens.
XX PN EP1118858-A2.
XX PD 25-JUL-2001.
XX PF 03-JAN-2001; 2001EP-00300020.
XX PR 12-JAN-2000; 2000GB-00000659.
XX PR 12-JAN-2000; 2000GB-00000661.

```

PR 12-JAN-2000; 2000GB-00000663.
XX (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
XX
XX
PI Dobbs S, Perros M, Rickett GA;
XX
XX WPI; 2001-477088/52.
DR N-PSDB; AAF87099.
XX
XX Determining if an agent can modulate CCR5-gp120 interaction, comprises
PT incubating the agent with CCR5 and gp120 and determining if the agent
PT modulates the interaction.
XX
XX Claim 1; Page 110; 113pp; English.
XX
XX This sequence represents the human CCR5 protein sequence. The invention
XX relates to a method for determining whether an agent is capable of
XX modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
XX with gp120, comprising incubating the agent with CCR5 and gp120 and
XX determining whether the agent modulates the interaction, where gp120 is
XX associated with CD4, and where the interaction is a low affinity binding.
XX The method is used to identify an agent capable of modulating the
XX interaction of CCR5 with gp120. An agent identified by the method is used
XX to prepare a pharmaceutical composition for the treatment of a disease or
XX condition associated with CCR5 and gp120 interaction, to treat a subject
XX with a disease or condition associated with CCR5 and gp120 interaction,
XX and for preparing a pharmaceutical for treating human immunodeficiency
XX virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
XX is commercially useful, amenable to high throughput screening, and
XX detects interaction of gp120 with cells expressing only CCR5
XX
XX Sequence 352 AA;
SQ
Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 25
AAB82948
ID AAB82948 standard; protein; 352 AA.
XX
XX AAB82948;
XX
XX 21-DEC-2001 (first entry)
XX
XX Human HIV-1 co-receptor CCR5.
XX
XX CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
XX infection; therapy; vaccine; anti-HIV-1.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Binding-site 2..18
FT /note= "binds to HIV-1 gp120"
XX
XX WO200164710-A2.
XX
XX 07-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US0066599.
XX
XX 29-FEB-2000; 2000US-0165667P.
XX
XX 19-MAY-2000; 2000US-0205839P.
XX
XX 07-FEB-2001; 2001US-0267231P.
XX
XX (PROG-) PROGENICS PHARM INC.
PA

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PA (AARO-) AARON DIAMOND AIDS RES CENT.
XX
XX Dragic T, Olson WC;
XX
XX WPI; 2001-611273/70.
DR N-PSDB; AAH26903.
XX
XX Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-
XX rector) amino terminal domain including negatively charged and two
XX sulfated tyrosine residues is useful for treating HIV infection in
XX humans.
XX
XX Claim 1; Page 30; 163pp; English.
XX
XX The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids
XX 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding
XX site that determines the specificity of the interaction between CCR5 and
XX HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the
XX CCR5 N-terminus is required for gp120 binding and may critically modulate
XX the susceptibility of target cells to HIV-1 infection in vivo. The
XX invention provides claimed sulfated peptides (see AAB82947) that are
XX based on the CCR5 N-terminal region and which are effective for
XX inhibiting HIV-1 binding to CCR5. These peptides are used in claimed
XX methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+
XX cells from becoming infected with HIV, of treating a subject whose CD4+
XX cells are infected with HIV, and of identifying an agent which inhibits
XX binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried
XX out in a subject, especially a human, infected (therapeutic method), not
XX infected with HIV (prophylactic method), or in a subject who is not
XX infected with, but has been exposed to, HIV
XX
XX Sequence 352 AA;
SQ
Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 26
AAU97150
ID AAU97150 standard; protein; 352 AA.
XX
XX AAU97150;
XX
XX 13-AUG-2002 (first entry)
XX
XX Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
XX
XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
XX immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
XX neurodegeneration; viral infection; Kaposi sarcoma; cancer;
XX hyperproliferative disease; neurological disease; receptor.
XX
XX Homo sapiens.
XX
XX US2002048786-A1.
XX
XX 25-APR-2002.
XX
XX 09-FEB-2001; 2001US-00779879.
XX
XX 09-FEB-2000; 2000US-0181258P.
XX
XX 09-MAR-2000; 2000US-0187999P.
XX
XX 22-SEP-2000; 2000US-0234336P.
XX
XX (ROSE/) ROSEN C A.
XX
XX (ROSC/) ROSCHKE V.
XX
XX (LIYV/) LI Y.
XX
XX (RUBE/) RUBEN S M.
PA

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XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2002-434754/46.
 DR N-PSDB; ABK51853.
 XX
 XX New nucleic acid encoding an antibody specific for the G-protein
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 PT inflammation.
 XX
 XX Claim 61; Fig 1; 180pp; English.
 XX
 XX The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
 CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune
 CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGNR10 #1
 XX
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QWDFGNTMCOLLTGLYFIGFPS 22
 DB 93 QWDFGNTMCOLLTGLYFIGFPS 114
 |||||
 |||||

RESULT 27
 AAU97152
 ID AAU97152 standard; protein; 352 AA.
 XX
 AC AAU97152;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 XX Human G-protein chemokine receptor (CCR5) HDGNR10 #2.
 XX
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.
 XX
 OS Homo sapiens.
 XX
 XX US2002048786-A1.
 XX
 XX 25-APR-2002.
 XX
 XX 09-FEB-2001; 2001US-00779879.
 XX
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 XX (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.

PA
 PA (LIY/) LI Y.
 XX (RUBE/) RUBEN S M.
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2002-434754/46.
 DR N-PSDB; ABK51870.
 XX
 XX New nucleic acid encoding an antibody specific for the G-protein
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 PT inflammation.
 XX
 XX Disclosure; Page 165-166; 180pp; English.
 XX
 XX The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
 CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune
 CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGNR10 #2
 XX
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QWDFGNTMCOLLTGLYFIGFPS 22
 DB 93 QWDFGNTMCOLLTGLYFIGFPS 114
 |||||
 |||||

RESULT 28
 AAM52829
 ID AAM52829 standard; protein; 352 AA.
 XX
 AC AAM52829;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 XX Human CCR5 Gln 55 variant.
 XX
 XX CCR5; CC chemokine receptor 5; human; HIV infection;
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
 KW drug screening; identification; variant.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 55
 FT Misc-difference 58 /note= "Glu replaces wild-type Leu; encoded by CTG"
 FT Misc-difference 58 /note= "Encoded by AGC"
 XX
 XX WO200171346-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 21-MAR-2001; 2001WO-US0009155.
 PF

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XX PR 21-MAR-2000; 2000US-0190946P.
XX PR 21-MAR-2000; 2000US-0190996P.
XX PR 21-MAR-2000; 2000US-0191299P.
XX PR 20-MAR-2001; 2001US-00813448.
XX PR 20-MAR-2001; 2001US-00813651.
XX PR 20-MAR-2001; 2001US-00813653.
XX PA (CONS-) CONSENSUS PHARM INC.
XX PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX DR N-PSDB; ABA02318.
XX DR WPI; 2002-010610/01.
XX PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX PT comprises binding a molecule from library to a molecule having binding
XX PT property corresponding to CCR5 and identifying bound molecule.
XX PS Example 3; Fig 4B; 50pp; English.
XX CC The invention relates to a method for identifying a binding compound for
XX CC CC chemokine receptor 5 (CCR5). The method involves screening a library
XX CC of test molecules (particularly peptides) with immobilised CCR5, and then
XX CC identifying those molecules which bind. The invention also relates to
XX CC CCR5-binding molecules identified using the method of the invention,
XX CC methods for identifying consensus motifs for CCR5-binding peptides, a
XX CC transfer vector encoding tagged CCR5, a computer-aided method for
XX CC determining the relative binding affinity of a test molecule to CCR5 and
XX CC a computer aided drug screening assay that utilises the three-dimensional
XX CC structure of CCR5. Compounds identified using the methods of the
XX CC invention are useful for treating or preventing HIV (human
XX CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
XX CC syndrome) in a patient. The methods of the invention may also be used to
XX CC identify agonists or antagonists of the interaction of CCR5 with its
XX CC natural ligand, and to determine a binding motif for CCR5. The present
XX CC sequence represents a naturally occurring variant of human CCR5 in which
XX CC there is a glutamine, rather than a leucine, at position 55
XX SQ Sequence 352 AA;
XX Query Match 100.0%; Score 126; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 QWDFGNTMCCQLLTGLYFIFGFFS 22
XX DB 93 QWDFGNTMCCQLLTGLYFIFGFFS 114
XX RESULT 29
XX AAMS2828
XX ID AAM52828 standard; protein; 352 AA.
XX AC AAM52828;
XX DT 22-FEB-2002 (first entry)
XX DE Human CC chemokine receptor 5 (CCR5).
XX KW CCR5; CC chemokine receptor 5; human; HIV infection;
XX KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
XX KW drug screening; identification.
XX OS Homo sapiens.
XX FN WO200171346-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009155.
XX PR 21-MAR-2000; 2000US-0190946P.

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PR 21-MAR-2000; 2000US-0190996P.
PR 21-MAR-2000; 2000US-0191299P.
PR 20-MAR-2001; 2001US-00813448.
PR 20-MAR-2001; 2001US-00813651.
PR 20-MAR-2001; 2001US-00813653.
XX XX (CONS-) CONSENSUS PHARM INC.
XX PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX DR N-PSDB; ABA02317.
XX DR WPI; 2002-010610/01.
XX PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX PT comprises binding a molecule from library to a molecule having binding
XX PT property corresponding to CCR5 and identifying bound molecule.
XX PS Example 3; Fig 4A; 50pp; English.
XX CC The invention relates to a method for identifying a binding compound for
XX CC CC chemokine receptor 5 (CCR5). The method involves screening a library
XX CC of test molecules (particularly peptides) with immobilised CCR5, and then
XX CC identifying those molecules which bind. The invention also relates to
XX CC CCR5-binding molecules identified using the method of the invention,
XX CC methods for identifying consensus motifs for CCR5-binding peptides, a
XX CC transfer vector encoding tagged CCR5, a computer-aided method for
XX CC determining the relative binding affinity of a test molecule to CCR5 and
XX CC a computer aided drug screening assay that utilises the three-dimensional
XX CC structure of CCR5. Compounds identified using the methods of the
XX CC invention are useful for treating or preventing HIV (human
XX CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
XX CC syndrome) in a patient. The methods of the invention may also be used to
XX CC identify agonists or antagonists of the interaction of CCR5 with its
XX CC natural ligand, and to determine a binding motif for CCR5. The present
XX CC sequence represents human CCR5
XX SQ Sequence 352 AA;
XX Query Match 100.0%; Score 126; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 QWDFGNTMCCQLLTGLYFIFGFFS 22
XX DB 93 QWDFGNTMCCQLLTGLYFIFGFFS 114
XX RESULT 30
XX ABG70597
XX ID ABG70597 standard; protein; 352 AA.
XX AC ABG70597;
XX DT 03-DEC-2002 (first entry)
XX DE Human G-protein chemokine receptor, HDGNR10.
XX KW Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;
XX KW haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;
XX KW chronic infection; leukaemia; T-cell mediated autoimmune disease;
XX KW parasitic infection; psoriasis; growth factor activity; allergy;
XX KW atherogenesis; anaphylaxis; malignancy; inflammation; histamine;
XX KW immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;
XX KW prostaglandin-independent fever; bone marrow failure; shock;
XX KW rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic;
XX KW immunosuppressive; antiparasitic; antipsoriatic; antiallergic;
XX KW antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;
XX KW antipyretic; receptor.
XX OS Homo sapiens.
XX PN US2002099176-A1.
XX XX

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PD 25-JUL-2002.
XX
PF 25-JUN-1999; 99US-00339912.
XX
PR 06-JUN-1995; 95US-00466343.
XX
PA (LIYY/) LI Y.
PI (RUBE/) RUBEN S M.
XX
XX Li Y, Ruben SM;
XX WPI; 2002-690494/74.
DR N-PSDB; ABS54272.
XX
XX Novel human G-protein chemokine receptor polypeptide useful for
PT identifying modulators for stimulating hematopoiesis, wound healing,
PT leukemia, for treating allergy, rheumatoid arthritis, shock and as
PT research agents.
XX
PS Claim 7; Fig 1; 22pp; English.
XX
XX The present invention relates to the isolation of human G-protein
CC chemokine receptor, HDGNR10 (CCR5), and the polynucleotide
CC sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences
CC are useful for diagnosing a disease or a susceptibility to a disease
CC related to underexpression of HDGNR10. They are useful for identifying
CC modulators for stimulating haematopoiesis, wound healing, coagulation,
CC angiogenesis, to treat solid tumours, chronic infections, leukaemia, T-
CC cell mediated autoimmune diseases, parasitic infections, psoriasis, or
CC for stimulating growth factor activity. The sequences are also useful for
CC preventing and/or treating allergy, atrogenesis, anaphylaxis,
CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
CC E (IGE)-mediated allergic reactions, prostatic and independent fever,
CC bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-
CC eosinophilic syndrome. Polynucleotide sequences encoding HDGNR10 can be
CC used in gene therapy to treat conditions related to underexpression of
CC HDGNR10. The present sequence represents human G-protein chemokine
CC receptor, HDGNR10
XX
XX Sequence 352 AA;
XX
Query Match 100.0%; Score 126; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
RESULT 31
ABG92883
ID ABG92883 standard; protein; 352 AA.
XX
AC ABG92883;
XX
XX 19-NOV-2002 (first entry)
XX
XX Human immunoglobulin variable heavy domain #1.
XX
XX Immunoglobulin; variable heavy chain; variable light chain; human;
KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
KW immunologic deficiency syndrome; blood protein disorder; nephritis;
KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
KW lymphocytopenia.
XX
XX Homo sapiens.
XX

PN WO200264612-A2.
XX
PD 22-AUG-2002.
XX
PF 08-FEB-2002; 2002WO-US003634.
XX
XX 09-FEB-2001; 2001US-00779880.
PR 09-FEB-2001; 2001WO-US004153.
PR 12-JUN-2001; 2001US-0297257P.
PR 08-AUG-2001; 2001US-0310458P.
PR 12-OCT-2001; 2001US-0328447P.
PR 21-DEC-2001; 2001US-0341725P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Roschke V, Rosen CA, Ruben SM;
PI WPI; 2002-643455/59.
XX N-PSDB; ABS68606.
XX
XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for
PT treating, preventing, ameliorating or monitoring diseases or disorders
PT associated with aberrant expression of HDGNR10 e.g. cancer.
XX
XX Example 55; Fig 4; 562pp; English.
XX
XX The invention describes an isolated polynucleotide encoding a first
CC antibody at least 95-100% identical to a second antibody consisting of an
CC amino acid sequence comprising at least one, two or three CDR regions of
CC a variable heavy (VH) or variable light (VL) domain of the antibody
CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,
CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
CC is useful treating, preventing, ameliorating, prognosing or monitoring
CC cancers or other diseases or disorders e.g. immunologic deficiency
CC syndromes such as blood protein disorders and ataxia telangiectasia,
CC inflammation associated disorders such as endotoxin lethality, nephritis
CC and inflammatory bowel disease, conditions associated with an increase in
CC certain haematopoietic cells such as histiocytosis, defective or aberrant
CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
CC an infectious disease, an autoimmune disease such as Addison's disease,
CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
CC poxvirus infection, a pneumocystis carinii infection, Kaposi's sarcoma,
CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
CC disease or disorder associated with aberrant expression of novel human G-
CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
CC sequence of human immunoglobulin sequence associated with the antibodies
CC against HDGNR10
XX
XX Sequence 352 AA;
XX
Query Match 100.0%; Score 126; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
RESULT 32
ABG92880
ID ABG92880 standard; protein; 352 AA.
XX
XX ABG92880;
XX
XX 19-NOV-2002 (first entry)
XX
XX Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
XX
XX Immunoglobulin; variable heavy chain; variable light chain; human;
KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
KW

immunologic deficiency syndrome; blood protein disorder; nephritis;
ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
histiocytosis; chemotaxis; infectious disease; autoimmune disease;
Addison's disease; dermatitis; rheumatoid arthritis; allergy;
neurodegenerative disorder; viral infection; poxvirus infection; HIV;
human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
lymphocytopenia.

OS Homo sapiens.

PN WC200364612-A2.

XX 22-AUG-2002.

XX 08-FEB-2002; 2002WO-US003634.

XX 09-FEB-2001; 2001US-00779880.

PR 09-FEB-2001; 2001WO-US004153.

PR 12-JUN-2001; 2001US-0297257P.

PR 08-AUG-2001; 2001US-0310458P.

PR 12-OCT-2001; 2001US-0328447P.

PR 21-DEC-2001; 2001US-0341725P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Roschke V, Rosen CA, Ruben SM;

PI WPI; 2002-643455/69.

DR N-PSDB; ABS68553.

XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for

PT treating, preventing, ameliorating or monitoring diseases or disorders

PT associated with aberrant expression of HDGNR10 e.g. cancer.

XX Disclosure; Fig 1A-B; 562pp; English.

XX The invention describes an isolated polynucleotide encoding a first
CC antibody at least 95-100% identical to a second antibody consisting of an
CC amino acid sequence comprising at least one, two or three CDR regions of
CC a variable heavy (VH) or variable light (VL) domain of the antibody
CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.1B85,
CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
CC is useful treating, preventing, ameliorating, prognosing or monitoring
CC cancers or other diseases or disorders e.g. immunologic deficiency
CC syndromes such as blood protein disorders and ataxia telangiectasia,
CC inflammation associated disorders such as endotoxin lethality, nephritis
CC and inflammatory bowel disease, conditions associated with an increase in
CC certain haematopoietic cells such as histiocytosis, defective or aberrant
CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
CC an infectious disease, an autoimmune disease such as Addison's disease,
CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
CC disease or disorder associated with aberrant expression of novel human G-
CC protein chemokine receptor (CCRS) HDGNR10. This is an amino acid sequence
CC of Human G-protein chemokine receptor (CCRS) HDGNR10 #1

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22

Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 33

AAE25808

ID AAE25808 standard; protein; 352 AA.
XX
AC AAE25808;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human G-protein chemokine receptor (CCRS), HDGNR10 #1.
XX
XX Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
KW inflammation; viral infection; autoimmune disease; neurodegeneration;
KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
KW hyperproliferative disease; receptor.
XX
OS Homo sapiens.

XX US2002061834-A1.

XX 23-MAY-2002.

XX 09-FEB-2001; 2001US-00779880.

XX 09-FEB-2000; 2000US-0181258P.

PR 09-MAR-2000; 2000US-0187999P.

PR 22-SEP-2000; 2000US-0234336P.

XX (ROSE/) ROSEN C A.

PA (ROSC/) ROSCHKE V.

PA (LIYY/) LI Y.

PA (RUBE/) RUBEN S M.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2002-499674/53.

DR N-PSDB; AAD42409.

XX New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,

PT useful for treatment, prevention and diagnosis of e.g. cancer, also

PT related antibodies.

XX Claim 61; Page 163-164; 186pp; English.

XX The invention relates to human G-protein chemokine receptor (CCRS), CCR5
CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
CC antibodies are used for the treatment or prevention of inflammation,
CC defective or aberrant chemotaxis of immune cells or T cell antigen-
CC presenting cell interaction, viral infections (specifically human immune
CC deficiency (including its early stages), cytomegalovirus or pox viruses),
CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
CC carinii infection, Kaposi's sarcoma or any condition associated with the
CC aberrant expression of CCR5 or their ligands. They are also used for the
CC detection, diagnosis, prognosis and monitoring of cancers or other
CC hyperproliferative diseases. The present sequence is human G-protein
CC chemokine receptor (CCRS), HDGNR10 DNA

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22

Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 34

AAE25811

ID AAE25811 standard; protein; 352 AA.

XX AAE25811;

XX 24-FEB-2003 (first entry)

DE Human G-protein chemokine receptor (CCR5), HDGMR10 #2.
 XX Human, G-protein chemokine receptor; CCR5; HDGMR10 protein; cancer;
 KW inflammation; viral infection; autoimmune disease; neurodegeneration;
 KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
 KW hyperproliferative disease; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002061834-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 09-FEB-2001; 2001US-00779880.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 03-MAR-2000; 2000US-0187999P.
 PR 22-SRP-2000; 2000US-0234336P.
 XX
 XX (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIYV/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2002-499674/53.
 DR N-PSDB; AAD42426.
 XX
 XX New nucleic acid encoding antibodies to the human CCR5 receptor HDGMR10,
 PT useful for treatment, prevention and diagnosis of e.g. cancer, also
 PT related antibodies.
 XX
 PS Disclosure; Page 170; 186pp; English.
 XX
 XX The invention relates to human G-protein chemokine receptor (CCR5),
 CC HDGMR10 proteins and nucleic acid molecules encoding such proteins. CCR5
 CC antibodies are used for the treatment or prevention of inflammation,
 CC defective or aberrant chemotaxis of immune cells or T cell antigen-
 CC presenting cell interaction, viral infections (specifically human immune
 CC deficiency including its early stages), cytomegalovirus or pox viruses),
 CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
 CC carinii infection, Kaposi's sarcoma or any condition associated with
 CC aberrant expression of CCR5 or their ligands. They are also used for the
 CC detection, diagnosis, prognosis and monitoring of cancers or other
 CC hyperproliferative diseases. The present sequence is human G-protein
 CC chemokine receptor (CCR5), HDGMR10 DNA
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCLLTGLYFIFGFFS 114
 RESULT 35
 ABB81054
 ID ABB81054 standard; protein; 352 AA.
 XX
 AC ABB81054;
 XX
 XX 05-NOV-2002 (first entry)
 DT
 DE G-protein chemokine receptor, HDGMR10.
 XX
 XX 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGMR10;
 KW G-protein chemokine receptor; haematopoietic; immunosuppressant;
 KW antiparasitic; antiproliferative; antiallergic; antiinflammatory; cytostatic;
 KW antineumatic; antiarthritic; gene therapy; human; receptor.

XX Homo sapiens.
 OS
 PN US2002076745-A1.
 XX
 PD 20-JUN-2002.
 XX
 PF 18-NOV-1998; 98US-00195662.
 XX
 PR 06-JUN-1995; 95US-00466343.
 XX
 PA (LIYV/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Li Y, Ruben SM;
 XX WPI; 2002-598724/64.
 DR N-PSDB; AEN86542.
 XX
 XX New polynucleotide encoding a human G protein chemokine receptor HDGMR10,
 PT useful e.g. for treating tumors.
 XX
 PS Claim 7; Fig 1; 22pp; English.
 XX
 XX The invention relates to a novel human 7-transmembrane receptor, HDGMR10,
 CC which has been identified as a G-protein chemokine receptor. The GPCR
 CC HDGMR10 polypeptide can be expressed by standard recombinant methodology.
 CC Compounds that activate or inhibit the receptor polypeptide, optionally
 CC expressed from DNA in gene therapy vectors, are used to treat diseases
 CC that require: (a) activation of the receptor (e.g. stimulation of
 CC haematopoiesis, treatment of solid tumors, T-cell stimulation of
 CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the
 CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis
 CC etc). The present sequence represents the human HDGMR10 receptor
 CC polypeptide
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCLLTGLYFIFGFFS 114
 RESULT 36
 ABB08343
 ID ABB08343 standard; protein; 352 AA.
 XX
 AC ABB08343;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human chemokine (C-C motif) receptor 5 polypeptide.
 XX
 XX Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
 KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
 KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
 KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;
 KW chromosome 3p21.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 55
 FT /label= Leu, Gln
 FT Misc-difference 182
 FT /label= Phe, Leu
 FT Misc-difference 223
 FT /label= Arg, Gln
 XX

PN WO200177125-A2.
 XX 18-OCT-2001.
 PD 04-APR-2001; 2001WO-US010708.
 PF 05-APR-2000; 2000US-0194361P.
 PR (GENA-) GENAISANCE PHARM INC.
 PA
 XX Choi JY, Klieh SE, Koshy B;
 XX WPI; 2002-041282/05.
 XX N-PSDB; ABA97318, ABA97319.
 DR
 XX
 PT New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful
 PT to diagnose and treat diseases associated with its abnormal expression or
 PT function, including human immunodeficiency virus-1 infection.
 XX
 PS Claim 29; Fig 3; 61pp; English.
 CC The present sequence is that of a polypeptide encoded by the human
 CC chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see
 CC ABA97319, ABA97319). The specification describes haplotyping the CCR5
 CC gene of an individual by determining if the individual has one of the
 CC CCR5 haplotypes or haplotype pairs fully defined in the specification.
 CC The specification also describes an isolated polynucleotide comprising a
 CC nucleotide sequence which is a polymorphic variant of the reference CCR5
 CC gene sequence and comprises an isogene defined by a haplotype described
 CC in the specification and its encoded polypeptide. The methods of the
 CC invention are useful to diagnose and develop treatment for diseases
 CC associated with abnormal expression or function of the gene. The CCR5
 CC isogenes and the screened compounds are useful for treating human
 CC immunodeficiency virus (HIV)-1 infection and the progression to acquired
 CC immunodeficiency syndrome (AIDS). The invention has antiviral
 CC applications. The specification describes genotyping the CCR5 gene of an
 CC individual; predicting a haplotype pair for the CCR5 gene of an
 CC individual; identifying an association between a trait and a haplotype or
 CC haplotype pair of the CCR5 gene. The specification describes a
 CC composition comprising a genotyping oligonucleotide for detecting a CCR5
 CC polymorphism; a recombinant non-human organism transformed with CCR5
 CC polynucleotide expressing a CCR5 protein encoded by the variant sequence;
 CC an isolated antibody specific for the CCR5 polypeptide and a method for
 CC screening drugs targeting the CCR5 polypeptide
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLTGLYFIGFSS 22
 DB 93 QWDFGNTWCQLLTGLYFIGFSS 114
 RESULT 37
 ABG75540
 ID ABG75540 standard; protein; 352 AA.
 XX
 AC ABG75540;
 XX
 DT 16-APR-2003 (first entry)
 XX Human G-protein chemokine receptor, HDGNR10, protein.
 XX Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor;
 KW HDGNR10; signal transduction; gene therapy; haematopoiesis;
 KW wound healing; coagulation; angiogenesis; tumour; chronic infection;
 KW leukaemia; T-cell mediated auto-immune disease; parasitic infection;
 KW psoriasis; growth factor; allergy; atherogenesis; anaphylaxis;
 KW malignancy; inflammation; histamine; IgE-mediated;
 KW prostaglandin-independent fever; bone marrow failure; silicosis;

KW sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.
 XX Homo sapiens.
 OS
 PN US2002132269-A1.
 XX 19-SEP-2002.
 PD 11-FEB-2000; 2000US-00502783.
 XX 06-JUN-1995; 95US-00466343.
 PF (HUMA-) HUMAN GENOME SCI INC.
 PR
 XX Li Y, Ruben SM;
 XX WPI; 2003-208944/20.
 DR N-PSDB; ABX10635.
 DR
 XX
 PT Novel human G-protein chemokine receptor polypeptide useful for
 PT diagnostic purposes and for identifying modulators of the polypeptide
 PT useful for treating leukemia, autoimmune diseases, psoriasis and allergic
 PT reactions.
 XX
 PS Claim 7; Fig 1; 22pp; English.
 CC The invention discloses a G-protein chemokine receptor (sometimes
 CC referred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the
 CC polynucleotide encoding it. G-protein chemokine receptors are involved in
 CC signal transduction pathways. The polynucleotide and polypeptide can be
 CC used to identify compounds which activate or inhibit activation of the
 CC protein and these compounds are useful for treating a patient having need
 CC to activate or inhibit a G-protein chemokine receptor. The compound is
 CC administered by providing to the patient DNA encoding the agonist or
 CC antagonist and expressing them in vivo (gene therapy). The
 CC polynucleotides and polypeptide are also useful for diagnosing a
 CC disease or susceptibility to a disease related to an under-expression of
 CC the protein, for chromosome identification or as immunogens for producing
 CC antibodies. Agonists are useful in stimulating haematopoiesis, wound
 CC healing, coagulation, angiogenesis, to treat solid tumours, chronic
 CC infections, leukaemia, T-cell mediated auto-immune diseases, parasitic
 CC infections, psoriasis and to stimulate growth factor activity.
 CC Antagonists are useful in the prevention and treatment of allergy,
 CC atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation,
 CC histamine and IgE-mediated allergic reactions, prostaglandin-independent
 CC fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis,
 CC shock and hyper-eosinophilic syndrome. The sequence presented is the
 CC human HDGNR10 protein
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLTGLYFIGFSS 22
 DB 93 QWDFGNTWCQLLTGLYFIGFSS 114
 RESULT 38
 ABR58602
 ID ABR58602 standard; protein; 352 AA.
 XX
 AC ABR58602;
 XX
 DT 09-JUL-2003 (first entry)
 XX Human cancer related protein SEQ ID NO:259.
 DE Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KW heart disease; atherosclerosis; endometriosis.
 XX

OS Homo sapiens.
 FN WO2003025138-A2.
 XX
 XX
 PD 27-MAR-2003.
 XX
 XX
 PF 17-SEP-2002; 2002WO-US029560.
 XX
 XX
 PR 17-SEP-2001; 2001US-0323469P.
 PR 20-SEP-2001; 2001US-0323887P.
 PR 13-NOV-2001; 2001US-0350866P.
 PR 08-FEB-2002; 2002US-0355145P.
 PR 08-FEB-2002; 2002US-0355257P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 XX (EOSB-) BOS BIOTECHNOLOGY INC.
 XX
 XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
 PI Zlotnick A;
 PI
 DR N-PSDB; ACC72740.
 DR WPI; 2003-354600/33.
 XX
 XX New genes that are up-regulated or down-regulated in cancers, useful as
 PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
 PT therapeutic targets for screening drugs for treating these diseases.
 XX
 PS Claim 12; Page 745; 767pp; English.
 XX
 XX The present invention describes an isolated nucleic acid molecule, which
 CC comprises the sequence of any of the genes that are up-regulated or down-
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer-
 CC related gene nucleotide sequences which encode the proteins given in
 CC ARK5821 to ARK58709. Also described: (1) determining the presence or
 CC absence of a pathological cell in a patient; (2) an expression vector
 CC comprising a nucleic acid molecule described above; (3) a host cell
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
 CC of (4); (6) specifically targeting a compound to a pathological cell in a
 CC patient by administering to the patient the antibody above; and (7) a
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or
 CC therapeutic targets. In particular, the nucleic acid is useful for
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in
 CC drug screening, particularly for identifying agents for treating these
 XX pathologies
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 6; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCCQLLTGLYFIFGFFS 22
 Db 93 QWDFGNTMCCQLLTGLYFIFGFFS 114
 RESULT 39
 AAO29514
 ID AAO29514 standard; protein; 352 AA.
 XX
 XX AAO29514;
 AC
 XX
 XX 27-AUG-2003 (first entry)
 DT
 DE Human C-C chemokine receptor type 5 (333) protein.
 XX
 XX Human; urological disorder; stress urinary incontinence; prostate cancer;
 KW benign prostatic hyperplasia; overactive bladder; oversensitive bladder;
 KW

KW overflow urinary incontinence; gene therapy; nephrotropic; prostatitis;
 KW kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
 OS Homo sapiens.
 XX
 XX WO2003039475-A2.
 PN
 XX
 PD 15-MAY-2003.
 XX
 XX 07-NOV-2002; 2002WO-US035824.
 PF
 XX
 XX 07-NOV-2001; 2001US-0344552P.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Silos-Santiago I;
 PI
 XX WPI; 2003-449396/42.
 DR N-PSDB; AAL59912.
 DR
 XX
 XX Identifying a compound, capable of treating urological disorder e.g.,
 PT benign prostatic hyperplasia, by assaying the ability of the compound to
 PT modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or
 PT polypeptide activity.
 XX
 PS Disclosure; Page 81; 87pp; English.
 XX
 XX The invention relates to a method for treating an urological disorder
 CC which comprises assaying the ability of the compound to modulate 313,
 CC 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide
 CC activity. The method is useful for identifying a compound for treating an
 CC urological disorder comprising urinary incontinence e.g., overactive/
 CC oversensitive bladder, overflow urinary incontinence, stress urinary
 CC incontinence caused by dysfunction of the bladder, urethra or central/
 CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
 CC prostate cancer or kidney disorders. It is also used in gene therapy. The
 CC present sequence is human C-C chemokine receptor type 5 (CCR5; 333).
 CC protein. This sequence is used to illustrate the method of the invention
 XX
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 126; DB 6; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCCQLLTGLYFIFGFFS 22
 Db 93 QWDFGNTMCCQLLTGLYFIFGFFS 114
 RESULT 40
 ABU61654
 ID ABU61654 standard; protein; 352 AA.
 XX
 XX ABU61654;
 AC
 XX
 XX 08-AUG-2003 (first entry)
 DT
 XX Human G-protein chemokine receptor (HDGMR10) polypeptide.
 DE
 XX Human; G-protein chemokine receptor; receptor; HDGMR10;
 KW 7-transmembrane receptor.
 KW
 XX Homo sapiens.
 OS
 XX US2003023044-A1.
 PN
 XX 30-JAN-2003.
 PD
 XX
 XX 03-SEP-2002; 2002US-00232686.
 PF
 XX
 XX 06-JUN-1995; 95US-00466343.
 PR
 XX 18-NOV-1998; 98US-00195662.
 PR

PR 25-JUN-1999; 99US-00339912.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Li Y, Ruben SM;
XX WPI; 2003-456307/43.
DR N-PSDB; ACA61721.
XX
PT Producing an antibody, involves immunizing an animal with a polypeptide
PT or with a polypeptide encoded by the human G-protein chemokine receptor
PT clone in ATCC 97183, and recovering the antibody.
XX
XX Claim 1; Fig 1; 23pp; English.
XX
CC The invention relates to a method of producing an antibody, involving
CC immunising an animal with a human G-protein chemokine receptor (HDGNR10)
CC polypeptide (also referred to as a human 7-transmembrane receptor) and
CC recovering an antibody which binds the polypeptide. The method is useful
CC for producing an antibody which binds specifically to the human G-protein
CC chemokine receptor polypeptide. This sequence represents the HDGNR10
CC polypeptide of the invention
XX
SQ Sequence 352 AA;
Query Match 100.0%; Score 126; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. NO. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114
Search completed: September 28, 2004, 09:03:37
Job time : 56.525 secs

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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:00:23 ; Search time 19.8 Seconds
(without alignments)
57.362 Million cell updates/sec

Title: US-10-084-813-12
Perfect score: 126
Sequence: 1 QWDFGNTMCOLLTLGYLFGFFS 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/aa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	126	100.0	184	US-08-833-752-4
2	126	100.0	215	US-09-087-232A-17
3	126	100.0	215	US-08-833-752-6
4	126	100.0	352	US-08-466-343D-2
5	126	100.0	352	US-09-087-232A-13
6	126	100.0	352	US-08-861-105-14
7	126	100.0	352	US-08-575-987A-2
8	126	100.0	352	US-09-045-583-52
9	126	100.0	352	US-09-517-605-5
10	126	100.0	352	US-09-534-185-52
11	126	100.0	352	US-08-833-752-5
12	126	100.0	352	US-09-502-783A-2
13	126	100.0	352	US-09-796-202-1
14	87	69.0	344	US-08-466-343D-9
15	87	69.0	347	US-08-461-244-3
16	87	69.0	360	US-08-450-393A-4
17	87	69.0	360	US-08-446-669-4
18	87	69.0	360	US-09-045-583-50
19	87	69.0	360	US-09-534-185-50
20	87	69.0	360	US-08-833-752-7
21	87	69.0	360	US-09-131-827A-2
22	87	69.0	360	US-09-131-827A-20
23	87	69.0	360	PCT-US95-00476-4
24	87	69.0	374	US-08-450-393A-2
25	87	69.0	374	US-08-446-669-2
26	87	69.0	374	PCT-US95-00476-2
27	83	65.9	269	US-08-307-499-30

Sequence 30, Appl
Sequence 2, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 2, Appl
Sequence 13, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 53, Appl
Sequence 53, Appl
Sequence 14, Appl
Sequence 5, Appl
Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-833-752-4
; Sequence 4, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbs, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-752-4

Query Match 100.0%; Score 126; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTLGYLFGFFS 22
Db 93 QWDFGNTMCOLLTLGYLFGFFS 114

RESULT 2

```
US-09-087-232A-17
; Sequence 17, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillient et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-17

Query Match 100.0%; Score 126; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFSS 22
DB 93 QWDFGNTMCQLLTGLYFIGFSS 114

RESULT 3
US-08-833-752-6
; Sequence 6, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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US-08-833-752-6
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-752-6

Query Match 100.0%; Score 126; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFSS 22
DB 93 QWDFGNTMCQLLTGLYFIGFSS 114

RESULT 4
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-2

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFSS 22
```

Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 5

US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quilliant et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519

INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-13

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22

Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 6

US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor

CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994

ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-861-105-14

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22

Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 7

US-08-575-967A-2
; Sequence 2, Application US/08575967A
; Patent No. 6265184
; GENERAL INFORMATION:
; APPLICANT: Gray et al.

TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,967A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

; NAME: No. 6265184and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32918
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-485-1900
; TELEFAX: 206-485-1662
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 9
US-09-517-605-5
; Sequence 5, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-605-5

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 10
US-09-534-185-52
; Sequence 52, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; TITLE OF INVENTION: Heptahelical Receptor Superfamily and Uses
; THEREFOR
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)742-4214
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-52

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NAME: No. 6265184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 8
US-09-045-583-52
; Sequence 52, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)742-4214
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-52
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;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 352 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match          100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFSS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFSS 114

RESULT 11
US-08-833-752-5
; Sequence 5, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: 5:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 352 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-752-5

Query Match          100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFSS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFSS 114

RESULT 12
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
```

```
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
; TITLE OF INVENTION: HDGNR10
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502.783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match          100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFSS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFSS 114

RESULT 13
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPN/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match          100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFSS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFSS 114

RESULT 14
US-08-466-343D-9
; Sequence 9, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-343D-9

Query Match 69.0%; Score 87; DB 3; Length 344;
Best Local Similarity 66.7%; Pred. No. 1.9e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIQFF 21
Db 88 EWVFGNAMCKLFTGLYHIGYF 108

RESULT 15
US-08-461-244-3
Sequence 3, Application US/08461244
Patent No. 5776729
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Vi, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Petrarro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-244-3

Query Match 69.0%; Score 87; DB 1; Length 347;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIQFF 21
Db 92 EWVFGNAMCKLFTGLYHIGYF 112

RESULT 16
US-08-450-393A-4
Sequence 4, Application US/08450393A
Patent No. 5707815
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Csert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-393A-4

Query Match 69.0%; Score 87; DB 1; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIQFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 17
US-08-446-669-4
Sequence 4, Application US/08446669
Patent No. 6132987
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nealey, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-669-4

Query Match 69.0%; Score 87; DB 3; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIQFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 18
US-09-045-583-50
Sequence 50, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-50

Query Match 69.0%; Score 87; DB 3; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIQFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 19

US-09-534-185-50
Sequence 50, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIQFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 20
US-08-833-752-7
; Sequence 7, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: 7:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
US-08-833-752-7

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFF 21
Db 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 21
US-09-131-827A-2
; Sequence 2, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-2

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFF 21
Db 105 EWVFGNACKLFTGLYHIGYF 125

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFF 21
Db 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 22
US-09-131-827A-20
; Sequence 20, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-20

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIFGFF 21
Db 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 23
PCT-US95-00476-4
; Sequence 4, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001


```

; TELEFAX: 310-977-1003
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-00476-4
Query Match 69.0%; Score 87; DB 5; Length 360;
Best Local Similarity 66.7%; Pred. No. 2le-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 24
US-08-450-393A-2
; Sequence 2, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-2
Query Match 69.0%; Score 87; DB 1; Length 374;
Best Local Similarity 66.7%; Pred. No. 2le-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 25
US-08-446-669-2
; Sequence 2, Application US/08446669

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; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neely, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-2
Query Match 69.0%; Score 87; DB 3; Length 374;
Best Local Similarity 66.7%; Pred. No. 2le-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 26
PCT-US95-00476-2
; Sequence 2, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```

```
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-00476-2

Query Match 69.0%; Score 87; DB 5; Length 374;
Best Local Similarity 66.7%; Pred. No. 2.1e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFF 21
Db 105 EWVFNAMCKLFTGLYHGYF 125

RESULT 27
US-08-307-499-30
; Sequence 30, Application US/08307499
; Patent No. 5651972
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,499
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-268-30

Query Match 65.9%; Score 83; DB 3; Length 269;
Best Local Similarity 54.5%; Pred. No. 6e-05;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 20 QWIFGNILCKIMSVLYYGVFFS 41

RESULT 28
US-09-299-268-30
; Sequence 30, Application US/09299268
; Patent No. 6217882
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/901,127
; FILING DATE:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-268-30

Query Match 65.9%; Score 83; DB 3; Length 269;
Best Local Similarity 54.5%; Pred. No. 6e-05;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
```

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Db      20 QWIFGNILCKMSVLYVGFPS 41
      || || || |:::| |:::| |:::| |:::|
      1 QWDFGNTMCLLTGLYFIFGFS 22
      || || || |:::| |:::| |:::| |:::|
      98 QWVFGTVMCKVSGFYIIGFYS 119

RESULT 30
US-08-461-244-2
; Sequence 2, Application US/08461244
; Patent No. 5776729
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GULFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-244-2

Query Match      65.1%; Score 82; DB 1; Length 355;
Best Local Similarity 54.5%; Pred. No. 0.00011;
Matches 12; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy      1 QWDFGNTMCLLTGLYFIFGFS 22
      || || || |:::| |:::| |:::| |:::|
      98 QWVFGTVMCKVSGFYIIGFYS 119

RESULT 31
US-09-534-185-56
; Sequence 56, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:

Qy      1 QWDFGNTMCLLTGLYFIFGFS 22
      || || || |:::| |:::| |:::| |:::|
      98 QWVFGTVMCKVSGFYIIGFYS 119

Db      20 QWIFGNILCKMSVLYVGFPS 41
      || || || |:::| |:::| |:::| |:::|
      1 QWDFGNTMCLLTGLYFIFGFS 22
      || || || |:::| |:::| |:::| |:::|
      98 QWVFGTVMCKVSGFYIIGFYS 119

RESULT 30
US-09-045-583-56
; Sequence 56, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-534-185-56

Query Match 65.1%; Score 82; DB 4; Length 355;
Best Local Similarity 54.5%; Pred. No. 0.00016;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCKLLTGLYIGF 22
DB 98 QWVFGNCKRVSGFYIGFYS 119

RESULT 32

US-09-045-583-51
Sequence 51, Application US/09045583
Patent No. 6287805

GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.

TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/045,583

FILING DATE: 20-MAR-98

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNI-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-09-045-583-51

Query Match 64.3%; Score 81; DB 3; Length 360;
Best Local Similarity 65.0%; Pred. No. 0.00016;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCKLLTGLYIGF 20
DB 105 EWVFGNCKRVSGFYIGFYS 124

RESULT 33

US-09-534-185-51

Sequence 51, Application US/09534185

Patent No. 6403767

GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24-Mar-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/045,583

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNI-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 51:

US-09-534-185-51

Query Match 64.3%; Score 81; DB 4; Length 360;

Best Local Similarity 65.0%; Pred. No. 0.00016;

Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCKLLTGLYIGF 20

DB 105 EWVFGNCKRVSGFYIGFYS 124

RESULT 34

US-08-724-984A-2

Sequence 2, Application US/08724984A

Patent No. 6388055

GENERAL INFORMATION:

APPLICANT: Dark Bergsma, Mary Brawner, and Usman Shabon

TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road, P.O. Box 1539

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM 486

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS

SOFTWARE: MICROSOFT WORD

CURRENT APPLICATION DATA:

APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
CLASSIFICATION: 800
FILE REFERENCE: 1488.1150006
CURRENT APPLICATION NUMBER: US/09/502.783A
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 329
TYPE: PRT
ORGANISM: Protein
US-09-502-783A-9

Query Match 63.5%; Score 80; DB 4; Length 354;
Best Local Similarity 57.1%; Pred. No. 0.00023;
Matches 12; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFICGFF 21
DB 95 EWIFGNIMCKVFTGVTHIYF 115

RESULT 35

US-09-886-319A-13
Sequence 13, Application US/09886319A
Patent No. 6585185
GENERAL INFORMATION:
APPLICANT: Wolf, Eckard
APPLICANT: Werner, Sabine
APPLICANT: Halle, Joern-Peter
APPLICANT: Regenbogen, Johannes
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 355
TYPE: PRT
ORGANISM: Mus musculus
US-09-886-319A-13

Query Match 50.3%; Score 76; DB 4; Length 355;
Best Local Similarity 52.4%; Pred. No. 0.00093;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 WDFGNTMCOLLTGLYFICGFFS 22
DB 99 WIFGDAMCKLLSGFYVLGLYS 119

RESULT 36

US-09-502-783A-9
Sequence 9, Application US/09502783A
Patent No. 6511826
GENERAL INFORMATION:
APPLICANT: Li, Yi

APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
CLASSIFICATION: 800
FILE REFERENCE: 1488.1150006
CURRENT APPLICATION NUMBER: US/09/502.783A
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 329
TYPE: PRT
ORGANISM: Protein
US-09-502-783A-9

Query Match 58.7%; Score 74; DB 4; Length 329;
Best Local Similarity 54.5%; Pred. No. 0.0017;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFICGFFS 22
DB 88 EWVFGNAMCKLFTGLYHIRYLA 109

RESULT 37

US-08-012-988A-2
Sequence 2, Application US/08012988A
Patent No. 5652133
GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning and Expression of Human
TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
TITLE OF INVENTION: alpha)/RANTES Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,988A
FILING DATE: 19930128
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-012-988A-2

Query Match 56.3%; Score 71; DB 1; Length 355;
Best Local Similarity 47.6%; Pred. No. 0.0053;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 WDFGNTMCOLLTGLYFICGFFS 22
DB 99 WVFGDAMCKLLSGFYVLGLYS 119

RESULT 38
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS: 14
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseer, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooLevPA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-450-393A-5
Query Match 56.3%; Score 71; DB 1; Length 355;
Best Local Similarity 47.6%; Pred. No. 0.0053;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 2 WDFGNTMCQLTGLYFICGFFS 22
Db 99 WVFSDAMCKILSGFYITGLYS 119
RESULT 39
US-08-446-669-5
; Sequence 5, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS: 14
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 35,207
; REFERENCE/DOCKET NUMBER: XAI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-450-393A-5

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816CooLevPA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-446-669-5
Query Match 56.3%; Score 71; DB 3; Length 355;
Best Local Similarity 47.6%; Pred. No. 0.0053;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 2 WDFGNTMCQLTGLYFICGFFS 22
Db 99 WVFSDAMCKILSGFYITGLYS 119
RESULT 40
US-09-045-583-53
; Sequence 53, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 35,207
; REFERENCE/DOCKET NUMBER: XAI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-53

Query Match 56.3%; Score 71; DB 3; Length 355;
Best Local Similarity 47.6%; Pred. No. 0.0053;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 WDFGNTMCQLLTGLYFIFGFFS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 99 WIFGDAMCKILSGFYVTGLYS 119

Search completed: September 28, 2004, 09:21:31
Job time : 20.8 secs

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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:06:23 ; Search time 72.875 Seconds
(without alignments)
97.074 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFGNTWCQLLTGLYFIFGFFS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US02_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	22	14	US-10-084-813-12
2	126	100.0	184	9	US-09-938-719-4
3	126	100.0	184	9	US-02-939-226-4
4	126	100.0	184	9	US-09-938-703-4
5	126	100.0	184	16	US-10-661-798-4
6	126	100.0	184	16	US-10-612-791-4
7	126	100.0	215	9	US-09-938-719-6
8	126	100.0	215	9	US-09-938-226-6
9	126	100.0	215	9	US-09-938-703-6
10	126	100.0	215	16	US-10-661-798-6
11	126	100.0	215	16	US-10-612-791-8
12	126	100.0	215	16	US-10-612-791-6
13	126	100.0	215	16	US-10-612-791-18
14	126	100.0	332	14	US-10-095-876A-2
15	126	100.0	352	9	US-09-725-285-2

16 126 100.0 352 9 US-09-759-841-2 Sequence 2, Appli
17 126 100.0 352 9 US-03-779-879A-2 Sequence 2, Appli
18 126 100.0 352 9 US-09-779-879A-22 Sequence 22, Appli
19 126 100.0 352 9 US-09-779-880A-2 Sequence 2, Appli
20 126 100.0 352 9 US-09-779-880A-22 Sequence 22, Appli
21 126 100.0 352 9 US-09-813-653-15 Sequence 15, Appli
22 126 100.0 352 9 US-09-813-653-17 Sequence 17, Appli
23 126 100.0 352 9 US-09-796-202-1 Sequence 1, Appli
24 126 100.0 352 9 US-09-135-862A-2 Sequence 2, Appli
25 126 100.0 352 9 US-09-339-912A-2 Sequence 2, Appli
26 126 100.0 352 9 US-09-938-719-5 Sequence 5, Appli
27 126 100.0 352 9 US-09-939-226-5 Sequence 5, Appli
28 126 100.0 352 9 US-09-938-703-5 Sequence 5, Appli
29 126 100.0 352 9 US-09-502-783A-2 Sequence 2, Appli
30 126 100.0 352 10 US-09-734-221A-14 Sequence 14, Appli
31 126 100.0 352 11 US-09-826-509-477 Sequence 477, Appli
32 126 100.0 352 12 US-10-151-274-5 Sequence 5, Appli
33 126 100.0 352 13 US-10-106-623-2 Sequence 2, Appli
34 126 100.0 352 13 US-10-106-623-20 Sequence 20, Appli
35 126 100.0 352 14 US-10-232-686-2 Sequence 2, Appli
36 126 100.0 352 14 US-10-086-814-1 Sequence 1, Appli
37 126 100.0 352 14 US-10-067-800-2 Sequence 2, Appli
38 126 100.0 352 14 US-10-067-800-22 Sequence 22, Appli
39 126 100.0 352 14 US-10-290-058A-6 Sequence 6, Appli
40 126 100.0 352 14 US-10-225-567A-352 Sequence 352, App
41 126 100.0 352 14 US-10-323-314-1 Sequence 1, Appli
42 126 100.0 352 14 US-10-072-301-1 Sequence 1, Appli
43 126 100.0 352 14 US-10-164-649-52 Sequence 52, Appli
44 126 100.0 352 14 US-10-071-866-1 Sequence 1, Appli
45 126 100.0 352 14 US-10-135-839-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-084-813-12
; Sequence 12, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-12

Query Match 100.0%; Score 126; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 1 QWDFGNTWCQLLTGLYFIFGFFS 22

RESULT 2

US-09-938-719-4
; Sequence 4, Application US/09938719
; Patent No. US20020106742A1

GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-719-4
Query Match 100.0%; Score 126; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
RESULT 3
US-09-939-226-4
Sequence 4, Application US/09939226
Patent No. US20020110805A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-226-4
Query Match 100.0%; Score 126; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
RESULT 4
US-09-938-703-4
Sequence 4, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-703-4

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Query Match      100.0%; Score 126; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QWDFGNTMCOLLTGLYFIFGFFS 22
      93 QWDFGNTMCOLLTGLYFIFGFFS 114
Db

RESULT 5
US-10-661-798-4
; Sequence 4, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Frederic, Libert
; TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV En
; FILE REFERENCE: 9409/2023F
; CURRENT APPLICATION NUMBER: US/10/661,798
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: 09/938,703
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: 08/810,028
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: EP 96870021.1
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: EP 96870102.9
; PRIOR FILING DATE: 1996-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-798-4

Query Match      100.0%; Score 126; DB 16; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QWDFGNTMCOLLTGLYFIFGFFS 22
      93 QWDFGNTMCOLLTGLYFIFGFFS 114
Db

RESULT 6
US-10-612-791-4
; Sequence 4, Application US/10612791
; Publication No. US20040161739A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; TITLE OF INVENTION: HIV Diagnostic Methods
; FILE REFERENCE: 9409/2023E
; CURRENT APPLICATION NUMBER: US/10/612,791
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/938,703
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: 08/810,028
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: EP 96870021.1
```

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; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: EP 96870102.9
; PRIOR FILING DATE: 1996-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-791-4

Query Match      100.0%; Score 136; DB 16; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QWDFGNTMCOLLTGLYFIFGFFS 22
      93 QWDFGNTMCOLLTGLYFIFGFFS 114
Db

RESULT 7
US-09-938-719-6
; Sequence 6, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michel
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Libert, Frederick
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-719-6

Query Match      100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QWDFGNTMCOLLTGLYFIFGFFS 22
      93 QWDFGNTMCOLLTGLYFIFGFFS 114
Db
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RESULT 8
US-09-939-226-6
; Sequence 6, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6
Query Match 100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114
RESULT 9
US-09-938-703-6
; Sequence 6, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6
Query Match 100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114
RESULT 10
US-10-661-798-6
; Sequence 6, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Frederic, Libert
; TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV Ent
; FILE REFERENCE: 9409/2023F
; CURRENT APPLICATION NUMBER: US/10/661,798
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: 09/938,703
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: 08/810,028
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: EP 96870021.1
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: EP 96870102.9
; PRIOR FILING DATE: 1996-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-798-6
Query Match 100.0%; Score 126; DB 16; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFS 22

Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 11

US-10-661-798-18

Sequence 18, Application US/10661798

Publication No. US20040110127A1

GENERAL INFORMATION:

APPLICANT: Samson, Michael

APPLICANT: Parmentier, Marc

APPLICANT: Vassart, Gilbert

APPLICANT: Frederic, Libert

TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV En

TITLE OF INVENTION: a Cell

FILE REFERENCE: 9409/2023F

CURRENT APPLICATION NUMBER: US/10/661,798

CURRENT FILING DATE: 2003-09-12

PRIOR APPLICATION NUMBER: 09/938,703

PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 09/626,939

PRIOR FILING DATE: 2000-07-27

PRIOR APPLICATION NUMBER: 08/833,752

PRIOR FILING DATE: 1997-04-09

PRIOR APPLICATION NUMBER: 08/810,028

PRIOR FILING DATE: 1997-03-03

PRIOR APPLICATION NUMBER: EP 96870021.1

PRIOR FILING DATE: 1996-03-01

PRIOR APPLICATION NUMBER: EP 96870102.9

PRIOR FILING DATE: 1996-08-06

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.1

SEQ ID NO 18

LENGTH: 215

TYPE: PRT

ORGANISM: Homo sapiens

US-10-661-798-18

Query Match 100.0%; Score 126; DB 16; Length 215;

Best Local Similarity 100.0%; Pred. No. 3.9e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFS 22

Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 12

US-10-612-791-6

Sequence 6, Application US/10612791

Publication No. US20040161739A1

GENERAL INFORMATION:

APPLICANT: Samson, Michael

APPLICANT: Parmentier, Marc

APPLICANT: Vassart, Gilbert

TITLE OF INVENTION: HIV Diagnostic Methods

FILE REFERENCE: 9409/2023E

CURRENT APPLICATION NUMBER: US/10/612,791

CURRENT FILING DATE: 2003-07-02

PRIOR APPLICATION NUMBER: 09/938,703

PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 09/626,939

PRIOR FILING DATE: 2000-07-27

PRIOR APPLICATION NUMBER: 08/833,752

PRIOR FILING DATE: 1997-04-09

PRIOR APPLICATION NUMBER: 08/810,028

PRIOR FILING DATE: 1997-03-03

PRIOR APPLICATION NUMBER: EP 96870021.1

PRIOR FILING DATE: 1996-03-01

PRIOR APPLICATION NUMBER: EP 96870102.9

PRIOR FILING DATE: 1996-08-06

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 215

TYPE: PRT

ORGANISM: Homo sapiens

US-10-612-791-6

Query Match 100.0%; Score 126; DB 16; Length 215;

Best Local Similarity 100.0%; Pred. No. 3.9e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFS 22

Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 13

US-10-612-791-18

Sequence 18, Application US/10612791

Publication No. US20040161739A1

GENERAL INFORMATION:

APPLICANT: Samson, Michael

APPLICANT: Parmentier, Marc

APPLICANT: Vassart, Gilbert

TITLE OF INVENTION: HIV Diagnostic Methods

FILE REFERENCE: 9409/2023E

CURRENT APPLICATION NUMBER: US/10/612,791

CURRENT FILING DATE: 2003-07-02

PRIOR APPLICATION NUMBER: 09/938,703

PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 09/626,939

PRIOR FILING DATE: 2000-07-27

PRIOR APPLICATION NUMBER: 08/833,752

PRIOR FILING DATE: 1997-04-09

PRIOR APPLICATION NUMBER: 08/810,028

PRIOR FILING DATE: 1997-03-03

PRIOR APPLICATION NUMBER: EP 96870021.1

PRIOR FILING DATE: 1996-03-01

PRIOR APPLICATION NUMBER: EP 96870102.9

PRIOR FILING DATE: 1996-08-06

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.1

SEQ ID NO 18

LENGTH: 215

TYPE: PRT

ORGANISM: Homo sapiens

US-10-612-791-18

Query Match 100.0%; Score 126; DB 16; Length 215;

Best Local Similarity 100.0%; Pred. No. 3.9e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFS 22

Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 14

US-10-095-876A-2

Sequence 2, Application US/10095876A

Publication No. US20030148294A1

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice; Bandman, Olga

APPLICANT: Coleman, Roger; Wilde, Craig G.

TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS

FILE REFERENCE: PF-0060-1 CON

CURRENT APPLICATION NUMBER: US/10/095,876A

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 08/638,081

PRIOR FILING DATE: 1996-04-26

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PERL Program

SEQ ID NO 2

LENGTH: 332

TYPE: PRT

LENGTH: 215

TYPE: PRT

ORGANISM: Homo sapiens

US-10-612-791-6

Query Match 100.0%; Score 126; DB 16; Length 215;

Best Local Similarity 100.0%; Pred. No. 3.9e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFS 22

Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 13

US-10-612-791-18

Sequence 18, Application US/10612791

Publication No. US20040161739A1

GENERAL INFORMATION:

APPLICANT: Samson, Michael

APPLICANT: Parmentier, Marc

APPLICANT: Vassart, Gilbert

TITLE OF INVENTION: HIV Diagnostic Methods

FILE REFERENCE: 9409/2023E

CURRENT APPLICATION NUMBER: US/10/612,791

CURRENT FILING DATE: 2003-07-02

PRIOR APPLICATION NUMBER: 09/938,703

PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 09/626,939

PRIOR FILING DATE: 2000-07-27

PRIOR APPLICATION NUMBER: 08/833,752

PRIOR FILING DATE: 1997-04-09

PRIOR APPLICATION NUMBER: 08/810,028

PRIOR FILING DATE: 1997-03-03

PRIOR APPLICATION NUMBER: EP 96870021.1

PRIOR FILING DATE: 1996-03-01

PRIOR APPLICATION NUMBER: EP 96870102.9

PRIOR FILING DATE: 1996-08-06

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.1

SEQ ID NO 18

LENGTH: 215

TYPE: PRT

ORGANISM: Homo sapiens

US-10-612-791-18

Query Match 100.0%; Score 126; DB 16; Length 215;

Best Local Similarity 100.0%; Pred. No. 3.9e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFS 22

Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 14

US-10-095-876A-2

Sequence 2, Application US/10095876A

Publication No. US20030148294A1

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice; Bandman, Olga

APPLICANT: Coleman, Roger; Wilde, Craig G.

TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS

FILE REFERENCE: PF-0060-1 CON

CURRENT APPLICATION NUMBER: US/10/095,876A

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 08/638,081

PRIOR FILING DATE: 1996-04-26

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PERL Program

SEQ ID NO 2

LENGTH: 332

TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2

Query Match 100.0%; Score 126; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 6e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
|||
DB 84 QWDFGNTMCQLLTGLYFIFGFFS 105
|||

RESULT 15
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
|||
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
|||

RESULT 16
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PCL0348PME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2

; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-841-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
|||
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
|||

RESULT 17
US-09-779-879A-2
; Sequence 2, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
|||
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
|||

RESULT 18
US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1489.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; LENGTH: 352

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-22

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 19
US-09-779-880A-2
; Sequence 2, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-2

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 20
US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens

; ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 21
US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 22
US-09-813-653-17
; Sequence 17, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-09-813-653-17

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 23

US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 24

US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGHR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 25

US-09-339-912A-2

; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGHR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 26

US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID-MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel B
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear


```

; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIIGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIIGFFS 114

RESULT 27
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92860
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIIGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIIGFFS 114

RESULT 28
US-09-938-703-5
; Sequence 5, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC

```

```

; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIIGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIIGFFS 114

RESULT 29
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. US20020132269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIIGFFS 22

```

DB 93 QWDFGNTMCQLLTGLTYFGFFS 114
|||||

RESULT 30

US-09-734-221A-14
; Sequence 14, Application US/09734221A
; Publication No. US20030096221A1
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; DENG, HONGKUI
; ELLMEIER, WILFRIED
; LANDAU, NATHANIEL R.
; LIU, RONG

TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/734,221A

FILING DATE: 11-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/666,020

FILING DATE: 19-JUN-1996

APPLICATION NUMBER: US 08/227,319

FILING DATE: 13-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1049-1-004 N2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-734-221A-14

Query Match 100.0%; Score 126; DB 10; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.3e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLTYFGFFS 22

DB 93 QWDFGNTMCQLLTGLTYFGFFS 114

RESULT 31

US-09-826-509-477

; Sequence 477, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: Patentin Version 2.1

; SEQ ID NO 477

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-826-509-477

Query Match 100.0%; Score 126; DB 11; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.3e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLTYFGFFS 22

DB 93 QWDFGNTMCQLLTGLTYFGFFS 114

RESULT 32

US-10-151-274-5

; Sequence 5, Application US/10151274

; Publication No. US20030064071A1

; GENERAL INFORMATION:

; APPLICANT: Littman, Dan R.

; APPLICANT: Kwon, Douglas S.

; APPLICANT: van Kooyk, Yvette

; APPLICANT: Geijtenbeek, Theo

; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

; TITLE OF INVENTION: INTO

; TITLE OF INVENTION: CELLS

; FILE REFERENCE: 1049-1-017

; CURRENT APPLICATION NUMBER: US/10/151,274

; CURRENT FILING DATE: 2002-05-20

; PRIOR APPLICATION NUMBER: US/09/517,605

; PRIOR FILING DATE: 2000-03-02

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 5

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-151-274-5

Query Match 100.0%; Score 126; DB 12; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.3e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLTYFGFFS 22

DB 93 QWDFGNTMCQLLTGLTYFGFFS 114

RESULT 33

US-10-106-623-2

; Sequence 2, Application US/10106623

; Publication No. US2002015088A1

; GENERAL INFORMATION:

; APPLICANT: Gray, Patrick W.

; APPLICANT: Schweickart, Vicky L.

; APPLICANT: Report, Carol J.

; TITLE OF INVENTION: Chemokine Receptor Materials and Methods

```
;/
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2

Query Match 100.0%; Score 126; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 34
US-10-106-623-20
; Sequence 20, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; SCHWEICKART, Vicky L.
; REPORT, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
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;/
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-106-623-20

Query Match 100.0%; Score 126; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 35
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCRS) HDGNE10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2

Query Match 100.0%; Score 126; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 36
US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
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; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-814-1

Query Match 100.0%; Score 126; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 37
US-10-067-800-2
; Sequence 2, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGHR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-2

Query Match 100.0%; Score 126; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 38
US-10-067-800-22
; Sequence 22, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGHR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-22

Query Match 100.0%; Score 126; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 39
US-10-290-058A-6
; Sequence 6, Application US/10290058A
; Publication No. US20030104455A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
; FILE REFERENCE: WPI01-289P1RM
; CURRENT APPLICATION NUMBER: US/10/290,058A
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/344,552
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-058A-6

Query Match 100.0%; Score 126; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 40
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-567A-352

Query Match      100.0%; Score 126; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QWDFGNTMCOLLTGLYFIGFFS 22
Db      93 QWDFGNTMCOLLTGLYFIGFFS 114

Search completed: September 28, 2004, 09:44:41
Job time : 74.875 secs
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:57:36 ; Search time 11.825 Seconds
(without alignments)
178.961 Million cell updates/sec

Title: US-10-084-813-12
Perfect score: 126
Sequence: 1 QWDFGNTMCOLLGLYFIQFFS 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:
1: Piri:
2: Piri2:
3: Piri3:
4: Piri4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126	100.0	352	A43113	chemokine (C-C) re
2	87	69.0	360	JC2443	chemokine (C-C) re
3	87	69.0	374	I38450	chemokine (C-C) re
4	82	65.1	355	JC5067	G protein-coupled
5	76	60.3	355	I49339	macrophage inflam
6	74	58.7	356	I49340	MIP-1 alpha recept
7	71	56.3	355	A45177	chemokine (C-C) re
8	70	55.6	359	I49341	MIP-1 alpha recept
9	67	53.2	355	G05436	chemokine (C-C) re
10	66	52.4	360	A57160	chemokine (C-C) re
11	65	51.6	344	JC5942	chemokine receptor
12	65	51.6	360	JC4587	chemokine (C-C) re
13	60	47.6	354	I59186	chemokine (C-C) re
14	59	46.8	369	JC5068	probable G protein
15	56	44.4	355	JC4304	G protein-coupled
16	55	43.7	383	S53594	orphan G protein-c
17	53.5	42.5	328	I38973	G protein-coupled
18	53	42.1	378	A55735	G protein-coupled
19	53	42.1	422	JC7080	G protein-coupled
20	52	41.3	378	A45680	melanin-concentrat
21	52	41.3	378	B55735	G protein-coupled
22	51	40.5	352	I27357	lymphocyte-specifi
23	50	39.7	350	JN0621	complement C5a ana
24	50	39.7	359	A48921	G protein-coupled
25	50	39.7	435	T37324	interleukin-8 rece
26	50	39.7	448	T16256	probable JNK-activ
27	49.5	39.3	359	I51372	hypothetical prote
28	49	38.9	354	B55733	angiotensin II rec
29	49	38.9	367	JE0349	G protein-coupled
					interferon-inducib

30	49	38.9	398	2	A57510	mu opiod receptor
31	49	38.9	425	2	A37512	thrombin receptor
32	49	38.9	427	2	S17148	alpha-thrombin rec
33	48.5	38.5	186	2	AG1086	hypothetical prote
34	48.5	38.5	706	2	A81848	probable TonB-depe
35	48	38.1	352	2	G00048	fusin (LESTRA) C
36	48	38.1	352	2	A45747	neuropeptide Y/pep
37	48	38.1	409	2	F5067	probable transport
38	48	38.1	409	2	F91091	probable transport
39	48	38.1	409	2	A85937	probable transport
40	48	38.1	420	2	I51667	thrombin receptor
41	48	38.1	482	2	S65766	G protein-coupled
42	48	38.1	937	2	T37241	olfactory channel
43	48	38.1	957	2	D88651	protein B0212.5 [i
44	47.5	37.7	370	2	J85549	heptahelical P2Y5-
45	47	37.3	334	2	JC4681	bradykinin B1 rece

ALIGNMENTS

RESULT 1

A43113
chemokine (C-C) receptor 5 - human
N:Alternate names: C-C CKR-5; CCR5
C:Species: Homo sapiens (man)
C:Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000
C:Accession: A43113; S71808; A58834; A58832; G02653; A58833
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A:Title: Molecular cloning and functional expression of a new human CC-chemokine recepto
A:Reference number: A43113; MUID:96241590; PMID:8639485
A:Accession: A43113
A:Molecule type: mRNA
A:Residues: 1-352 <SAM1>
A:Cross-references: GB:X91492; NID:gl262810; PIDN:CAA62796.1; PID:gl262811
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragost
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa
Nature 382, 722-725, 1996
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles (c
A:Reference number: S71808; MUID:96345670; PMID:8751444
A:Accession: S71808
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206; 207-230 <SAM2>
A:Accession: A58834
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184, 'IKDSLHGAPAAACHGILLGNPKNSASVSK' <SAM3>
A:Cross-references: GB:X93933; NID:gl524062; PIDN:CAA67767.1; PID:gl524063
A>Note: this frameshift mutation results in a non-functional receptor but confers a deg
nd may have had a selective advantage by conferring resistance to Yersinia plague infect
R:Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec
A:Reference number: A58832; MUID:96295970; PMID:8699119
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:gl502408; PIDN:AAB17071.1; PID:gl502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadiere, C.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89, 'L', 91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine
A:Reference number: A58833; MUID:96291862; PMID:8663314

A/Accession: A58833
 A/Molecule type: mRNA
 A/Residues: 1-352 <RAP>
 A/Cross-references: GB:U54994; NID:G1457945; PIDN:BA050598.1; PID:G1457946
 C/Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30575) and dual-tropic strains of HIV-1 bind to a complex of chemokine (see PIR:A30576) and dual-tropic strains of HIV-1 bind to a complex of chemokine (see PIR:A30577).
 C/Genetics:
 A/Gene: GDB:CMKBR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
 A/Cross-references: GDB:1230510; OMIM:601373
 A/Map position: 3p21-3p21
 C/Function:
 A/Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES.
 A/Note: Probably acts to control granulocyte proliferation and differentiation.
 C/Superfamily: vertebrate rhodopsin
 F/32-56/Domain: transmembrane #status predicted <TM1>
 F/37-87/Domain: transmembrane #status predicted <TM2>
 F/103-124/Domain: transmembrane #status predicted <TM3>
 F/142-166/Domain: transmembrane #status predicted <TM4>
 F/193-218/Domain: transmembrane #status predicted <TM5>
 F/236-257/Domain: transmembrane #status predicted <TM6>
 F/285-300/Domain: transmembrane #status predicted <TM7>
 F/20-269/Domain: transmembrane #status predicted
 F/268/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/336.337,342/Binding site: phosphate (Ser) (covalent) #status predicted
 F/340.343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.08; Score 126; DB 2; Length 352;
 Best Local Similarity 100.08; Pred. NO. 1.6e-11; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0

QY 1 QWDFGNTMCCQLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCCQLTGLYFIFGFFS 114

RESULT 2
 JC2443
 Chemokine (C-C) receptor 2, splice form B - human
 N/Alternate names: C-C CRK-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine receptor 1
 C/Species: Homo sapiens (man)
 C/Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
 C/Accession: JC2443; I38463
 R/Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
 A/Title: CDNA cloning and functional expression of a human monocyte chemoattractant protein 1
 A/Reference number: JC2443; MUID:94324942; PMID:8048929
 A/Accession: JC2443
 A/Molecule type: mRNA
 A/Residues: 1-360 <YAM>
 A/Cross-references: DBJ:J29584; NID:G531246; PIDN:BA06253.1; PID:G531247
 R/Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A/Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2
 A/Reference number: A53477; MUID:94195821; PMID:8146186
 A/Accession: I38463
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-360 <RES>
 A/Cross-references: EMBL:U03505; NID:G472557; PIDN:AAA19120.1; PID:G472558
 A/Map position: 3p21-3p21
 C/Superfamily: vertebrate rhodopsin
 F/41-70/Domain: transmembrane #status predicted <TM1>
 F/81-100/Domain: transmembrane #status predicted <TM2>
 F/115-136/Domain: transmembrane #status predicted <TM3>
 F/154-178/Domain: transmembrane #status predicted <TM4>
 F/207-226/Domain: transmembrane #status predicted <TM5>
 F/244-265/Domain: transmembrane #status predicted <TM6>
 F/287-309/Domain: transmembrane #status predicted <TM7>

F/14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/113-190/Disulfide bonds: #status predicted

Query Match 69.08; Score 87; DB 2; Length 360;
 Best Local Similarity 66.78; Pred. NO. 1.4e-05; Indels 0; Gaps 0;
 Matches 14; Conservative 3; Mismatches 4

QY 1 QWDFGNTMCCQLTGLYFIFGFF 21
 DB 105 EWVFGNACKLFTGLYHIGVF 125

RESULT 3

I38450
 Chemokine (C-C) receptor 2, splice form A - human
 N/Alternate names: C-C CRK-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine receptor 1
 C/Species: Homo sapiens (man)
 C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
 C/Accession: I38450
 R/Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A/Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2
 A/Reference number: A53477; MUID:94195821; PMID:8146186
 A/Accession: I38450
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-374 <RES>
 A/Cross-references: EMBL:U03882; NID:G472555; PIDN:AAA19119.1; PID:G472556
 C/Genetics:
 A/Gene: GDB:CMKBR2
 A/Map position: 3p21-3p21
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
 F/44-68/Domain: transmembrane #status predicted <TM1>
 F/79-99/Domain: transmembrane #status predicted <TM2>
 F/115-136/Domain: transmembrane #status predicted <TM3>
 F/154-178/Domain: transmembrane #status predicted <TM4>
 F/208-226/Domain: transmembrane #status predicted <TM5>
 F/244-265/Domain: transmembrane #status predicted <TM6>
 F/292-309/Domain: transmembrane #status predicted <TM7>
 F/14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/32-277,113-190/Disulfide bonds: #status predicted

Query Match 69.08; Score 87; DB 2; Length 374;
 Best Local Similarity 66.78; Pred. NO. 1.5e-05; Indels 0; Gaps 0;
 Matches 14; Conservative 3; Mismatches 4

QY 1 QWDFGNTMCCQLTGLYFIFGFF 21
 DB 105 EWVFGNACKLFTGLYHIGVF 125

RESULT 4

JC5067
 G protein-coupled receptor CRK-L1 - human
 N/Alternate names: chemokine receptor-like protein TER1; GPR-CY6
 C/Species: Homo sapiens (man)
 C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C/Accession: JC5067; G02776; G02387
 R/Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A/Title: Molecular cloning and RNA expression of two new human chemokine receptor-like 9
 A/Reference number: JC5067; MUID:97040707; PMID:8886020
 A/Accession: JC5067
 A/Molecule type: DNA
 A/Residues: 1-355 <ZAB>
 A/Cross-references: EMBL:Z79782; NID:G1668735; PIDN:CA02142.1; PID:G1668736
 R/Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
 submitted to the EMBL Data Library, June 1996
 A/Reference number: H01714
 A/Accession: G02776
 A/Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-355 <NAP>
 A:Cross-references: EMBL:U62556; NID:G1468978; PID:G1468979
 R:Bonner, T.I.
 submitted to the EMBL Data Library, January 1996
 A:Reference number: H01154
 A:Accession: G02387
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-355 <BON>
 A:Cross-references: EMBL:U45983; NID:G1245056; PID:G1245057
 C:Comment: This protein belongs to the family of beta chemokine receptors.

C:Genetics:
 A:Gene: GDB:CMKBR8; CMKBR2; TER1; CKR-L1
 A:Cross-references: GDB:6053733; OMIM:601834
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:36-63/Domain: transmembrane #status predicted <TM1>
 F:73-94/Domain: transmembrane #status predicted <TM2>
 F:108-129/Domain: transmembrane #status predicted <TM3>
 F:147-171/Domain: transmembrane #status predicted <TM4>
 F:200-222/Domain: transmembrane #status predicted <TM5>
 F:233-260/Domain: transmembrane #status predicted <TM6>
 F:281-304/Domain: transmembrane #status predicted <TM7>

Query Match 65.1%; Score 82; DB 2; Length 355;
 Best Local Similarity 54.5%; Pred. No. 7.9e-05;
 Matches 12; Conservative 6; Mismatches 4; Indels 0;

QY 1 QWDFGNTMCKLTLGLYFIFGFS 22
 DB 98 QWFGTVMCKVSGFYIIGLYS 119

RESULT 5

I49339
 macrophage inflammatory protein-1 alpha receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 A:Accession: I49339
 R:Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
 A:Reference number: I49339; MUID:95340546; PMID:7542241
 A:Accession: I49339
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-355 <RES>
 A:Cross-references: EMBL:U28404; NID:G881547; PIDN:AAA89153.1; PID:G881548
 C:Superfamily: vertebrate rhodopsin

Query Match 60.3%; Score 76; DB 2; Length 355;
 Best Local Similarity 52.4%; Pred. No. 0.00065;
 Matches 11; Conservative 6; Mismatches 4; Indels 0;

QY 2 WDFGNTMCKLTLGLYFIFGFS 22
 DB 99 WIFGDAMCKLLSGFYIIGLYS 119

RESULT 6

I49340
 MIP-1 alpha receptor like-1 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 A:Accession: I49340
 R:Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
 A:Reference number: I49339; MUID:95340546; PMID:7542241
 A:Accession: I49340
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-356 <RES>
 A:Cross-references: EMBL:U28405; NID:G881549; PIDN:AAA89154.1; PID:G881550
 C:Superfamily: vertebrate rhodopsin

Query Match 58.7%; Score 74; DB 2; Length 356;
 Best Local Similarity 47.6%; Pred. No. 0.0013;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 WDFGNTMCKLTLGLYFIFGFS 22
 DB 100 WIFGDAMCKFVSGFYIIGLYS 120

RESULT 7

A45177
 chemokine (C-C) receptor 1 - human
 N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 A:Accession: A45177; I55671
 R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
 Cell 72, 415-425, 1993
 A:Title: Molecular cloning, functional expression, and signaling characteristics of a C-
 A:Reference number: A45177; MUID:93161416; PMID:7679328
 A:Accession: A45177
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-355 <NEO>
 A:Cross-references: GB:L10918; NID:G292416; PIDN:AAA36543.1; PID:G292417
 A:Experimental source: HL60 cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:124876)
 R:Gao, J.

J. Exp. Med. 177, 1421-1427, 1993
 A:Title: Structure and functional expression of the human macrophage inflammatory 1 alp
 A:Reference number: I55671; MUID:93240122; PMID:7683036
 A:Accession: I55671

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-355 <RES>

A:Cross-references: GB:L10918; NID:G292416; PIDN:AAA36543.1; PID:G292417

C:Genetics:

A:Gene: GDB:CMKBR1; CMKR-1

A:Cross-references: GDB:1138446; OMIM:601159

A:Map position: 3p21-3p21

C:Superfamily: vertebrate rhodopsin

C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tr

F:36-60/Domain: transmembrane #status predicted <TM1>

F:71-91/Domain: transmembrane #status predicted <TM2>

F:108-129/Domain: transmembrane #status predicted <TM3>

F:147-171/Domain: transmembrane #status predicted <TM4>

F:205-223/Domain: transmembrane #status predicted <TM5>

F:240-264/Domain: transmembrane #status predicted <TM6>

F:288-305/Domain: transmembrane #status predicted <TM7>

F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:24-273,106-183/Disulfide bonds: #status predicted

F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 56.3%; Score 71; DB 2; Length 355;
 Best Local Similarity 47.6%; Pred. No. 0.0038;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 WDFGNTMCKLTLGLYFIFGFS 22
 DB 99 WIFGDAMCKILSGFYIIGLYS 119

RESULT 8

I49341
 MIP-1 alpha receptor like-2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
 A:Accession: I49341

R:Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
 A:Reference number: I49339; MUID:95340546; PMID:7542241
 A:Accession: I49341
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <RES>
 A:Cross-references: EMBL:U28406; NID:G881551; PID:G881552
 A:Superfamily: vertebrate rhodopsin

Query Match 55.6%; Score 70; DB 2; Length 359;
 Best Local Similarity 40.9%; Pred. NO. 0.0054;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFVIGFFS 22
 DB 102 EWGFHYNCKMLSGFYIALYS 123

RESULT 9
 G02436
 Chemokine (C-C) receptor 3 - human
 N:Alternate names: C-C CKR-3
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
 C:Accession: G02436; A57237
 R:Penh, P.D.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: H01272
 A:Accession: G02436
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-355 <PON>
 A:Cross-references: EMBL:U49727; NID:gl477560; PIDN:AAB09726.1; PID:gl477561
 R:Compadriere, C.; Ahuja, S.K.; Murphy, P.M.
 J. Biol. Chem. 270, 16491-16494, 1995
 A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
 A:Reference number: A57237; MUID:95348056; PMID:7622448
 A:Accession: A57237
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
 A:Cross-references: GB:U28694; NID:gl199579; PIDN:AAC50469.1; PID:gl199580
 A:Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.
 C:Genetics:
 A:Gene: GDB:CMKBR3
 A:Cross-references: GDB:579624; OMIM:601268
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F:36-60/Domain: transmembrane #status predicted <TM1>
 F:71-91/Domain: transmembrane #status predicted <TM2>
 F:108-129/Domain: transmembrane #status predicted <TM3>
 F:147-171/Domain: transmembrane #status predicted <TM4>
 F:205-223/Domain: transmembrane #status predicted <TM5>
 F:240-261/Domain: transmembrane #status predicted <TM6>
 F:288-305/Domain: transmembrane #status predicted <TM7>
 F:24-273,106-183/Disulfide bonds: #status predicted
 F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 53.2%; Score 67; DB 2; Length 355;
 Best Local Similarity 52.4%; Pred. NO. 0.015;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 WDFGNTMCLLTGLYFVIGFFS 22
 DB 99 WVFHGMCKLISGFVHTGLYS 119

RESULT 10
 A57160
 Chemokine (C-C) receptor 4 - human

N:Alternate names: C-C CKR-4
 C:Species: Homo sapiens (man)
 C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 A:Reference number: I49339; MUID:95340546; PMID:7542241
 A:Accession: A57160
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <RES>
 A:Cross-references: EMBL:U28406; NID:G881551; PID:G881552
 A:Superfamily: vertebrate rhodopsin

Query Match 52.4%; Score 66; DB 2; Length 360;
 Best Local Similarity 40.9%; Pred. NO. 0.022; 5; Indels 0; Gaps 0;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFVIGFFS 22
 DB 102 QWVFLGLCKMISWYLVGFYS 123

RESULT 11
 JCS942
 Chemokine receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: JCS942
 R:Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
 Biochem. Biophys. Res. Commun. 243, 264-268, 1998
 A:Title: Cloning and characterization of a novel human chemokine receptor.
 A:Reference number: JCS942; MUID:98139902; PMID:9473515
 A:Accession: JCS942
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-344 <PAN>
 A:Cross-references: GB:U97123; NID:G2897070; PIDN:AAC39595.1; PID:G2897071
 C:Superfamily: vertebrate rhodopsin

Query Match 51.8%; Score 65; DB 2; Length 344;
 Best Local Similarity 55.6%; Pred. NO. 0.03;
 Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 GNTMCLLTGLYFVIGFFS 22
 DB 99 GDPVCKILIGLVFVGLYS 116

RESULT 12
 JC4587
 Chemokine (C-C) receptor 4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000

C;Accession: JC4587
R;Hogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CCR-4 and high affinity binding of chemokines to
A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Accession: JC4587
A;Molecule type: mRNA
A;Residues: 1-360 <HOO>
A;Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ccr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 51.6%; Score 65; DB 2; Length 360;
Best Local Similarity 40.9%; Pred. No. 0.031;
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 QWDFGNTMQLLTGLYFIFGFFS 22
DB 102 QWVFLGLCKIVSMYLVGFYS 123
||| |:::|:|:|

RESULT 13
I58186
Probable G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C;Accession: I58186
R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and b
A;Reference number: I58186; MUID:94323113; PMID:8047298
A;Accession: I58186
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>
A;Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 47.6%; Score 60; DB 2; Length 354;
Best Local Similarity 62.5%; Pred. No. 0.18;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 NTWCQLLTGLYFIFGFF 21
DB 100 NAMCKLTATFAFFIGFF 115
||| |:::|:|:|

RESULT 14
JC5068
G protein-coupled receptor CXR-L3 - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C;Accession: JC5068
R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like g
A;Reference number: JC5067; MUID:97040707; PMID:8886020
A;Accession: JC5068
A;Molecule type: DNA
A;Residues: 1-369 <ZAB>
A;Cross-references: EMBL:Z79784; NID:g1668737; PIDN:CAB02144.1; PID:g1668738
C;Comment: This protein belongs to the family of alpha chemokine receptors.
C;Genetics:
A;Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CXR-L3; GPR-CY4
A;Cross-references: GDB:5370639; OMIM:601835

A;Map position: 6q27-6q27
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;42-68/Domain: transmembrane #status predicted <TM1>
F;79-99/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;160-180/Domain: transmembrane #status predicted <TM4>
F;212-233/Domain: transmembrane #status predicted <TM5>
F;250-271/Domain: transmembrane #status predicted <TM6>
F;292-315/Domain: transmembrane #status predicted <TM7>

Query Match 46.8%; Score 59; DB 2; Length 369;
Best Local Similarity 52.6%; Pred. No. 0.26;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 WDFGNTMQLLTGLYFIFGFF 20
DB 106 WVFSNATCKLLKGIYAINF 124
||| |:::|:|:|

RESULT 15
JC4304
orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C;Accession: JC4304
R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to g
A;Reference number: JC4304; MUID:96011651; PMID:7590284
A;Accession: JC4304
A;Molecule type: mRNA
A;Residues: 1-355 <RAP>
A;Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signal
C;Genetics:
A;Gene: V28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;275-296/Domain: transmembrane #status predicted <TM7>

Query Match 44.4%; Score 56; DB 2; Length 355;
Best Local Similarity 56.2%; Pred. No. 0.72;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 NTWCQLLTGLYFIFGFF 21
DB 99 NAMCKTATFAFFIGFF 114
||| |:::|:|:|

RESULT 16
S55594
G protein-coupled receptor E1 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C;Accession: S55594
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: the DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55594
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA

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A;Residues: 1-383 <TEL>
A;Cross-references: GB:U20824; NID:9695172; PIDN:AA13788.1; PID:9695173
A;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 43.7%; Score 55; DB 2; Length 383;
Best Local Similarity 38.1%; Pred. No. 1.1;
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 2 WDFGNTWCQLLTGLYFIFGFFS 22
Db 138 WTFGSLCKLGRVCYMSLYS 158

RESULT 17
I38973
G protein-coupled receptor 7 - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1995 #sequence_revision 24-May-1996 #text_change 21-Jul-2000
C;Accession: I38973
R;O'Dowd, B.F.; Scheideler, M.A.; Nguyen, T.; Cheng, R.; Rasmussen, J.S.; Zastawny, R.;
Genomics 28, 84-91, 1995
A;Title: The cloning and chromosomal mapping of two novel human opicoid-somatostatin-like
A;Reference number: A57647; MUID:96070436; PMID:7590751
A;Accession: I38973
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-328 <RES>
A;Cross-references: EMBL:U22491; NID:9553232; PIDN:AA150197.1; PID:9553233
C;Genetics:
A;Gene: GDB:GPR7
A;Cross-references: GDB:371714; OMIM:600730
A;Map position: 10q11.2-10q21.1
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 42.5%; Score 53.5; DB 2; Length 328;
Best Local Similarity 35.5%; Pred. No. 1.6;
Matches 11; Conservative 4; Mismatches 7; Indels 9; Gaps 1;

QY 1 QWDFGNTWCQLTGLYFIFGFFS 22
Db 101 QWPFGLCKLIVADQNTFSSLYFLTVMS 131

RESULT 18
A55735
G protein-coupled receptor EB11 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C;Accession: A55735
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.;
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: A55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:L31580; NID:9468340; PIDN:AAA74232.1; PID:9468341
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 42.1%; Score 53; DB 2; Length 378;
Best Local Similarity 42.9%; Pred. No. 2.2;
Matches 9; Conservative 5; Mismatches 7; Indels 7; Gaps 0;

QY 2 WDFGNTWCQLLTGLYFIFGFFS 22
Db 122 WIFGVLCCKGIFGIYKUSFFS 142

RESULT 19
A5735
Lymphocyte-specific G protein-coupled receptor EB11 - human
A;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: B55735; S52443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.;
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: B55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:L31581; NID:9468319; PIDN:AAA74231.1; PID:9468320
R;Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995

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JC7080
melanin-concentrating hormone receptor [validated] - human
A;Alternate names: MCHR; orphan somatostatin-like receptor 1 (SLC-1)
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: JC7080
R;Shimomura, Y.; Mori, M.; Sugo, T.; Ishibashi, Y.; Abe, M.; Kurokawa, T.; Onda, H.; Nis
Biochem. Biophys. Res. Commun. 261, 622-626, 1999
A;Title: Isolation and identification of melanin-concentrating hormone as the endogenous
A;Reference number: JC7080; MUID:99373129; PMID:10441476
A;Accession: JC7080
A;Molecule type: mRNA
A;Residues: 1-422 <SHI>
A;Note: It is uncertain whether Met-1, Met-6 or Met-70 is the initiation codon
C;Superfamily: neurokinin 1 receptor
C;Keywords: hormone receptor; transmembrane protein

Query Match 42.1%; Score 53; DB 2; Length 422;
Best Local Similarity 57.1%; Pred. No. 2.5;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 WDFGNTWCQLLTGL 15
Db 178 WHFGTCTLTITAM 191

RESULT 20
A45680
G protein-coupled peptide receptor EBI 1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A45680
R;Birkenbach, M.; Josefsen, K.; Valamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p
A;Reference number: A45680; MUID:93188173; PMID:8363238
A;Accession: A45680
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-378 <BIR>
A;Cross-references: GB:L08176; NID:gi833484; PID:gi833485
A;Experimental source: B-lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBI:127094, NCBI:127095)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 41.3%; Score 52; DB 2; Length 378;
Best Local Similarity 42.9%; Pred. No. 3.1;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 WDFGNTWCQLLTGLYFIFGFFS 22
Db 122 WIFGVHFCFLIFAIYKUSFFS 142

RESULT 21
B55735
Lymphocyte-specific G protein-coupled receptor EB11 - human
A;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: B55735; S52443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.;
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: B55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:L31581; NID:9468319; PIDN:AAA74231.1; PID:9468320
R;Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995

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A;Description: The expression of the chemokine receptor BLR2/EB11 is specifically transcribed in the brain.
 A;Reference number: S52443
 A;Accession: S52443
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 21-378

 A;Cross-references: EMBL:X84702
 C;Genetics:
 A;Gene: GDB:CMKBR7; EB11; BLR2; CCR7
 A;Cross-references: GDB:342065; OMIM:600242
 A;Map position: 17q12-17q21.2
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor

Query Match 41.3%; Score 52; DB 2; Length 378;
 Best Local Similarity 42.9%; Pred. No. 3.1;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 WDFGNTWCOLLTGLYFIFGFS 22
 Db 122 WVFQVHFCKLIFAIYKMSFFS 142

RESULT 22
 S27357
 Complement C5a anaphylatoxin receptor - dog
 C;Species: Canis lupus familiaris (dog)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: S27357
 R;Perret, J.J.; Raspe, E.; Vassart, G.; Parmentier, M.
 Biochem. J. 288, 911-917, 1992
 A;Title: Cloning and functional expression of the canine anaphylatoxin C5a receptor. Evidences for a G protein-coupled receptor.
 A;Reference number: S27357; MUID:93111969; PMID:1472004
 A;Accession: S27357
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-352 <PER>
 A;Cross-references: EMBL:X65860; NID:g878; PIDN:CAA46690.1; PID:g879
 C;Function:
 A;Description: mediates the inflammatory and chemotactic responses of polymorphonuclear neutrophils

C;Superfamily: vertebrate rhodopsin
 C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorphism
 F;1-38/Domain: extracellular #status predicted <EX1>
 F;39-62/Domain: transmembrane #status predicted <TM1>
 F;63-72/Domain: intracellular #status predicted <IN1>
 F;73-95/Domain: transmembrane #status predicted <TM2>
 F;96-111/Domain: extracellular #status predicted <EX2>
 F;112-133/Domain: transmembrane #status predicted <TM3>
 F;134-150/Domain: intracellular #status predicted <IN2>
 F;151-175/Domain: transmembrane #status predicted <TM4>
 F;176-208/Domain: extracellular #status predicted <EX3>
 F;209-229/Domain: transmembrane #status predicted <TM5>
 F;230-244/Domain: intracellular #status predicted <IN3>
 F;245-266/Domain: transmembrane #status predicted <TM6>
 F;267-285/Domain: extracellular #status predicted <EX4>
 F;286-309/Domain: transmembrane #status predicted <TM7>
 F;310-352/Domain: intracellular #status predicted <IN4>
 F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.5%; Score 51; DB 1; Length 352;
 Best Local Similarity 33.3%; Pred. No. 4.1;
 Matches 7; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 WDFGNTWCOLLTGLYFIFGFS 22
 Db 103 WFGNAACRLPSLLNNYA 123

RESULT 23
 JN0621
 G protein-coupled receptor type B - bovine
 C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
 C;Accession: JN0621
 R;Matsumoto, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
 Biochem. Biophys. Res. Commun. 194, 504-511, 1993
 A;Title: Identification of novel members of G-protein coupled receptor superfamily expressed in the brain.
 A;Reference number: JN0621; MUID:93326166; PMID:8392843
 A;Accession: JN0621
 A;Molecule type: mRNA
 A;Residues: 1-350 <MAT>
 A;Cross-references: GB:S63848; NID:g399710; PIDN:AAB27547.1; PID:g399711
 A;Experimental source: tongue taste papillae
 C;Comment: This protein is involved in modulating taste sensitivity or regeneration of taste buds.
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
 F;42-66/Domain: transmembrane #status predicted <TM1>
 F;67-99/Domain: transmembrane #status predicted <TM2>
 F;114-135/Domain: transmembrane #status predicted <TM3>
 F;154-175/Domain: transmembrane #status predicted <TM4>
 F;200-222/Domain: transmembrane #status predicted <TM5>
 F;242-265/Domain: transmembrane #status predicted <TM6>
 F;284-306/Domain: transmembrane #status predicted <TM7>
 F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.7%; Score 50; DB 2; Length 350;
 Best Local Similarity 38.1%; Pred. No. 5.8;
 Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 WDFGNTWCOLLTGLYFIFGFS 22
 Db 105 WVLGKIMCKVTSALYTNFVS 125

RESULT 24
 A48921
 Interleukin-8 receptor type B - mouse
 N;Alternate names: G-protein coupled receptor GPCR16
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
 C;Accession: A48921; A53677; I49348; I55421; H48909; I53774
 R;Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert, Genomics 18, 410-413, 1993
 A;Title: The murine homologue of the human interleukin-8 receptor type B maps near the IL-8 gene.
 A;Reference number: A48921; MUID:94117014; PMID:8288247
 A;Accession: A48921
 A;Molecule type: DNA
 A;Residues: 1-359 <CER>
 A;Cross-references: GB:L23637; NID:g435093; PIDN:AAA39305.1; PID:g435094
 R;Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
 J. Biol. Chem. 269, 18263-18266, 1994
 A;Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding to the IL-8 protein.
 A;Reference number: A53677; MUID:94308043; PMID:7518426
 A;Accession: A53677
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-359 <SUZ>
 A;Cross-references: GB:L26549
 A;Note: sequence extracted from NCBI backbone (NCBI:149812)
 R;Lee, J.; Cacciano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
 J. Immunol. 155, 2159-2164, 1995
 A;Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
 A;Reference number: I49348; MUID:95363183; PMID:7636264
 A;Accession: I49348
 A;Status: preliminary; translated from GB/EMBL/DBSJ
 A;Molecule type: DNA
 A;Residues: 1-359 <RES>
 A;Cross-references: EMBL:U31207; NID:g950174; PIDN:AAC52239.1; PID:g950175
 R;Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
 J. Biol. Chem. 269, 29355-29358, 1994
 A;Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression of the murine interleukin 8 type B receptor homologue and its ligands. Expression of the murine interleukin 8 type B receptor homologue and its ligands.
 A;Reference number: I55421; MUID:95050766; PMID:7961509
 A;Accession: I55421
 A;Status: preliminary; translated from GB/EMBL/DBSJ
 A;Molecule type: DNA

A:Residues: 1-359 <RE2>
A:Cross-references: GB:IL1239; NID:g293665; PIDN:AAA62109.1; PTD:g293666
R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.
Genomics 18, 175-184, 1993
A:Title: Identification, chromosomal location, and genome organization of mammalian G-protein coupled receptor 18
A:Reference number: A48909; MUID:94116980; PMID:8288218
A:Accession: H48909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 145-258 <WL>
A:Cross-references: GB:IL20337; NID:9439800; PIDN:AAA16853.1; PTD:9438801
R:Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
Gene 142, 297-300, 1994
A:Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
A:Reference number: IS3774; MUID:94252584; PMID:8194768
A:Accession: IS3774
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <RE3>
A:Cross-references: GB:DL17630; NID:9493671; PIDN:BAA04536.1; PTD:9493672
C:Genetics:
A:Gene: IL8xb
A:Introns: #status absent
A:Superfamily: G protein-coupled receptor; glycoprotein; transmembrane protein
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:49-74/Domain: transmembrane #status predicted <M1>
F:74-106/Domain: transmembrane #status predicted <M2>
F:120-141/Domain: transmembrane #status predicted <M3>
F:163-182/Domain: transmembrane #status predicted <M4>
F:213-234/Domain: transmembrane #status predicted <M5>
F:251-271/Domain: transmembrane #status predicted <M6>
F:308-328/Domain: transmembrane #status predicted <M7>

Query Match 39.7%; Score 50; DB 2; Length 359;
Best Local Similarity 33.3%; Pred. No. 6;
Matches 7; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 WDFGNMTCQLLTGLYFIFGFS 22
DB 111 WTFGSTLCKIFSVKVEFTFS 131

RESULT 25
T37324
C:Probable JNK-activating protein kinase (EC 2.7.1.-) JNK-1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T37324
R:Kawasaki, M.; Hisamoto, N.; Iino, Y.; Yamamoto, M.; Ninomiya-Tsuji, J.; Matsumoto, K.
EMBO J. 18, 3604-3615, 1999
A:Title: A Caenorhabditis elegans JNK signal transduction pathway regulates coordinated
A:Reference number: Z21686; MUID:99321749; PMID:10393177
A:Accession: T37324
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-435 <KAW>
A:Cross-references: EMBL:AB024086; NID:g5668698; PIDN:BAA82641.1; PTD:g5668699
C:Genetics:
A:Gene: jnk-1
C:Function:
A:Description: activation of JNK-1
A:Pathway: JNK signaling pathway
A:Note: JNK pathway functions in type-D GABAergic motor neurons and thereby modulates co
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; signal transduction

Query Match 39.7%; Score 50; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 7.3;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 WDFGNMTCQLLTGLY 16
DB 307 WSLGIVTVLVITGLY 321

Query Match 39.3%; Score 49.5; DB 2; Length 359;
 Best Local Similarity 50.0%; Pred. No. 7.1;
 Matches 9; Conservative 4; Mismatches 1; Gaps 1;

QY 1 QWDFGNTWCQLLT-GLYF 17
 DB 93 QWPGNCLCKLASAGISF 110

RESULT 28
 B55733
 G protein-coupled receptor GPR2 - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 26-Aug-1999
 C:Accession: B55733
 R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, H.H.Q.; Tsui, I.
 Genomics 23, 609-618, 1994
 A:Title: Cloning of human genes encoding novel G protein-coupled receptors.
 A:Reference number: A55733; MUID:95154831; PMID:7851889
 A:Accession: B55733
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-354 <MAR>
 A:Cross-references: GB:U13667
 C:Genetics:
 A:Gene: GDB:GPR2
 A:Cross-references: GDB:371708; OMIM:600240
 A:Map position: 17q21.1-17q21.3
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor

Query Match 38.9%; Score 49; DB 2; Length 354;
 Best Local Similarity 36.8%; Pred. No. 8.4;
 Matches 7; Conservative 4; Mismatches 0; Gaps 0;

QY 2 WDFGNTWCQLLTGLYFIFGF 20
 DB 98 WSLGSATCRTISGLYSASF 116

RESULT 29
 JE0349
 interferon-inducible protein 10 (IP-10) receptor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
 C:Accession: JE0349
 R:Tamaru, M.; Tomimaga, Y.; Yatsunami, K.; Narumi, S.
 Biochem. Biophys. Res. Commun. 251, 41-48, 1998
 A:Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its
 A:Reference number: JE0349; MUID:99009219; PMID:9790904
 A:Accession: JE0349
 A:Molecule type: mRNA
 A:Residues: 1-367 <TAM>
 A:Cross-references: DDBJ:AB003174; NID:g3798731; PIDN:BAA34045.1; PID:g3798732
 C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
 C:Superfamily: vertebrate rhodopsin

Query Match 38.9%; Score 49; DB 2; Length 367;
 Best Local Similarity 36.4%; Pred. No. 8.7;
 Matches 8; Conservative 6; Mismatches 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGF 22
 DB 115 QWVFGPLCKVGAUFNIFYA 136

RESULT 30
 A57510
 mu opioid receptor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999
 C:Accession: A57510; I48665; S66513; I49300
 R:Kaufman, D.L.; Keith Jr., D.E.; Anton, B.; Tian, J.; Magendzo, K.; Newman, D.; Tran, T.

J. Biol. Chem. 270, 15877-15883, 1995
 A:Title: Characterization of the murine mu opioid receptor gene.
 A:Reference number: A57510; MUID:95318184; PMID:7797593
 A:Accession: A57510
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-398 <KAU>
 A:Cross-references: GB:U19380
 R:Min, B.H.; Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.; Loh, H.H.
 Proc. Natl. Acad. Sci. U.S.A. 91, 9081-9085, 1994
 A:Title: Genomic structure analysis of promoter sequence of a mouse mu opioid receptor y
 A:Reference number: I48665; MUID:94377496; PMID:8090773
 A:Accession: I48665
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-398 <RES>
 A:Cross-references: EMBL:U10561; NID:9555696; PIDN:AAB60673.1; PID:9565069
 R:Rossi, G.C.; Pan, Y.X.; Brown, G.P.; Pasternak, G.W.
 FEBS Lett. 369, 192-196, 1995
 A:Title: Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing
 A:Reference number: I49300; MUID:95377399; PMID:7649256
 A:Accession: S66513
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-398 <ROS>
 A:Cross-references: EMBL:U26915; NID:g1055230; PIDN:AAA81170.1; PID:g1055231
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
 C:Genetics:
 A:Gene: MOR-1
 A:Introns: 95/2; 213/1; 386/3
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran

Query Match 38.9%; Score 49; DB 2; Length 398;
 Best Local Similarity 28.6%; Pred. No. 9.5;
 Matches 6; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 WDFGNTWCQLLTGLYFIFGF 22
 DB 133 WPGNLCIKVISIDYNNFT 153

RESULT 31
 A37912
 thrombin receptor precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
 C:Accession: A37912
 R:Vu, T.K.H.; Hung, D.T.; Wheaton, V.I.; Coughlin, S.R.
 Cell 64, 1057-1068, 1991
 A:Title: Molecular cloning of a functional thrombin receptor reveals a novel proteolytic
 A:Reference number: A37912; MUID:91168254; PMID:1672265
 A:Accession: A37912
 A:Molecule type: mRNA
 A:Residues: 1-425 <VUA>
 A:Cross-references: GB:M62424; NID:g339676; PIDN:AAA36743.1; PID:g339677
 C:Genetics:
 A:Gene: GDB:F2R
 A:Cross-references: GDB:I127737; OMIM:187930
 A:Map position: 5q13-5q13
 C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-425/Product: thrombin receptor #status predicted <MAT>

Query Match 38.9%; Score 49; DB 2; Length 425;
 Best Local Similarity 23.8%; Pred. No. 10;
 Matches 5; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 WDFGNTWCQLLTGLYFIFGF 22
 DB 168 WQFGSELRFVTAFCNNYA 188

A:Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PID:CA884785.1; PID:g7380101
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1558

Query Match 38.5%; Score 48.5; DB 2; Length 706;
Best Local Similarity 54.5%; Pred. No. 20;
Matches 12; Conservative 1; Mismatches 2; Indels 7; Gaps 2;

QY 2 WDFG---NTMCOLLTGLYFIFGF 20
||| ||| ||| ||| ||| |||
DB 41 WQFGESNT----LTGLYFRGY 58

RESULT 35
G00048
fusin (LESTRA) - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 26-Aug-1999
C:Accession: G00048
R:Tatsumi, M.
submitted to GenBank, July 1996
A:Reference number: H00048
A:Accession: G00048
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <TAR>
A:Cross-references: GB:D86579; NID:g1468948; PID:g1468949
C:Superfamily: vertebrate rhodopsin

Query Match 38.1%; Score 48; DB 2; Length 352;
Best Local Similarity 33.3%; Pred. No. 12;
Matches 7; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 WDFGNTMCOLLTGLYFIFGF 22
||| ||| ||| ||| ||| |||
DB 102 WYFGNPLCKAVHVIYTVNLVS 122

RESULT 36
A45747
neuropeptide Y/peptide YY receptor Y3 - human
N:Alternate names: fusin; RM89; leukocyte-derived seven-transmembrane receptor LESTR; re
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: A45747; A53103; I53006; I59444; I69203; S32761
R:Pederspiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewis
Genomics 16, 707-712, 1993
A:Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a pu
A:Reference number: A45747; MUID:93315164; PMID:8325644
A:Accession: A45747
A:Molecule type: mRNA
A:Residues: 1-352 <FED>
A:Cross-references: GB:M99293; NID:g292516; PID:AAA16617.1; PID:g292517
R:Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; Moser, B.
J. Biol. Chem. 269, 232-237, 1994
A:Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly e
A:Reference number: A53103; MUID:94103215; PMID:8276799
A:Accession: A53103
A:Molecule type: mRNA
A:Residues: 1-352 <LOE>
A:Cross-references: EMBL:X71635; NID:g297099; PID:CAA50641.1; PID:g297100
R:Herzog, H.; Hort, Y.J.; Shine, J.; Seibie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A:Title: Molecular cloning, characterization, and localization of the human homolog to t
A:Reference number: I53006; MUID:93319629; PMID:8329116
A:Accession: I53006
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <HER>
A:Cross-references: GB:L06797; NID:g414929; PID:AAA03209.1; PID:g414928
R:Jazini, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Walker, M.W.; Salton, J.; Lar
Regul. Pept. 47, 247-258, 1993

alpha-thrombin receptor - Chinese hamster
C:Species: Cricetus griseus (Chinese hamster)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S17148
R:Rasmussen, U.B.; Vouret-Craviari, V.; Jallat, S.; Schlesinger, Y.; Pages, G.; Pavirani
FEBS Lett. 288, 123-128, 1991
A:Title: cDNA cloning and expression of a hamster alpha-thrombin receptor coupled to Ca
A:Reference number: S17148; MUID:91348247; PMID:1652467
A:Accession: S17148
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-427 <RAS>
A:Cross-references: EMBL:X61958; NID:g940495; PID:CAA43957.1; PID:g49538
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 38.9%; Score 49; DB 2; Length 427;
Best Local Similarity 28.6%; Pred. No. 10;
Matches 6; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 WDFGNTMCOLLTGLYFIFGF 22
||| ||| ||| ||| ||| |||
DB 170 WQFGSCMCRFAATAFYCNYYA 190

RESULT 37
AG1086
hypothetical protein lmo0094 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AG1086
R:Glaser, P.; Francoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Trier, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1086
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-186 <GLA>
A:Cross-references: GB:NC_003210; PID:CA98309.1; PID:g16409453; GSPDB:GM00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0094

Query Match 38.5%; Score 48.5; DB 2; Length 186;
Best Local Similarity 45.5%; Pred. No. 5.1;
Matches 10; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

QY 6 NTMCQ-----LTLTGLYFIFGF 22
||| ||| ||| ||| ||| |||
DB 115 NEMIQLAGLLITALYFVGYYFA 136

RESULT 38
A81848
probable TonB-dependent receptor protein NMA1558 [imported] - Neisseria meningitidis (st
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81848
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: AB1775; MUID:20222556; PMID:10761919
A:Accession: A81848
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-706 <PAR>

A;Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homoid.
A;Reference number: I59444; MUID:94052833; PMID:8234909
A;Accession: I59444
A;Status: preliminary; translated from GE/EMBL/DBDU
A;Molecule type: mRNA
A;Residues: 1-352 <RE2>

A;Cross-references: GB:L01639; NID:G189313; PIDN:AAA15594.1; PID:G189314
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A;Title: Molecular cloning of cDNAs encoding a Ld78 receptor and putative leukocyte chemokine
A;Reference number: 154751; MUID:94092629; PMID:7505609
A;Accession: I69203
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-352 <RES>
A;Cross-references: GB:D10924; NID:G219868; PIDN:AAA01722.1; PID:G219869

C;genetics:
A;Gene: GDB:NPY3R; NPYX3
A;cross-references: GDB:230002; OMIM:163643
A;Map position: 2q21-2q21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

	Query Match	38.1%	Score 48;	DB 2;	Length 352;
	Best Local Similarity	33.3%;	Pred. No. 12;		
	Matches	7;	Conservative	6;	Mismatches 8; Indels 0; Gaps 0;
QY	2	WDFGNTMCQLLTGLYPIGFPS	22		
Db	102	WYFGNPLCKXAVHVIYTNLYS	122		

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RESULT 37
F65067
C:Probable transporter protein b2845 [similarity] - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: F65067

```

R. Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, D.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997

Article: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: F65067

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-409 <BLAT>

A:Cross-references: GB:AE000368; GB:U00096; NID:92367165; PIDN:AACT5884.1; PID:gl789211;

A:Experimental source: strain K-12, substrain MG1655

A:Superfamily: threonine-serine permease

Tue Sep 28 15:49:55 2004

us-10-084-813-12.rpr

Page 12

Job time : 13.075 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:55:11 ; Search time 6.875 Seconds
(without alignments)
166.624 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFGNVTCQLLGLYFIFGFFS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	352	1	CKR5_CERAE
2	126	100.0	352	1	CKR5_CERP
3	126	100.0	352	1	CKR5_CERTO
4	126	100.0	352	1	CKR5_GORGO
5	126	100.0	352	1	CKR5_HUMAN
6	126	100.0	352	1	CKR5_HYLE
7	126	100.0	352	1	CKR5_HYLM
8	126	100.0	352	1	CKR5_HYLSY
9	126	100.0	352	1	CKR5_MACMU
10	126	100.0	352	1	CKR5_PANTR
11	126	100.0	352	1	CKR5_PAPHA
12	126	100.0	352	1	CKR5_PONPY
13	126	100.0	352	1	CKR5_PYGBI
14	126	100.0	352	1	CKR5_PYGNE
15	126	100.0	352	1	CKR5_TRAFR
16	126	100.0	352	1	CKR5_TRAPH
17	89	70.6	353	1	CKR8_MOUSE
18	87	69.0	374	1	CKR2_HUMAN
19	86	68.3	373	1	CKR2_RAT
20	84	66.7	354	1	CKR5_RAT
21	83	65.9	289	1	VC03_SPVKA
22	83	65.9	370	1	VK02_SPVKA
23	83	65.9	373	1	CKR2_MOUSE
24	82	65.1	355	1	CKR8_HUMAN
25	82	65.1	356	1	CKR8_MACMU
26	81	64.3	360	1	CKR2_MOUSE
27	80	63.5	354	1	CKR5_MOUSE
28	79	62.7	358	1	CKR1_CAVPO
29	76	60.3	355	1	CKR1_MOUSE
30	75	59.5	359	1	CKR3_RAT
31	74	58.7	356	1	CKR1_MOUSE
32	71	56.3	355	1	CKR1_HUMAN
33	71	56.3	355	1	CKR1_MACMU

34	70	55.6	359	1	CKR3_MOUSE
35	67	53.2	355	1	CKR3_HUMAN
36	66	52.4	342	1	CKR6_CERAE
37	66	52.4	360	1	CKR4_HUMAN
38	65	51.6	342	1	CKR6_HUMAN
39	65	51.6	342	1	CKR6_MACNE
40	65	51.6	342	1	CKR6_PANTR
41	65	51.6	343	1	CKR6_PACPA
42	65	51.6	343	1	CKR6_VACMU
43	65	51.6	360	1	CKR4_MOUSE
44	61	48.4	381	1	VQ3L_CAPVK
45	60	47.6	354	1	CX31_MOUSE

ALIGNMENTS

RESULT 1

CKR5_CERAE

ID CKR5_CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RC MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses";
RL J. Virol. 71:8642-8656(1997).

SEQUENCE FROM N.A.

RN [2]
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
gene";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announcement/>
or send an email to license@isb-sib.ch).

EMBL; U83324; AAC51795.1; -;
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EMBL; AB015944; BAA31328.1; -;
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PROSITE; PS00237; G PROTEIN RECEPTOR; 1.
PROSITE; PS00262; G PROTEIN RECEPTOR; 2.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
Polymorphism.
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 FT TRANSMEM 7737 7754 425 (POTENTIAL).
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 FT DOMAIN 8331 8348 458 (POTENTIAL).
 FT TRANSMEM 8349 8366 459

increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 DR EMBL; AF051905; AAC39833.1; -
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 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
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 FT VARIANT 146 146 26 (POTENTIAL).
 FT VARIANT 340 340 27 (POTENTIAL).
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QY 1 QWDFGNTMCQLLTGLYFIGPFS 22
 DB 93 QWDFGNTMCQLLTGLYFIGPFS 114

RESULT 4
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 DT 15-JUL-1998 (Rel. 36, Last sequence update)
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 RP MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharron M., Sanson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RA "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by

CC-chemokine receptor gene.";
RL Biochemistry 35:3362-3367(1996).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=96291862; PubMed=8663314;
RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
RT "Molecular cloning and functional characterization of a novel human
CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";
RL J. Biol. Chem. 271:17161-17166(1996).
[3]
SEQUENCE FROM N.A.
RX MEDLINE=96295970; PubMed=8699119;
RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
RT "Cloning and functional expression of CC CKR5, a human monocyte CC
chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RANTES.";
RL J. Leukoc. Biol. 60:147-152(1996).
[4]
SEQUENCE FROM N.A.
RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gao J., La Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinski K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
[6]
SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
[7]
SEQUENCE FROM N.A.
RX MEDLINE=98049523; PubMed=9388201;
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
with 5' end heterogeneity, dual promoter usage, and evidence for
RT polymorphisms within the regulatory regions and noncoding exons.";
RL J. Biol. Chem. 272:30662-30671(1997).
[8]
SEQUENCE FROM N.A., AND VARIANT ARG-178.
RX Magierowska M., Barre-Sinoussi F., Issatras H., Theodorou I.,
RA Debre P.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[9]
SEQUENCE FROM N.A.
RX Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
[10]
CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96260017; PubMed=8649511;
RA Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
RA di Marzio P., Broder C., Spector R.E., Hill C.M., Davis C.B.,
RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
RT "Identification of a major co-receptor for primary isolates of
RT HIV-1.";
RL Nature 381:661-666(1996).
[11]
CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96260018; PubMed=8649512;

RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
RA Nagashima K.A., Cayan C., Maddon P.J., Koup R.A., Moore J.P.,
RA Paxton W.A.;
RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
RT CC-CKR-5.";
RL Nature 381:667-673(1996).
[12]
SUBMISSION.
RX MEDLINE=99189752; PubMed=1009882;
RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
RT entry.";
RL Cell 96:667-676(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and Rantes and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation. Acts as co-receptor with CD4 for primary non-
CC syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1
CC virus. It promotes Env-mediated fusion of the virus.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Found in promyelocytic cells.
CC -!- PTM: Sulfation contributes to the efficiency of HIV-1 entry.
CC -!- PTM: Modified by O-linked glycosylation, but not by N-linked
CC glycosylation.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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RT "Genetically divergent strains of simian immunodeficiency virus use
 RL CCR5 as a coreceptor for entry.";
 RN J. Virol. 71:2705-2714(1997).
 RP [3]
 RC SPECIES=V.mullatta; PubMed=11461684;
 RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mullatta, M.fascicularis, and M.nemestrina;
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amodeo A., Miller K., Doranz B.J., Endres M.,
 RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
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 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
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 DR Pfam; PF00001; 7tm 1; 1.
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 DR PROSITE; PS00282; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
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 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 FT CARBOHYD 268 268
 FT CONFLICT 241 241 M -> I (IN REF. 3).
 FT CONFLICT 292 292 I -> M (IN REF. 3).
 SQ SEQUENCE 352 AA; 58936C85909FACB2 CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 |||||
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
 |||||
 RESULT 10
 ID CCR5_PANTR STANDARD; PRT; 352 AA.
 AC P56440; O02778;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS).
 GN CCR5 OR CMKBR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]_TaxID=9598;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amodeo A., Miller K., Doranz B.J., Endres M.,
 RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 CC [2]
 CC SEQUENCE FROM N.A.
 RA Zimmerman P.A., Buckler-White A., Alkhatib G.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98022612; PubMed=9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97426118; PubMed=9282822;
 RA Zacharova V., Zachar V., Goustin A.S.;
 RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
 HIV type 1 host.";
 RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98090115; PubMed=9430250;
 RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Buter C.;
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RT "Sequence comparison of the CCR5 gene in primates and primate
 phylogeny.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Db	93 QWDFGNTMCQLLTGLYFIGFFS 114	
RESULT 12		
CKR5_PONPY	STANDARD; PRT; 352 AA.	
ID CKR5_PONPY		
AC 097881;		
DT 30-MAY-2000 (Rel. 39, Created)		
DT 30-MAY-2000 (Rel. 39, Last sequence update)		
DT 28-FEB-2003 (Rel. 41, Last annotation update)		
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).		
GN CKR5 OR CMKR5.		
OS Pongo pygmaeus (Orangutan).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.		
OX NCBI_TaxID=9600;		
RN [1]		
RP SEQUENCE FROM N.A.		
RX MEDLINE=99416438; PubMed=10486970;		
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;		
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";		
RL Mol. Biol. Evol. 16:1145-1154(1999).		
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,		
CC MIP-1-beta and RANTES and subsequently transduces a signal by		
CC increasing the intracellular calcium ions level. May play a role		
CC in the control of granulocytic lineage proliferation or		
CC differentiation.		
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.		
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.		
CC		
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CC or send an email to license@isb-sib.ch).		
CC		
CC EMBL; AF075446; AAD19858.1; -		
DR InterPro; IPR000276; GPCR_Rhodpsn.		
DR Pfam; PF00001; 7tm 1; 1.		
DR PRINTS; PR00237; GPCRHHODPSN.		
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.		
DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.		
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.		
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).		
FT TRANSMEM 31 58 1 (POTENTIAL).		
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).		
FT TRANSMEM 69 89 2 (POTENTIAL).		
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).		
FT TRANSMEM 103 124 3 (POTENTIAL).		
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).		
FT TRANSMEM 142 166 4 (POTENTIAL).		
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).		
FT TRANSMEM 199 218 5 (POTENTIAL).		
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).		
FT TRANSMEM 236 260 6 (POTENTIAL).		
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).		
FT TRANSMEM 278 301 7 (POTENTIAL).		
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).		
FT DISULFID 101 178 BY SIMILARITY.		
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).		
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).		
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).		
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).		
SQ SEQUENCE 352 AA; 40527 NW; F4E2F47135AF658A CRC64;		
Query Match	100.0%; Score 126; DB 1; Length 352;	
Best Local Similarity	100.0%; Pred. No. 1e-11;	
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 QWDFGNTMCQLLTGLYFIGFFS 22	

Db	93 QWDFGNTMCQLLTGLYFIGFFS 114	
RESULT 13		
CKR5_PYGBI	STANDARD; PRT; 352 AA.	
ID CKR5_PYGBI		
AC 097880;		
DT 30-MAY-2000 (Rel. 39, Created)		
DT 30-MAY-2000 (Rel. 39, Last sequence update)		
DT 28-FEB-2003 (Rel. 41, Last annotation update)		
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).		
GN CKR5 OR CMKR5.		
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;		
OC Pygathrix.		
OX NCBI_TaxID=61621;		
RN [1]		
RP SEQUENCE FROM N.A.		
RX MEDLINE=99416438; PubMed=10486970;		
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;		
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";		
RL Mol. Biol. Evol. 16:1145-1154(1999).		
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,		
CC MIP-1-beta and RANTES and subsequently transduces a signal by		
CC increasing the intracellular calcium ions level. May play a role		
CC in the control of granulocytic lineage proliferation or		
CC differentiation.		
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.		
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.		
CC		
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CC or send an email to license@isb-sib.ch).		
CC		
CC EMBL; AF075445; AAD19857.1; -		
DR InterPro; IPR000276; GPCR_Rhodpsn.		
DR Pfam; PF00001; 7tm 1; 1.		
DR PRINTS; PR00237; GPCRHHODPSN.		
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.		
DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.		
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.		
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).		
FT TRANSMEM 31 58 1 (POTENTIAL).		
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).		
FT TRANSMEM 69 89 2 (POTENTIAL).		
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).		
FT TRANSMEM 103 124 3 (POTENTIAL).		
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).		
FT TRANSMEM 142 166 4 (POTENTIAL).		
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).		
FT TRANSMEM 199 218 5 (POTENTIAL).		
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).		
FT TRANSMEM 236 260 6 (POTENTIAL).		
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).		
FT TRANSMEM 278 301 7 (POTENTIAL).		
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).		
FT DISULFID 101 178 BY SIMILARITY.		
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).		
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).		
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).		
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).		
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;		
Query Match	100.0%; Score 126; DB 1; Length 352;	
Best Local Similarity	100.0%; Pred. No. 1e-11;	
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 QWDFGNTMCQLLTGLYFIGFFS 22	

Db 93 QWDFGNTMCQLLTGLYFIGFFS 114
|||||

RESULT 14
CKR5 PYGNE
ID CKR5 PYGNE STANDARD; PRT; 352 AA.
AC Q97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCRS).
GN CCR5 OR CCR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OC NCBI_TaxID=54133;
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: AF075448; AAD19860.1;
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm1.1.
CC PRINTS: PR00237; GPCRHHODPSN.
CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 31 58
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 59 68
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 69 89
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 90 102
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 103 124
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 125 141
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 142 166
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 167 198
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 199 218
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 219 235
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 236 260
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 261 277
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 278 301
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 302 352
BY SIMILARITY.
FT DISULFID 101 178
SULFATION (BY SIMILARITY).
FT MOD_RES 3 3
SULFATION (BY SIMILARITY).
FT MOD_RES 10 10
SULFATION (BY SIMILARITY).
FT MOD_RES 14 14
SULFATION (BY SIMILARITY).
FT MOD_RES 15 15
SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3E861 CRC64;
Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
|||||
DB 93 QWDFGNTMCQLLTGLYFIGFFS 114
|||||

RESULT 15
CKR5 TRAPR
ID CKR5 TRAPR STANDARD; PRT; 352 AA.
AC Q97878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCRS).
GN CCR5 OR CCR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OC NCBI_TaxID=54180;
OX NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF075442; AAD19854.1;
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm1.1.
CC PRINTS: PR00237; GPCRHHODPSN.
CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 31 58
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 59 68
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 69 89
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 90 102
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 103 124
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 125 141
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 142 166
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 167 198
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 199 218
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 219 235
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 236 260
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 261 277
EXTRACELLULAR (POTENTIAL).
FT DOMAIN 278 301
CYTOPLASMIC (POTENTIAL).
FT DOMAIN 302 352
BY SIMILARITY.
FT DISULFID 101 178
SULFATION (BY SIMILARITY).
FT MOD_RES 3 3
SULFATION (BY SIMILARITY).
FT MOD_RES 10 10
SULFATION (BY SIMILARITY).
FT MOD_RES 14 14
SULFATION (BY SIMILARITY).
FT MOD_RES 15 15
SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;
Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;

FT DOMAIN 262 278 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 279 302 7 (POTENTIAL).
FT DOMAIN 303 353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 104 181 BY SIMILARITY.
FT CARBOHYD 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 353 AA; 40045 MW; 31EC4B642CDB9AE5 CRC64;

Query Match 70.6%; Score 89; DB 1; Length 353;
Best Local Similarity 63.6%; Pred. No. 4e-06; 3; Indels 0; Gaps 0;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLGLYPIGFPS 22
DB 96 QWVGFTAMCKVSLGYIGFPS 117
|||||:|||||
|||:|||||

RESULT 18
CKR2 HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
GN (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
DE CCR2 OR CCKBR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=94195821; PubMed=8146186;
RX Charo I.F., Myers S.J., Herman A., Francis C., Connolly A.J.,
RA Coughlin S.R.;
RT "Molecular cloning and functional expression of two monocyte
chemoattractant protein 1 receptors reveals alternative splicing of
the carboxyl-terminal tails."
RT Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94324942; PubMed=8048929;
RA Yanagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
RT "cDNA cloning and functional expression of a human monocyte
chemoattractant protein 1 receptor."
RL Biochem. Biophys. Res. Commun. 202:1156-1162 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97150864; PubMed=8995400;
RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking."
RL J. Biol. Chem. 272:1038-1045 (1997).
RN [4]
RP SEQUENCE FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nham M., Farnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., Ia Bastide M., Kaplan N., Greco T., Touchman J., Tang M.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Powell E.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.
RA Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.
RX MEDLINE=20501139; PubMed=11046064;
RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,

RA Chakravarty L., Kolattukudy P.E.;
RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
has tyrosine sulfation in a conserved extracellular N-terminal
region."
RL J. Immunol. 165:5295-5303 (2000).
CC FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
level. Alternative coreceptor with CD4 for HIV-1 infection.
CC SUBCELLULAR LOCATION: Integral membrane protein.
CC ALTERNATIVE PRODUCTS:
CC Events=Alternative splicing; Named isoforms=2;
CC Name=A; IsoId=P41597-1; Sequence=Displayed;
CC Name=B; IsoId=P41597-2; Sequence=VSP_001893;
CC PTM: N-glycosylated.
CC SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U03882; AAA19119.1; -;
CC EMBL; U03905; AAA19120.1; -;
CC EMBL; D29984; BAA06253.1; -;
CC EMBL; U80924; AAC51637.1; -;
CC EMBL; U80924; AAC51636.1; -;
CC EMBL; U95626; AAB57791.1; -;
CC EMBL; U95626; AAB57792.1; -;
CC EMBL; AFS45480; AAN16400.1; -;
CC PIR; I38450; I38450.
CC PIR; JC2443; JC2443.
CC PDB; 1KPI; 14-AUG-02.
CC PDB; 1KPI; 23-JAN-02.
CC Genew; HGNC:1603; CCR2.
CC MIM; 601267; -;
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005625; C: soluble fraction; TAS.
CC GO; GO:0004950; F: chemokine receptor activity; TAS.
CC GO; GO:0006960; F: antimicrobial humoral response (sensu Inver. . .); TAS.
CC GO; GO:0006968; P: cellular defense response; TAS.
CC GO; GO:0006935; P: chemotaxis; TAS.
CC GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
CC GO; GO:0006954; P: inflammatory response; TAS.
CC GO; GO:0007125; P: invasive growth; TAS.
CC GO; GO:0007259; P: JAK-STAT cascade; TAS.
CC GO; GO:0007194; P: negative regulation of adenylate cyclase ac. . .; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Polymorphism; Alternative splicing; 3D-structure.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 70 1 (POTENTIAL).
FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 100 2 (POTENTIAL).
FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 136 3 (POTENTIAL).
FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 178 4 (POTENTIAL).
FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 374 CYTOPLASMIC (POTENTIAL).

DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_2; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 33 60 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 91 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 105 126 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 168 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 201 220 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 238 262 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 280 303 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 304 354 BY SIMILARITY.
FT DISULFID 103 180 N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 270 270 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 66.7%; Score 84; DB 1; Length 354;
Best Local Similarity 61.9%; Pred. No. 2.3e-05;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCKLFTGIYHGF 21
DB 95 EWDFGNTMCKLFTGIYHGF 115

RESULT 21
VC03 SPVKA
ID VC03 SPVKA STANDARD; PRT; 269 AA.
AC P32229;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE G-protein coupled receptor homolog C3.
GN C3L.
OS Swinepox virus (strain Kasza) (SPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Suipoxvirus.
ON NCBI_TaxID=10277;
DR EMBL; L22013; AAC37868.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODPSN
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_2; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 61 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 62 82 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 83 94 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 95 115 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 116 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 152 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 153 171 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 172 192 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 193 223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 224 244 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 245 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 286 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 287 301 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 302 321 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 322 370 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 370 AA; 43171 MW; 76D08613327B0CC0 CRC64;

Query Match 65.9%; Score 83; DB 1; Length 370;
Best Local Similarity 54.5%; Pred. No. 3.3e-05;

SQ SEQUENCE 269 AA; 31509 MW; CE1A192CCAB999A3 CRC64;

Query Match 65.9%; Score 83; DB 1; Length 269;
Best Local Similarity 54.5%; Pred. No. 2.4e-05;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 QWDFGNTMCKLFTGIYHGF 22
DB 20 QWDFGNTMCKLFTGIYHGF 41

RESULT 22
VK02 SPVKA
ID VK02 SPVKA STANDARD; PRT; 370 AA.
AC Q08520;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE G-protein coupled receptor homolog K2.
GN K2R.
OS Swinepox virus (strain Kasza) (SPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Suipoxvirus.
ON NCBI_TaxID=10277;
DR EMBL; L21931; AAC37873.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODPSN
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_2; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEPT_F1_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 61 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 62 82 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 83 94 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 95 115 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 116 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 152 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 153 171 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 172 192 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 193 223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 224 244 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 245 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 286 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 287 301 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 302 321 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 322 370 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 370 AA; 43171 MW; 76D08613327B0CC0 CRC64;

Query Match 65.9%; Score 83; DB 1; Length 370;
Best Local Similarity 54.5%; Pred. No. 3.3e-05;

GO; GO:0006954; P:inflammatory response; IMP.
GO; GO:0030334; P:regulation of cell migration; IMP.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHOOPS
PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
DOMAIN 1 55
EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 56 83
1 (POTENTIAL).
FT DOMAIN 84 93
CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 94 114
2 (POTENTIAL).
FT DOMAIN 115 127
EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 128 149
3 (POTENTIAL).
FT DOMAIN 150 166
CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 191
4 (POTENTIAL).
FT DOMAIN 192 219
EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 239
5 (POTENTIAL).
FT DOMAIN 240 256
CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 281
6 (POTENTIAL).
FT DOMAIN 282 299
EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 299 322
7 (POTENTIAL).
FT DOMAIN 323 373
CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 203
BY SIMILARITY.
FT CONFLICT 39 39 Y -> H (IN REF. 1).
FT CONFLICT 184 184 A -> G (IN REF. 1).
FT CONFLICT 264 264 V -> G (IN REF. 1).
SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 65.9%; Score 83; DB 1; Length 373;
Best Local Similarity 61.9%; Pred. No. 3.4e-05;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 QWDFGNTWCQLLTGLGYFGFF 21
: ||| ||| : ||| ||| :
DBB 118 EWVFNIMCKVFTGLYHIGYF 138

RESULT 24
CKR8_HUMAN
IID CKR8_HUMAN STANDARD; PRT; 355 AA.
AC F51685;
DT 01-OCT-1996 (Rel. 34, Created)
DDT 01-OCT-1996 (Rel. 34, Last sequence update)
DST 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 8 (C-C CKR-8) (CCR-8) (GPR-CY6)
DE (GPCY6) (Chemokine receptor-like 1) (CKR-L1) (TERI) (CMKRL2) (CC-
DE chemokine receptor CMKRL1).
DE CCR8 OR CMKBR8 OR CKRL1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RR MEDLINE=97351133; PubMed=9207005;
RA Tiffany H.-L., Lautens L.L., Gao J.-L., Pease J., Locati M.,
RB Combadiere C., Modi W., Bonner T.I., Murphy P.M.;
RC "Identification of CCR8: a human monocyte and thymus receptor for the
RD CC chemokine I-309";
RE J. Exp. Med. 186:165-170(1997).
RF [2]
RG SEQUENCE FROM N.A.
RH MEDLINE=98129363; PubMed=9469461;
RI Goya I., Gutierrez J., Varona R., Kremer L., Zaballos A., Marquez G.;
RS "Identification of CCR8 as the specific receptor for the human beta-
RT chemokine I-309: cloning and molecular characterization of murine
RU CCR8 as the receptor for rCA-3";
RV J. Immunol. 160:1975-1981(1998).
RW [3]
RX SEQUENCE FROM N.A.
RY MEDLINE=97040707; PubMed=8886020;
ZABALLOS A., VARONA R., GUTIERREZ J., LIND P., MARQUEZ G.

RT "Molecular cloning and RNA expression of two new human chemokine
 RT receptor-like genes.";
 RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
 RN [4]

RN SEQUENCE FROM N.A.

RX MEDLINE=97131825; PubMed=8977299;

RA Samson M., Stordeur P., Labbe O., Soullard P., Vassart G.,
 RA Parmentier M.;

RA "Molecular cloning and chromosomal mapping of a novel human gene,
 RT Chem1, expressed in T lymphocytes and polymorphonuclear cells and
 RT encoding a putative chemokine receptor.";
 RL Eur. J. Immunol. 26:3021-3028(1996).
 RN [5]

RN SEQUENCE FROM N.A.

RA Nakajima T., Yoshida R., Harada S.;

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]

RN LIGAND BINDING.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

RN SEQUENCE FROM N.A.

RX MEDLINE=98180363; PubMed=9521068;

RA Bernardini G., Hedrick J., Sezzani S., Iaini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;

RA "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 RN [7]

FT DOMAIN 172 202 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 203 222 5 (POTENTIAL).

FT DOMAIN 223 238 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 239 263 6 (POTENTIAL).

FT DOMAIN 264 280 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 281 304 7 (POTENTIAL).

FT DOMAIN 305 355 CYTOPLASMIC (POTENTIAL).

FT DISULFID 106 183 BY SIMILARITY.

FT SEQUENCE 355 AA; 40844 MW; BC14A153CF695361 CRC64;

Query Match 65.1%; Score 82; DB 1; Length 355;

Best Local Similarity 54.5%; Pred. No. 4.5e-05;

Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCCLLTGLYFIFGFFS 22

DB 98 QWFGTVMCKVSGFYIFGYS 119

RESULT 25

CCR8 MACMU STANDARD; PRT; 356 AA.

AC 097653; (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 8 (C-CR-8) (CCR-8).

GN CCR8.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

OX NCBI_TaxID=9544;

RP [1]

SEQUENCE FROM N.A.

RC TISSUE=Splice;

RC MEDLINE=2135176; PubMed=11461684;

RX Maguiness B.J., Hauer D.A., Clements J.E.;

RA "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).

CC -!- FUNCTION: Receptor for the chemokines SCY1/I-309, SCY44/MIP-1-
 CC beta and SCY17/TARC. May regulate monocyte chemotaxis and thymic
 CC cell line apoptosis (By similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; AF100205; AAC72403.1; -

DR InterPro; IPR004068; CC 8 receptor.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR01530; CHEMOKINER8.

DR PRINTS; PR00237; GPCR_Rhodopsin.

DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.

DR PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 36 63 1 (POTENTIAL).

FT DOMAIN 64 93 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 74 93 2 (POTENTIAL).

FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 108 129 3 (POTENTIAL).

FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 147 172 4 (POTENTIAL).

FT DOMAIN 173 203 EXTRACELLULAR (POTENTIAL).

```
FT TRANSMEM 204 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 356 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 184 BY SIMILARITY.
SQ SEQUENCE 356 AA; 41210 MW; 1979628DEE4845B CRC64;

Query Match 65.1%; Score 82; DB 1; Length 356;
Best Local Similarity 54.5%; Pred. No. 4.6e-05;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCCOLLGLYFIFGS 22
DB 98 QWVFGVNCVKSQVSGFYIFGYS 119

RESULT 26
CKR2 MACMU STANDARD; PRT; 360 AA.
ID CKR2 MACMU STANDARD; PRT; 360 AA.
AC O18793;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
DE CKR2 OR CMKBR2
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461584;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=B;
CC IsoId=O18793-1; Sequence=Displayed;
CC Name=A;
CC IsoId=O18793-2; Sequence=Not described;
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
CC EMBL; AF013958; AAD11572.1;
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1.1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
CC Alternative splicing.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 70 1 (POTENTIAL).
FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 100 2 (POTENTIAL).
FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
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FT TRANSMEM 115 136 3 (POTENTIAL).
FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 178 4 (POTENTIAL).
FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC... ) (POTENTIAL).
FT MOD_RES 26 26 SULFATION (BY SIMILARITY).
FT DISULFID 113 190 BY SIMILARITY.
SQ SEQUENCE 360 AA; 41139 MW; 4B2552BC913FE9F CRC64;

Query Match 64.3%; Score 81; DB 1; Length 360;
Best Local Similarity 65.0%; Pred. No. 6.5e-05;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCCOLLGLYFIFG 20
DB 105 EWVFGNACMKLFTGLYHIGY 124

RESULT 27
CKR5 MOUSE STANDARD; PRT; 354 AA.
ID CKR5 MOUSE STANDARD; PRT; 354 AA.
AC P51682; O35313; O35891; P97308; P97405; Q61867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
DE alpha receptor).
DE CCR5 OR CMKBR5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SVJ; TISSUE=Spleen;
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Montecarlo F.S., Lulis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9."
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96278910; PubMed=862890;
RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Cloning and characterization of a novel murine macrophage
RT inflammatory protein-1 alpha receptor."
RL J. Biol. Chem. 271:14445-14451(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=129/Ola;
RX Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RN Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
RX MEDLINE=98001397; PubMed=9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses."
RL J. Virol. 71:8642-8656(1997).
RN [5]
RP SEQUENCE FROM N.A.
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SQ SEQUENCE 358 AA; 41623 MW; 7B73FAB7A3BC3670 CRC64;
Query Match 62.7%; Score 79; DB 1; Length 358;
Best Local Similarity 50.0%; Pred. No. 0.00013;
Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
DB 102 KWFVGHFMCKLIISGLYVGLFS 123

RESULT 29
CKR3 MOUSE
ID CKR3_MOUSE STANDARD; PRT; 355 AA.
AC P51675; Q91VP9;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)
DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
DE (RANTES-R)
DE GN
DE CCR1 OR CMKBR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Peritoneal macrophage;
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA Gerard C.;
RT "Molecular characterization of two murine eosinophil beta chemokine
RT receptors.";
RL J. Immunol. 155:5299-5305 (1995).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a
RT functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501 (1995).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC RANTES, AND LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC PROLIFERATION.

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CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in the heart, spleen, lung,
CC peritoneal exudate cells and leukocytes.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC -----
CC EMBL; U29678; AAA86119.1; -.
CC EMBL; U28404; AAA89153.1; -.
CC EMBL; BC011092; AAH11092.1; -.
CC PIR; I49339; I49339.
CC MGD; MGI:104618; Ccr1.
CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0030595; P:immune cell chemotaxis; IDA.
CC GO; GO:0006954; P:inflammatory response; IMP.
CC GO; GO:0030099; P:myeloid blood cell differentiation; IMP.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane.
CC DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 35 60 1 (POTENTIAL).
CC DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 65 91 2 (POTENTIAL).
CC DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 108 129 3 (POTENTIAL).
CC DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 147 171 4 (POTENTIAL).
CC DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 198 223 5 (POTENTIAL).
CC DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 240 264 6 (POTENTIAL).
CC DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 282 305 7 (POTENTIAL).
CC DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
CC DISULFID 106 183 BY SIMILARITY.
CC CONFLICT 55 55 M -> V (IN REF. 2 AND 3).
CC CONFLICT 149 149 L -> F (IN REF. 3).
CC CONFLICT 278 278 H -> Q (IN REF. 3).
CC SEQUENCE 355 AA; 40901 MW; FCE9FF70E6F38B1 CRC64;
Query Match 60.3%; Score 76; DB 1; Length 355;
Best Local Similarity 52.4%; Pred. No. 0.00037;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 2 WDFGNTWCQLLTGLYFIFGFFS 22
DB 99 WIFGDAMCKLLSGFYVGLYS 119
RESULT 30
CKR3 RAT
ID CKR3_RAT STANDARD; PRT; 359 AA.
AC O54814; O55169;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR3)
DE (CCR3).
DE GN CCR3 OR CMKBR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

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DE (RANTES-R) (HM145) (LD78 receptor).
GN CCR1 OR CMK3R1 OR CMK3R1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93161416; PubMed=7679328;
RA Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
RT "Molecular cloning, functional expression, and signaling
RT characteristics of a C-C chemokine receptor.";
RL Cell 72:415-425 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93240122; PubMed=7683036;
RA Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
RT Murphy P.M.;
RT "Structure and functional expression of the human macrophage
RT inflammatory protein 1 alpha/RANTES receptor.";
RL J. Exp. Med. 177:1421-1427 (1993).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Monocytes;
RX MEDLINE=94092629; PubMed=7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT leukocyte chemotactic peptide receptors.";
RL Int. Immunol. 5:1239-1249 (1993).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-
CC beta or MCP-1 and subsequently transduces a signal by increasing
CC the intracellular calcium ions level. Responsible for affecting
CC stem cell proliferation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed in different hematopoietic
CC cells.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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DR EMBL; L09230; AAA58408.1; -;
DR EMBL; L10918; AAA36543.1; -;
DR EMBL; D10925; BA01723.1; -;
DR EMBL; A45177; A45177.
DR Genbank; HGNC:1602; CCR1.
DR MIM; 601159; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004950; P:chemokine receptor activity; TAS.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR GO; GO:0007265; P:cell-cell signaling; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0007125; P:invasive growth; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1_1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT

FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFLICT 337 337 E -> D (IN REF. 3).
SQ SEQUENCE 355 AA; 41172 MW; 52C100FFED275985 CRC64;
Query Match 56.3%; Score 71; DB 1; Length 355;
Best Local Similarity 47.6%; Pred. No. 0.0021;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
Oy 2 WDRGNTMCQLLTGLYTGPF 22
Db 99 WFGDAMCKILSGFYTGLYS 119
RESULT 33
ID_CCR1_MACMU STANDARD; PRT; 355 AA.
AC PS6482;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 1 (C-CR-1) (CCR-1) (CCR1).
GN CCR1 OR CMK3R1
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2134176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors.";
RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC RANTES, MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC PROLIFERATION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
DR EMBL; AF017282; AAB70526.1; -;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1_1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT

```

FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 6 (POTENTIAL).
FT TRANSMEM 240 264 7 (POTENTIAL).
FT DOMAIN 265 281 7 (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
SQ SEQUENCE 355 AA; 41198 MW; 41CAEA7CC19D23D4 CRC64;

Query Match 56.3%; Score 71; DB 1; Length 355;
Best Local Similarity 47.6%; Pred. No. 0.0021;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 WDFGNMTCOLLTGLYFIFGFS 22
Db 99 WIFGDAMCKILSGFYTGILYS 119

RESULT 34
CKR3_MOUSE
ID CKR3_MOUSE STANDARD; PRT; 359 AA.
AC PS1678;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3)
DE (CCR3) (CCR3) (Macrophage inflammatory protein-1 alpha receptor-like
DE 2) (MIP-1 alpha RL2).
DE GN CCR3 OR CMKBR3 OR CMKBR1L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA Gerard C.;
RT "Molecular characterization of two murine eosinophil beta chemokine
RT receptors";
RL J. Immunol. 155:5299-5305(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a
RT functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501(1995).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
CC amounts in leukocytes.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC EMBL; U29677; AAA86118.1; -.
DR EMBL; U28406; AA89155.1; -.
DR MGI; MGI:104616; CCR3.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0006935; P:chemotaxis; IDA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECP Fl_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP Fl_2; 1.
DR G-protein coupled receptor; Transmembrane.
KW DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 39 64 1 (POTENTIAL).
FT DOMAIN 65 68 1 (POTENTIAL).
FT TRANSMEM 69 95 2 (POTENTIAL).
FT DOMAIN 96 111 3 (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 4 (POTENTIAL).
FT TRANSMEM 151 175 4 (POTENTIAL).
FT DOMAIN 176 201 5 (POTENTIAL).
FT TRANSMEM 202 227 5 (POTENTIAL).
FT DOMAIN 228 243 6 (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 7 (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 359 7 (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
FT CONFLICT 270 270 R -> S (IN REF. 2).
SQ SEQUENCE 359 AA; 41825 MW; AC1ED6E283CEAF CRC64;

Query Match 55.6%; Score 70; DB 1; Length 359;
Best Local Similarity 40.9%; Pred. No. 0.003;
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 QWDFGNMTCOLLTGLYFIFGFS 22
Db 102 EWGFGHYMCKLSGFIYLYLIS 123

RESULT 35
CKR3_HUMAN
ID CKR3_HUMAN STANDARD; PRT; 355 AA.
AC PS1677; Q15748; Q85WD2; Q9ULY8;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
DE (CCR3) (Eosinophil eotaxin receptor).
DE GN CCR3 OR CMKBR3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Monocytes;
RX MEDLINE=95348056; PubMed=7622448;
RA Combadiere C., Ahuja S.K., Murphy P.M.;
RT "Cloning and functional expression of a human eosinophil CC chemokine
RT receptor.";
RL J. Biol. Chem. 270:16491-16494(1995).
RN [2]
RP ERZATUM.
RA Combadiere C., Ahuja S.K., Murphy P.M.;
RL J. Biol. Chem. 270:30235-30235(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96235044; PubMed=8642344;
RA Daugherty B.L., Siciliano S.J., Demartino J.A., Malkowitz L.,
RA Sirotina A., Springer M.S.;
RT "Cloning, expression, and characterization of the human eosinophil
RT

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CC -----
DR EMBL; U28694; AAC50469.1; -
DR EMBL; U51241; AAB16831.1; -
DR EMBL; U49727; AAB09726.1; -
DR EMBL; AF026535; AAB82589.1; -
DR EMBL; AB023887; BAA86964.1; -
DR EMBL; AF247361; AAL85154.1; -
DR EMBL; AY221092; AAC65970.2; -
DR EMBL; BC033514; AAB33514.1; -
DR PIR; G02436; G02436.
DR Genew; HGNC:1604; CCR3.
DR MIM; 601268; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004350; F:chemokine receptor activity; TAS.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0007188; P:G-protein signaling, coupled to CAMP nucleo. .; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0007125; P:invasive growth; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G PROTEIN RECP FL_1; 1.
DR PROSITE; PS0262; G PROTEIN RECP FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Polymorphism.
KW DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 35 62 1 (POTENTIAL).
FT FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 73 93 2 (POTENTIAL).
FT FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 108 129 3 (POTENTIAL).
FT FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 147 171 4 (POTENTIAL).
FT FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 204 223 5 (POTENTIAL).
FT FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 240 264 6 (POTENTIAL).
FT FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 282 305 7 (POTENTIAL).
FT FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT FT DISULFID 106 133 BY SIMILARITY.
FT FT VARIANT 218 218 C -> S (polymorphism found in about 7% of
FT FT the population; may show reduced
FT FT activity).
FT FT CONFLICT 276 276 S -> T (IN REF. 4 AND 5).
FT FT SEQUENCE 355 AA; 41043 MW; E95DCD7A6C643874 CRC64;
/FTIG=VAR 010668.
Query Match 53.2%; Score 67; DB 1; Length 355;
Best Local Similarity 52.4%; Pred. No. 0.0083;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 2 WDFGNTMCCOLLGLYFIFGFFS 22
DB 99 WYFGHGMCKLLSGFYHTGLYS 119
| | | | | | | | | |
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| | | | | | | | | |
RESULT 36
CCR6_CERAE STANDARD; PRT; 342 AA.
AC O18983;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-WAR-2004 (Rel. 43, Last annotation update)
DE C-X-c chemokine receptor type 6 (CXC-R6) (CXCR-6) (G protein-coupled
DE receptor bonzo).

```

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
PP TISSUE=Spleen;
X MEDLINE=96370289; PubMed=7642634;
X Power C.A., Meyer A., Neneth K., Bacon K.B., Hoogewerf A.J.,
A Proudfoot A.E.I., Wells T.N.C.;
A "Molecular cloning and functional expression of a novel CC chemokine
T receptor cDNA from a human basophilic cell line.";
L J. Biol. Chem. 270:19495-19500(1995).
[2]
X SEQUENCE FROM N.A.; AND VARIANTS VAL-130 AND SER-178.
X MEDLINE=21040311; PubMed=11196669;
X Kato H., Teuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
A Hirai K., Tokunaga K.;
A "New variations of human CC-chemokine receptors CCR3 and CCR4.";
L Genes Immun. 1:97-104(1999).
[3]
X SEQUENCE FROM N.A.
X Kopatz S.A., Aronstam R.S., Sharma S.V.;
X "cDNA clones of human proteins involved in signal transduction
subsequent by the Guthrie cDNA resource center (www.cdna.org).";
L Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
[4]
PP FUNCTION.
X MEDLINE=97313486; PubMed=9169480;
X Inai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
X "The T cell-directed CC chemokine TARC is a highly specific
biological ligand for CC chemokine receptor 4.";
L J. Biol. Chem. 272:15036-15042(1997).
[5]
PP FUNCTION.
X MEDLINE=98104168; PubMed=9430724;
X Inai T., Chantry D., Report C.J., Wood C.L., Nishimura M., Godiska R.,
X Yoshie O., Gray P.W.;
X "Macrophage-derived chemokine is a functional ligand for the CC
chemokine receptor 4.";
L J. Biol. Chem. 273:1764-1768(1998).
[6]
PP FUNCTION.
X MEDLINE=99394604; PubMed=10466728;
X Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P.,
X Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher E.C.;
X "The chemokine receptor CCR4 in vascular recognition by cutaneous but
not intestinal memory T cells.";
L Nature 400:776-780(1999).
[7]
PP FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.
X MEDLINE=20219238; PubMed=10754297;
X Ingber J., Damaj B., Maghazachi A.A.;
X "Human NK cells express CC chemokine receptors 4 and 8 and respond to
thymus and activation-regulated chemokine, macrophage-derived
chemokine, and I-309.";
L J. Immunol. 164:4048-4054(2000).
X -I- FUNCTION: High affinity receptor for the C-C type chemokines
TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is
mediated by G(i) proteins which activate a phosphatidylinositol-
calcium second messenger system. Can function as a chemoattractant
homing receptor on circulating memory lymphocytes and as a
coreceptor for some primary HIV-2 isolates. In the CNS, could
mediate hippocampal-neuron survival.
X -I- SUBCELLULAR LOCATION: Integral membrane protein.
X -I- TISSUE SPECIFICITY: Predominantly expressed in the thymus, in
peripheral blood leukocytes, including T cells, mostly cd4+ cells,
and basophils, and in platelets; at lower levels, in the spleen
and in monocytes. Detected also in macrophages, IL-2-activated
natural killer cells and skin-homing memory T cells, mostly the
ones expressing the cutaneous lymphocyte antigen (CLA). Expressed
in brain microvascular and coronary artery endothelial cells.
X -I- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.

C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled receptor bonzo) (G protein-coupled receptor STRL33).
CXCR6 OR BONZO OR STRL33 OR TYMSR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxId=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=97373958; PubMed=3230441;
"Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.:
"Expression cloning of new receptors used by simian and human immunodeficiency viruses";
Nature 388:296-300(1997).
[2]
SEQUENCE FROM N.A., AND VARIANT ALA-25.
MEDLINE=973111099; PubMed=9166430;
Liao F., Alkhatib G., Peden K.W.C., Sharma G., Berger E.A., Farber J.M.;
"STRL33, A novel chemokine receptor-like protein, functions as a fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-1.";
J. Exp. Med. 185:2015-2023(1997).
[3]
SEQUENCE FROM N.A.
TISSUE=Blood;
MEDLINE=97431687; PubMed=9285716;
Loetscher M., Anara A., Oberlin E., Brass N., Lecler D.F., Virlizier J.L., Loetscher P., D'Amico M., Meese E.U., Rousset D., Virlizier J.L., Baggiolini M., Arenzana-Seisdedos F., Moser B.;
"TYMSR, a putative chemokine receptor selectively expressed in activated T cells, exhibits HIV-1 coreceptor function";
Curr. Biol. 7:652-660(1997).
[4]
SEQUENCE FROM N.A.
Kopatz S.A., Aronstam R.S., Sharma S.V.;
"cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";
Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
TISSUE=Pancreas;
MEDLINE=22389257; PubMed=12477932;
Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh P., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Expressed in lymphoid tissues and activated T cells.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC coreceptor by sIVs and by strains of HIV-2 and m-tropic HIV-1.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF084229; RAD52041.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 33 59 1 (POTENTIAL).
FT DOMAIN 60 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 125 3 (POTENTIAL).
FT DOMAIN 126 143 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 164 4 (POTENTIAL).
FT DOMAIN 165 187 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 188 215 5 (POTENTIAL).
FT DOMAIN 216 231 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 232 259 6 (POTENTIAL).
FT DOMAIN 260 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 293 7 (POTENTIAL).
FT DOMAIN 294 342 CYTOPLASMIC (POTENTIAL).
FT DISULFID 102 180 BY SIMILARITY.
FT CARBOHYD 16 16 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 342 AA; 39273 MW; 5B58003797806B2A CRC64;
```

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Query Match 51.6%; Score 65; DB 1; Length 342;
Best Local Similarity 45.5%; Pred. No. 0.016;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QWDFGNTWCCLLTGLYFIGFFS 22
Db :||| ||: ||: ||:
94 EWVFGQVMCKSLGIYITINFT 115
```

Search completed: September 28, 2004, 09:04:05
Job time : 7.875 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:56:16 ; Search time 35.2 Seconds
(without alignments)
197.199 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFGNTMCQLLTGLYFIFGFS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	215	4	075303
2	126	100.0	333	4	014694
3	126	100.0	339	4	Q9UN24
4	126	100.0	339	4	Q9UN23
5	126	100.0	339	4	Q9UB77
6	126	100.0	339	4	Q9UN25
7	126	100.0	339	4	Q9UN27
8	126	100.0	339	4	Q9UBT9
9	126	100.0	339	4	Q9UN28
10	126	100.0	339	6	Q9TQW0
11	126	100.0	339	6	Q9TUX1
12	126	100.0	339	6	Q9TUX8
13	126	100.0	339	6	Q9TUT4
14	126	100.0	339	6	Q9TUT9
15	126	100.0	339	6	Q9TUX8
16	126	100.0	339	6	Q9TQW4

17	126	100.0	339	6	Q9TUX4
18	126	100.0	339	6	Q9TQW7
19	126	100.0	339	6	Q9TUX3
20	126	100.0	339	6	Q9TUX9
21	126	100.0	339	6	Q9TQW0
22	126	100.0	339	6	Q9TUT9
23	126	100.0	339	6	Q9TSN2
24	126	100.0	339	6	Q9TUX6
25	126	100.0	339	6	Q9TQV6
26	126	100.0	339	6	Q9TUX6
27	126	100.0	339	6	Q9TUX9
28	126	100.0	339	6	Q9TSN3
29	126	100.0	339	6	Q9TUX7
30	126	100.0	339	6	Q9TQV0
31	126	100.0	339	6	Q9TUX5
32	126	100.0	339	6	Q9TUX7
33	126	100.0	339	6	Q9TUX3
34	126	100.0	339	6	Q9TUX3
35	126	100.0	339	6	Q9TUX5
36	126	100.0	339	6	Q9TUX0
37	126	100.0	339	6	Q9TQV2
38	126	100.0	339	6	Q9TQV3
39	126	100.0	339	6	Q9TUX8
40	126	100.0	339	6	Q9TQW2
41	126	100.0	339	6	Q9TUX1
42	126	100.0	339	6	Q9TUX6
43	126	100.0	339	6	Q9TSQ4
44	126	100.0	339	6	Q9TUT3
45	126	100.0	339	6	Q9TUT0

ALIGNMENTS

RESULT 1

075303 PRELIMINARY; PRT; 215 AA.
 ID O75303
 DT 01-NOV-1998 (TREMELrel. 08, Created)
 DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE CC-chemokine receptor.
 GN CCR-5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tse L., Ehrenberg P.K., Chang G., Michael N.L.;
 RT "Genomic Organization and Functional Characterization of the Complete
 RT Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-
 RT Receptor for HIV-1";
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF009962; AAC23944.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; P:receptor activity; IEA.
 DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 215 AA; 23946 MW; 3C9146C768A416F7 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22

|||||

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Db      93 QWDFGNTMCQLLTGLYFIFGFFS 114
RESULT 2
O14694      PRELIMINARY;      PRT;      333 AA.
AC O14694
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011504; AB85704.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 333 333
SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 100.0%; Score 126; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 74 QWDFGNTMCQLLTGLYFIFGFFS 95

RESULT 3
Q9UN24      PRELIMINARY;      PRT;      339 AA.
AC Q9UN24
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161919; AAD4767.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 5
Q9UBJ7      PRELIMINARY;      PRT;      339 AA.
AC Q9UBJ7
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161919; AAD4767.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.

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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 4
Q9UN23      PRELIMINARY;      PRT;      339 AA.
AC Q9UN23
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD4767.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 5
Q9UBJ7      PRELIMINARY;      PRT;      339 AA.
AC Q9UBJ7
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD4767.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 5
Q9UBJ7      PRELIMINARY;      PRT;      339 AA.
AC Q9UBJ7
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD4767.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.

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RN  SEQUENCE FROM N.A.
RP  Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF161921; AAD47678.1; -.
DR  EMBL; AF161917; AAD47674.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm.1; 1.
DR  PRINTS; PR00237; GPCRHOPOPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
FT  NON_TER 339 339
FT  NON_TER 339 339
SQ  SEQUENCE 339 AA; 39128 MW; 9C3369FF1F2F27A CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIGFFS 22
    |||||
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 6
Q9UN25 PRELIMINARY; PRT; 339 AA.
AC Q9UN25;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B48E2CB4EC2 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIGFFS 22
    |||||
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 8
Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47667.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
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Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 7
Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B48E2CB4EC2 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIGFFS 22
    |||||
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 8
Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47667.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
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DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F47 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFGFFS 107
|||||

RESULT 9
Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFGFFS 107
|||||

RESULT 10
Q9TQW0 PRELIMINARY; PRT; 339 AA.
AC Q9TQW0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFGFFS 22
DB 86 QWDFGNTMCQLLTGLYFGFFS 107
|||||

RESULT 11
Q9TUX1 PRELIMINARY; PRT; 339 AA.
ID Q9TUX1
AC Q9TUX1;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257FBB834C4AE CRC64;

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Query Match          100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 12
Q9TUT8 PRELIMINARY; PRT; 339 AA.
ID Q9TUT8 AC Q9TUT8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; P:G-protein coupled receptor protein signalin. .; IEA.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39079 MW; 44A79753DA2F7AAF CRC64;

Query Match          100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 13
Q9TUT4 PRELIMINARY; PRT; 339 AA.
ID Q9TUT4 AC Q9TUT4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; P:G-protein coupled receptor protein signalin. .; IEA.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39079 MW; 44A79753DA2F7AAF CRC64;

Query Match          100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 14
Q9TUT9 PRELIMINARY; PRT; 339 AA.
ID Q9TUT9 AC Q9TUT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29069;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39024 MW; EC4CE48DEEF107E CRC64;

Query Match          100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 15
Q9TUT8 PRELIMINARY; PRT; 339 AA.
ID Q9TUT8 AC Q9TUT8;
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DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 DE CCR5.
 OS Cercopithecus diana (Diana monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheinae; Cercopithecus.
 OX NCBI_TaxID=36224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161949; AAD47705.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39049 MW; 6DIA93F6270F3ED CRC64;

 Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
 DB 86 QWDFGNTMCQLLTGLYFIFGFS 107
 [1]

RESULT 16
 Q9TQW4
 ID Q9TQW4 PRELIMINARY; PRT; 339 AA.
 AC Q9TQW4;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 DE CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161903; AAD47660.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39159 MW; 8E599E882BAC0E84 CRC64;

 Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
 DB 86 QWDFGNTMCQLLTGLYFIFGFS 107
 [1]

RESULT 18
 Q9TQW7
 ID Q9TQW7 PRELIMINARY; PRT; 339 AA.
 AC Q9TQW7;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 DE CCR5.
 OS Cercopithecus nictitans (white-nosed guenon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheinae; Cercopithecus.
 OX NCBI_TaxID=36228;
 RN [1]

```

RN
RP SEQUENCE FROM N.A.
RA Kunsman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -
DR EMBL; AF162042; AAD47797.1; -
DR EMBL; AF162044; AAD47799.1; -
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signaling. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
DR Receptor.
FT NON TER 1
FT NON TER 339
FT NON TER 339
SQ SEQUENCE 339 AA; 39150 MW; 847D5F92BB03B6E2 CRC64;

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Query Match      100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 QWDFGNTMCQLLTGLYFIGFFS 22
db 86 QWDFGNTMCQLLTGLYFIGFFS 107

RESULT 19
Q9TUU3
ID Q9TUU3
PRELIMINARY;
PRT; 339 AA.

DT	01-MAY-2000 (TReMBUrel. 13, Created)
DT	01-MAY-2000 (TReMBUrel. 13, Last sequence update)
DT	01-MAY-2003 (TReMBUrel. 24, Last annotation update)
DE	C-C chemokine receptor 5 (fragment).
DE	CCR5
OC	Macaca mulatta (Rhesus macaque).
OC	Macaca mulatta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC	Cercopitheciinae; Macaca.
EN	NCBI_TaxID=9544;
EN	[1]_TaxID=9544;
EN	[1]

SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RP Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.,
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.",
RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.
RL EMBL; AF161961; AAD47716.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein-coupled receptor protein signalin. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECEPT_F1.1; 1.
DR PROSITE; PS00362; G PROTEIN RECEPT_F1.2; 1.
DR PROSITE; PS00362; G PROTEIN RECEPT_F1.2; 1.

FT	1	1	
FT	339	339	
SQ	339 AA;	39121 MW;	AFB6E3EE4D6D3484 CRC64;

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Query Match      100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy.	1	QWDFGNTMCQLLTGLYFIGFFS	22
db	86	QWDFGNTMCQLLTGLYFIGFFS	107

RESULT 20

Q9TUR3	PRELIMINARY;	PRT;	339 AA.
ID			
AC			
CD			
DT			
ED			
HE			
NA			
OR			
OS			
OC			
OX			
RN			
RP			
RR			
RT			
SA			
SC			
SE			
SI			
SL			
SM			
SN			
SO			
SP			
SR			
SS			
ST			
SV			
SW			
SY			
TA			
TE			
TF			
TM			
TS			
TT			
TX			
TY			
UN			
UP			
UR			
US			
UT			
UU			
UV			
UW			
UX			
UY			
UZ			
VA			
VB			
VC			
VD			
VE			
VF			
VG			
VH			
VI			
VJ			
VK			
VL			
VM			
VN			
VO			
VP			
VQ			
VR			
VS			
VT			
VU			
VV			
VO			
VF			
VG			
VH			
VI			
VJ			
VK			
VL			
VM			
VN			
VO			
VP			
VQ			
VR			
VS			
VT			
VU			
VV			
VO			
VF			
VG			
VH			
VI			
VJ			
VK			
VL			

EMBL; AF162015; AAD4770.1; -;
GO: GO:0016021: C: integral to membrane: TEA.

DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR Rhodopsn.

DR PIAM; PF00001; 7cm 1; 1.
DR PRINTS: PR00237: GPCRPHODPSN.

DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.

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DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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KW	Receptor.	1
FT	NON TER	1

FT	NON_TER	339	339
FT	NON_TER	339	339

SQ SEQUENCE 339 AA; 39

Query Match 100.0%: Score 126: DB 6: Length 339:

Query Match 100.0%; Score 120; Length 333;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
db 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 21

	Q9TQT0	PRELIMINARY; PRT; 339 AA.
IID	Q9TQT0	
AAC	Q9TQT0;	
DIT	01-MAY-2000 (TREMBLrel. 13, Created)	
DDI	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DEE	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DED	C-C chemokine receptor 5 (Fragment).	
GNG	CCRS.	
OOS	Macaca fascicularis (Crab eating macaque) (<i>Cynomolgus monkey</i>). Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopitheciidae; Catarrhini; Primates; Cercopithecinae; Macaca. <i>[1]</i>	
RNP	NCBI_TaxId=9541; SEQUENCE FROM N.A. [1] RN RN RP	

RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., pillai S., Kuiken C., Marx P., Wolinksy S.

"Sequences of the CCR5 genes from diverse simian and prosimian

RT species.";

Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AF161954; AAD47710.1; -

EMBL; AF161950; AAD47706.1; -.

DR EMBL; AF161952; AAD47708.1; -.

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DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 22
Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF161972; AAD4727.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39067 MW; 5BFCB5BA96C2F9E CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 23
Q9TSN2 PRELIMINARY; PRT; 339 AA.
AC Q9TSN2
DT 01-MAY-2000 (TRENBLrel. 13, Created)

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DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF161953; AAD4709.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39137 MW; 9E626ED3288607C1 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 24
Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopitheidae.
OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF162026; AAD4781.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 1

```

FT	NON_TER	339	339
SQ	SEQUENCE	339 AA; 39178 MW;	9DF2A6F446C55AED CRC64;
Query Match		100.0%;	Score 126; DB 6; Length 339;
Best Local Similarity		100.0%;	Pred. No. 3.1e-11;
Matches	22; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 QWDFGNTMCQLLTGLYFIGFFS	22	
DB	86 QWDFGNTMCQLLTGLYFIGFFS	107	
RESULT 25			
Q9TVQ6	PRELIMINARY;	PRT;	339 AA.
ID	Q9TVQ6		
AC	Q9TVQ6		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DE	01-JUN-2003 (TrEMBLrel. 13, Last sequence update)		
DE	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
GN	C-C chemokine receptor 5 (fragment).		
OS	Colobus guereza (Black-and-white colobus monkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;		
OC	Colobus.		
OX	NCB1_TaxID=33548;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agly M.,		
RA	Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;		
RT	"Sequences of the CCR5 genes from diverse simian and prosimian		
RT	species."		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AF162005; AAD47760.1; -		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin.. . ; IEA.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCRRHODPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.		
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.		
KW	Receptor.		
FT	NON TER		
FT	NON TER	339	339
SQ	SEQUENCE	339 AA; 39103 MW;	4038C132D024CSA4 CRC64;
Query Match		100.0%;	Score 126; DB 6; Length 339;
Best Local Similarity		100.0%;	Pred. No. 3.1e-11;
Matches	22; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 QWDFGNTMCQLLTGLYFIGFFS	22	
DB	86 QWDFGNTMCQLLTGLYFIGFFS	107	
RESULT 27			
Q9TUQ9	PRELIMINARY;	PRT;	339 AA.
ID	Q9TUQ9		
AC	Q9TUQ9		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DE	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DE	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
GN	C-C chemokine receptor 5 (fragment).		
OS	Cercopithecus mona.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC	Cercopithecinae; Cercopithecus.		
OX	NCB1_TaxID=36226;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agly M.,		
RA	Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;		
RT	"Sequences of the CCR5 genes from diverse simian and prosimian		
RT	species."		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AF162041; AAD47796.1; -		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin.. . ; IEA.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCRRHODPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.		
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.		
KW	Receptor.		
FT	NON TER		
FT	NON TER	339	339
SQ	SEQUENCE	339 AA; 39168 MW;	6A4BF72FBFF566F CRC64;
Query Match		100.0%;	Score 126; DB 6; Length 339;
Best Local Similarity		100.0%;	Pred. No. 3.1e-11;
Matches	22; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 QWDFGNTMCQLLTGLYFIGFFS	22	
DB	86 QWDFGNTMCQLLTGLYFIGFFS	107	
RESULT 26			
Q9TWU6	PRELIMINARY;	PRT;	339 AA.
ID	Q9TWU6		
AC	Q9TWU6		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DE	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DE	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
GN	C-C chemokine receptor 5 (fragment).		
OS	Fan troglodytes (Chimpanzee).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 28

Q9TSN3 PRELIMINARY; PRT; 339 AA.
 AC Q9TSN3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161951; AAD47707.1; -.
 DR GO; GO:0036021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 DR NON_TER 1
 FT NON_TER 339
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39098 MW; F01328B8C44EF829 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 29

Q9TUU7 PRELIMINARY; PRT; 339 AA.
 AC Q9TUU7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Macaca fuscata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161955; AAD47711.1; -.
 DR GO; GO:0036021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 30

Q9TVQV PRELIMINARY; PRT; 339 AA.
 AC Q9TVQV;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Papio papio (Guinea baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=100937;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161989; AAD47744.1; -.
 DR EMBL; AF161988; AAD47743.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39113 MW; 7F9803EAO50AF9ED CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 86 QWDFGNTMCQLLTGLYFIFGFFS 107

RESULT 31

Q9TOU5 PRELIMINARY; PRT; 339 AA.
 AC Q9TOU5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)


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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecoidea.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162046; AAD47801.1; -.
DR EMBL; AF162043; AAD47798.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339
FT SEQUENCE 339 AA; 39178 MW; 8478936B00E6E2 CRC64;
SQ SEQUENCE 339 AA; 39178 MW; 8478936B00E6E2 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 32
Q9TUS7 PRELIMINARY; PRT; 339 AA.
ID Q9TUS7
AC Q9TUS7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161995; AAD47750.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT SEQUENCE 1
SQ SEQUENCE 1

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 33
Q9TUS7 PRELIMINARY; PRT; 339 AA.
ID Q9TUS7
AC Q9TUS7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161899; AAD47656.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT SEQUENCE 1
SQ SEQUENCE 1

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 34
Q9TUS7 PRELIMINARY; PRT; 339 AA.
ID Q9TUS7
AC Q9TUS7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161895; AAD47750.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT SEQUENCE 1
SQ SEQUENCE 1
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RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161908; AAD47665.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.

DR Pfam; PF00001; 7tm1.1; .
 DR PRINTS; PR00237; GPCR_Rhodopsn.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON_TER 1

FT NON_TER 339

SQ SEQUENCE 339 AA; 39103 MW; 4350C4625FB0657C CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22

DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 35

ID Q9TUS5 PRELIMINARY; PRT; 339 AA.

AC Q9TUS5;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Papio papio (Guinea baboon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopitheidae; Papio.

OX NCBI_TaxID=100937;

RN [1]_TaxID=100937;

SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

RT species";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161997; AAD47752.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0004872; F: receptor activity; IEA.

DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.

DR Pfam; PF00001; 7tm1.1; .

DR PRINTS; PR00237; GPCR_Rhodopsn.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON_TER 1

FT NON_TER 339

SQ SEQUENCE 339 AA; 39028 MW; 8C9C978FD80B936 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22

DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 36

Q9TUU0 PRELIMINARY; PRT; 339 AA.

AC Q9TUU0;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopitheidae; Macaca.

OX NCBI_TaxID=9544;

RN [1]_TaxID=9544;

SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

RT species";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161970; AAD47725.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0004872; F: receptor activity; IEA.

DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm1.1; .

DR PRINTS; PR00237; GPCR_Rhodopsn.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON_TER 1

FT NON_TER 339

SQ SEQUENCE 339 AA; 39155 MW; 3D1B503B9E24C82 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22

DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 37

Q9TQV2 PRELIMINARY; PRT; 339 AA.

AC Q9TQV2;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Papio papio (Guinea baboon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopitheidae; Papio.

OX NCBI_TaxID=100937;

RN [1]_TaxID=100937;

SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

RT species";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161993; AAD47748.1; -.
 DR EMBL; AF161987; AAD47742.1; -.
 DR EMBL; AF161990; AAD47745.1; -.
 DR EMBL; AF161991; AAD47746.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.

[illegible]

Best Local Similarity 100.0%; Pred. No. 3.le-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 86 QWDFGNTMCQLLTGLYFIGFFS 107

Search completed: September 28, 2004, 09:06:18
Job time : 36.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:51:21 ; Search time 42.975 Seconds
(without alignments)
118.345 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96

Sequence: 1 SQYQFWKNFQTLKIVILG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: Geneseqp29Jan04.*
 - 2: Geneseqp1980s.*
 - 3: Geneseqp1990s.*
 - 4: Geneseqp2000s.*
 - 5: Geneseqp2001s.*
 - 6: Geneseqp2002s.*
 - 7: Geneseqp2003as.*
 - 8: Geneseqp2003bs.*
 - 9: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	4 AAB88954	Aab88954 HIV gp120
2	96	100.0	18	4 AAB88995	Aab88995 HIV gp120
3	96	100.0	352	2 AAW27407	Aaw27407 Human CCR
4	96	100.0	352	2 AAW27123	Aaw27123 Human che
5	96	100.0	352	2 AAW07602	Aaw07602 Human G-P
6	96	100.0	352	2 AAW23835	Aaw23835 Human CC
7	96	100.0	352	2 AAW88232	Aaw88232 HIV-1 co-
8	96	100.0	352	3 AAY80128	Aay80128 Human G-P
9	96	100.0	352	4 AAG79089	Aag79089 Amino aci
10	96	100.0	352	4 AAE07045	Aae07045 Human G-P
11	96	100.0	352	4 AAE07048	Aae07048 Human G-P
12	96	100.0	352	4 AAG80111	Aag80111 Human CCR
13	96	100.0	352	4 AAE04321	Aae04321 Human che
14	96	100.0	352	4 AAE07037	Aae07037 Human G-P
15	96	100.0	352	4 AAE07039	Aae07039 Human G-P
16	96	100.0	352	4 AAB46858	Aab46858 Human HDG
17	96	100.0	352	4 ABB56342	Abb56342 Non-endog
18	96	100.0	352	4 AAB83354	Aab83354 Human CCR
19	96	100.0	352	4 AAB82948	Aab82948 Human HIV
20	96	100.0	352	5 AAU97150	Aau97150 Human G-P
21	96	100.0	352	5 AAU97152	Aau97152 Human CCR
22	96	100.0	352	5 AAM52829	Aam52829 Human CCR
23	96	100.0	352	5 AAM52828	Aam52828 Human CC
24	96	100.0	352	5 AEG70597	Aeg70597 Human G-P
25	96	100.0	352	5 AEG92883	Aeg92883 Human imm

ALIGNMENTS

RESULT 1

AAB88954

ID AAB88954 standard; peptide; 18 AA.

XX AAB88954;

DT 23-MAY-2001 (first entry)

DE HIV gp120 protein binding peptide #47.

KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.

OS Homo sapiens.

PN WO200116182-A2.

PD 08-MAR-2001.

PP 25-AUG-2000; 2000WO-US023505.

PR 27-AUG-1999; 99US-0151270P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions.

PS Example 1; Page 37; 114pp; English.

XX The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention

SQ Sequence 18 AA;

Query Match 100.0%; Score 96; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.2e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18

```

Db      1  SQYQFWKNFQTLKIVILG 18
|||||
RESULT 2
AAAB88995
ID  AAB88995 standard; peptide; 18 AA.
XX
AC  AAB88995;
XX
DT  23-MAY-2001 (first entry)
XX
DE  HIV gp120 protein binding peptide #88.
XX
KW  Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW  replication; CCR5; CXCR4; CD4; STRL33.
XX
OS  Homo sapiens.
XX
FN  WO200116182-A2.
XX
PD  08-MAR-2001.
XX
PF  25-AUG-2000; 2000WO-US023505.
XX
PR  27-AUG-1999; 99US-0151270P.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Saxinger C;
XX
DR  WPI; 2001-244398/25.
XX
PT  Novel polypeptides useful for treating HIV infection, have homology to
PT  regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT  and binds to HIV gp120 under physiological conditions.
XX
PS  Claim 21; Page 38; 114pp; English.
XX
CC  The present invention describes a number of peptides which are able to
CC  bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC  chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC  useful in the treatment of HIV, as they prevent replication of the virus.
CC  The present sequence is an example of a peptide of the invention
XX
XX  Sequence 18 AA;
XX
Query Match 100.0%; Score 96; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  SQYQFWKNFQTLKIVILG 18
Db      1  SQYQFWKNFQTLKIVILG 18
|||||
RESULT 3
AAW27407
ID  AAW27407 standard; protein; 352 AA.
XX
AC  AAW27407;
XX
DT  14-APR-1998 (first entry)
XX
DE  Human CCR5.
XX
KW  Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
KW  type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
KW  inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
KW  idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
KW  atherosclerosis; autoimmune disorder.
XX
OS  Homo sapiens.

```

```

XX  WO9732019-A2.
XX
PD  04-SEP-1997.
XX
PF  28-FEB-1997; 97WO-BE000023.
XX
PR  01-MAR-1996; 96EP-00870021.
PR  06-AUG-1996; 96EP-00870102.
XX
PA  (EURO-) EUROSCREEN SA.
XX
PI  Samson M, Parmentier M, Vassart G, Libert F;
XX
DR  WPI; 1997-479829/44.
DR  N-PSDB; AAT90117.
XX
PT  Active and inactive forms of human CC chemokine receptor CCR-5 - useful
PT  to diagnose, prevent and/or treat inflammatory disorders, autoimmune
PT  disease and viral infection.
XX
PS  Claim 4; Fig 1b-c; 94pp; English.
XX
CC  The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
CC  which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but
CC  not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,
CC  interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
CC  chemokines. Active CCR-5 is also a receptor of human immunodeficiency
CC  virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its CDNA can be used to
CC  diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
CC  arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
CC  psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
CC  atherosclerosis and autoimmune disorders
XX
SQ  Sequence 352 AA;
XX
Query Match 100.0%; Score 96; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  SQYQFWKNFQTLKIVILG 18
Db      185  SQYQFWKNFQTLKIVILG 202
|||||
RESULT 4
AAW27123
ID  AAW27123 standard; protein; 352 AA.
XX
AC  AAW27123;
XX
DT  14-DEC-1997 (first entry)
XX
DE  Human chemokine receptor 88C.
XX
KW  Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
KW  asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
KW  diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
KW  modulator; antibody; human.
XX
OS  Homo sapiens.
XX
Key Location/Qualifiers
FH Domain 1..32 /label= Extracellular_domain
FT Domain 56..67 /label= Intracellular_domain
FT Domain 89..112 /label= Extracellular_domain
FT Domain 125..145 /label= Extracellular_domain
FT Domain 166..191 /label= Intracellular_domain
FT Domain /label= Extracellular_domain

```


FT Region 261..276
 FT /note= "extracellular loop-3 (Claim 19)"
 FT Domain 277..300
 FT /label= VII
 FT /note= "transmembrane domain"
 XX
 PN WO9745543-A2.
 XX
 PD 04-DEC-1997.
 XX
 XX 28-MAY-1997; 97WO-US009586.
 PF 28-MAY-1996; 96US-0018508P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
 PI Broder CC, Kennedy PE;
 XX WPI; 1998-032650/03.
 DR N-PSDB; AAT76920.
 XX
 XX CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
 PT between HIV and a target cell.
 PT
 XX Claim 68; Fig 1C; 70pp; English.
 PS
 XX This protein sequence comprises of a novel human macrophage-selective CC
 CC chemokine receptor that has been designated CCR5. The sequence was
 CC deduced from an isolated cDNA clone (see AAT76920). An Alai27Leu variant
 CC (see W238340 of CCR5 was also identified. The susceptibility of human
 CC macrophages to HIV infection depends on cell surface expression of CD4
 CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
 CC protein coupled cell surface molecules. It plays an essential role in the
 CC membrane fusion step of infection by some HIV isolates. The establishment
 CC of stable, non-human cell lines and transgenic mammals having cells that
 CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV
 CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
 CC agents capable of blocking membrane fusion between HIV and target cells
 CC represent potential anti-HIV therapeutics for macrophage tropic strains
 CC of HIV
 CC
 SQ Sequence 352 AA;
 XX
 Query Match 100.0%; Score 96; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No; 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SOYQFWKNFQTLKIVILG 18
 Db |||||
 185 SOYQFWKNFQTLKIVILG 202
 RESULT 7
 AAW88232
 ID AAW88232 standard; protein; 352 AA.
 XX
 AC AAW88232;
 XX
 XX 15-MAR-1999 (first entry)
 DT
 XX HIV-1 co-receptor CCR5.
 DE
 XX HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
 KW gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 32..56
 FT /note= "transmembrane domain 1"
 FT Domain 67..87
 FT /note= "transmembrane domain 2"
 FT

FT Misc-difference 101
 FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA
 FT (Stop) in CCR5m303"
 FT 103..124
 FT Domain /note= "transmembrane domain 3"
 FT 142..167
 FT Domain /note= "transmembrane domain 4"
 FT 200..223
 FT Domain /note= "transmembrane domain 5"
 FT 236..260
 FT Domain /note= "transmembrane domain 6"
 FT 275..301
 FT Domain /note= "transmembrane domain 7"
 XX
 PN WO9854317-A1.
 XX
 XX 03-DEC-1998.
 PD
 XX 29-MAY-1998; 98WO-EP003437.
 PF
 XX 30-MAY-1997; 97US-0048057P.
 PR
 XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 PA Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
 PI WPI; 1999-059835/05.
 XX N-PSDB; AAW84126.
 DR
 XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 PT resistance of CCR5-expressing cells to HIV-1 infection.
 PT
 XX Disclosure; Page 34-35; 55pp; English.
 PS
 XX This is the amino acid sequence of wild-type human CCR5, which serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see
 CC AAW8231), designated CCR5m303, comprising the first two transmembrane
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
 CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a
 CC positive correlation with resistance to infection with M-tropic HIV-1
 CC strains, and may indicate slower progression of the disease. The
 CC detection of CCR5 variants may be used to identify individuals at lower
 CC risk of infection relative to the general population who, if infected,
 CC may exhibit slower progression to AIDS. Probes and primers (see AAW8412-
 CC 36) are provided for use in diagnostic methods for detecting the presence
 CC of such variants. A method is provided for inhibiting HIV-1 infection of
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number
 CC of functional CCR5 molecules present on the cell surface
 CC
 SQ Sequence 352 AA;
 XX
 Query Match 100.0%; Score 96; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No; 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SOYQFWKNFQTLKIVILG 18
 Db |||||
 185 SOYQFWKNFQTLKIVILG 202
 RESULT 8
 AAY80128
 ID AAY80128 standard; protein; 352 AA.
 XX
 AC AAY80128;
 XX
 XX 19-MAY-2000 (first entry)
 DT
 XX Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
 DE
 XX Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
 KW

KW diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
 KW tumour; infection; leukaemia; psoriasis; allergy;
 KW T-cell mediated autoimmune disease; atherogenesis; anaphylaxis;
 KW inflammation; allergic reaction; silicosis; sarcoidosis;
 KW rheumatoid arthritis; hyper-eosinophilia syndrome.
 XX
 OS Homo sapiens.
 XX
 PN US6025154-A.
 XX
 XX 15-FEB-2000.
 XX
 XX 06-JUN-1995; 95US-00466343.
 XX
 XX 06-JUN-1995; 95US-00466343.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Li Y, Ruben SM;
 XX
 XX WPI; 2000-181807/16.
 XX
 XX N-PSDB; AAZ91481.
 XX
 XX Isolated nucleic acid encoding human G-protein chemokine receptor useful
 XX for diagnostic assays, scientific research and screening for compounds
 XX which bind to and activate or inhibit activation of the receptor
 XX polypeptides.
 XX
 XX Claim 1; Fig 1; 22pp; English.
 XX
 XX The present sequence represents a human G-protein chemokine receptor
 XX designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
 XX screening for compounds which bind to and either: (1) activate the
 XX HDGNR10 polypeptides causing stimulation of haematopoiesis, wound
 XX healing, coagulation, and angiogenesis; treatment of solid tumours,
 XX chronic infections, leukaemia, T-cell mediated autoimmune diseases,
 XX parasitic infections, psoriasis, and to stimulate growth factor activity;
 XX or (2) inhibit activation of the HDGNR10 polypeptides which is useful for
 XX preventing and/or treating allergy, atherogenesis, anaphylaxis,
 XX malignancy, chronic and acute inflammation, histamine and immunoglobulin
 XX E-mediated allergic reactions, prostaglandin-independent fever, bone
 XX marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
 XX hyper-eosinophilia syndrome. The polynucleotides are also useful for
 XX diagnostic assays for detecting diseases related to mutations in the
 XX nucleic acid sequences encoding the polypeptides and for detecting an
 XX altered level of the soluble form of the receptor polypeptides. The
 XX polynucleotides are also useful for in vitro purposes related to
 XX scientific research, synthesis of DNA and manufacture of DNA vectors
 XX
 XX Sequence 352 AA;
 XX
 XX Query Match 100.0%; Score 96; DB 3; Length 352;
 XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 SOYQFWKNFQTLKIVILG 18
 XX |||||
 XX 185 SOYQFWKNFQTLKIVILG 202
 XX
 XX
 XX RESULT 9
 XX AAG79089
 XX ID AAG79089 standard; protein; 352 AA.
 XX
 XX AC AAG79089;
 XX
 XX 10-DEC-2001 (first entry)
 XX
 XX Amino acid sequence of human CCR5 protein.
 XX
 XX Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
 KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
 XX

OS Homo sapiens.
 XX
 PN WO200164752-A2.
 XX
 PD 07-SEP-2001.
 XX
 XX 28-FEB-2001; 2001WO-US006322.
 XX
 XX 02-MAR-2000; 2000US-00517605.
 XX
 XX (UYNY) UNIV NEW YORK STATE.
 XX (UYNI-) UNIV NIJMEGEN.
 XX
 XX Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
 XX WPI; 2001-602565/68.
 XX
 XX An antibody for the treatment or prevention of HIV-infection comprises a
 XX gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
 XX DC-SIGN due to concomitant conformational change.
 XX
 XX Disclosure; Page 118-119; 131pp; English.
 XX
 XX The specification describes an antibody which is specific for an
 XX antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
 XX is exposed upon gp120 binding of DC-SIGN due to concomitant
 XX conformational change. DC-SIGN is a receptor that is specifically
 XX expressed on dendritic cells and facilitates infection of T lymphocytes
 XX with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
 XX -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 XX with high affinity. The antibody of the invention inhibits the trans
 XX enhancement of HIV entry into a T cell or macrophage facilitated by
 XX dendritic cells. The antibody is useful to treat or prevent HIV
 XX infection. The present sequence represents a human CCR5 protein, which is
 XX a translocation promoting agent that interacts with CD4. This receptor
 XX functions in HIV-1 entry into cells
 XX
 XX Sequence 352 AA;
 XX
 XX Query Match 100.0%; Score 96; DB 4; Length 352;
 XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 SOYQFWKNFQTLKIVILG 18
 XX |||||
 XX 185 SOYQFWKNFQTLKIVILG 202
 XX
 XX
 XX RESULT 10
 XX AAE07046
 XX ID AAE07046 standard; protein; 352 AA.
 XX
 XX AC AAE07046;
 XX
 XX 16-OCT-2001 (first entry)
 XX
 XX Human G-protein chemokine receptor (CCRS) HDGNR10 protein #1.
 XX
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1.36
 FT Domain /label= Extracellular_domain
 FT

Domain 37..305
/label= Transmembrane_domain
Domain 37..58
/label= Transmembrane_domain
/note= "Segment 1"
Domain 59..67
/label= Intracellular_loop_1
Domain 68..88
/label= Transmembrane_domain
/note= "Segment 2"
Domain 89..102
/label= Extracellular_loop_1
Domain 103..124
/label= Transmembrane_domain
/note= "Segment 3"
Domain 125..141
/label= Intracellular_loop_2
Domain 142..166
/label= Transmembrane_domain
/note= "Segment 4"
Domain 167..195
/label= Extracellular_loop_2
Domain 196..223
/label= Transmembrane_domain
/note= "Segment 5"
Domain 224..235
/label= Intracellular_loop_3
Domain 236..260
/label= Transmembrane_domain
/note= "Segment 6"
Domain 261..274
/label= Extracellular_loop_3
Domain 287..305
/label= Transmembrane_domain
/note= "Segment 7"
Domain 306..352
/label= Intracellular_domain
WO200158916-A2.
16-AUG-2001.
09-FEB-2001; 2001WO-US004153.
09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Roschke V, Li Y, Ruben SM;
WPI; 2001-488966/53.
N-PSDB; AAD13282.
Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
Claim 102; Fig 1; 518pp; English.
The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack

of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis) ; cardiovascular disorders (myocardial ischaemias) and wound healing. The present sequence is human CCR5 HDGNR10 protein
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQYQFWKMFQTLKIVILG 18
DB 185 SQYQFWKMFQTLKIVILG 202
RESULT 11
AAE07048
ID AAE07048 standard; protein; 352 AA.
XX AC AAE07048;
XX DT 16-OCT-2001 (first entry)
XX DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
XX KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnary;
KW cytostatic; immunosuppressive; neutropic; neuroprotective; gene therapy;
KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
KW cardiovascular disorder; myocardial ischaemia.
XX OS Homo sapiens.
XX PN WO200158916-A2.
XX PD 16-AUG-2001.
XX PF 09-FEB-2001; 2001WO-US004153.
XX PR 09-FEB-2000; 2000US-0181258P.
XX PR 09-MAR-2000; 2000US-0187999P.
XX PR 22-SEP-2000; 2000US-0234336P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX WPI; 2001-488966/53.
XX DR N-PSDB; AAD13299.
XX PT Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
XX PS Example 40; Page 504-505; 518pp; English.
XX CC The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder

CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC disease or disorder may be associated with aberrant CCR5 expression, lack
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGNR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The
 CC present sequence is human CCR5 HDGNR10 protein
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
 DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 12
 AAG80111
 ID AAG80111 standard; protein; 352 AA.

AC AAG80111;

XX 17-JAN-2002 (first entry)

DT Human CCR5 protein.

DE Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.

XX Homo sapiens.

OS WO200172830-A2.

PN 04-OCT-2001.

PD 02-APR-2001; 2001WO-EP003708.

PF 31-MAR-2000; 2000DE-01016013.

XX (IPFP-) IPF PHARM GMBH.

XX (FORS/) FORSMANN U.

PI Forssmann W, Adermann K, Heitland A, Spodsborg N;

XX WPI; 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.

XX Disclosure; Page 10; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in

CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation) or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
 DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 13

AAG804321
 ID AAG804321 standard; protein; 352 AA.

XX AAE04321;

XX 04-SEP-2001 (first entry)

DT Human chemokine receptor (CKR), CC-CKR-5 related protein #2.

DE Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CKR-5; envelope glycoprotein; anti-HIV.

XX Homo sapiens.

OS US6258527-B1.

PN 10-JUL-2001.

PD 21-MAY-1997; 97US-00861105.

PF 20-MAY-1996; 96US-0017157P.

PR 19-JUN-1996; 96US-0020043P.

XX 19-MAY-1997; 97US-00858660.

XX (AARO-) AARON DIAMOND AIDS RES CENT.

PA (UANY) UNIV NEW YORK STATE.

XX Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;

XX WPI; 2001-417127/44.

DR N-PSDB; AAD08577.

XX Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
 PT and HIV LTR for identification of drugs and antibodies for treatment of
 PT HIV.

PS Disclosure; Col 47-50; 37pp; English.

XX The present invention relates to a transformed mammalian cell that
 CC contains a gene encoding CD4, a construct encoding a reporter gene under
 CC the regulation of an human immuno deficiency virus (HIV) long terminal
 CC repeat (LTR) and that has been transduced with a vector encoding a human
 CC chemokine receptor (CKR) where the CD4 and the CKR are present on the
 CC cell surface of transformed mammalian cell. The invention is useful for

CC identifying drugs or antibodies that interfere with the translocation of
 CC HIV into transformed mammalian cell or for identifying a human chemokine
 CC receptor that facilitates the infection of a particular HIV strain into
 CC the transformed mammalian cell. Compounds identified can be used to treat
 CC cellular dysfunction and to prevent or combat HIV infection. The present
 CC sequence is a human chemokine receptor (CCR), CC-CR-5 related protein.
 CC CC-CR-5 is the principal cofactor for entry, mediated by the envelope
 CC glycoproteins of primary macrophage-tropic strains of HIV-1
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
 Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 14
 ID AAE07037 standard; protein; 352 AA.
 AC AAE07037;

DT 16-OCT-2001 (first entry)
 XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW Human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 1..36 /label= Extracellular_domain
 FT Domain 37..305 /label= Transmembrane_domain
 FT Domain 37..58 /label= Transmembrane_domain
 FT /note= "Segment 1"
 FT Domain 59..67 /label= Intracellular_loop_1
 FT Domain 68..88 /label= Transmembrane_domain
 FT /note= "Segment 2"
 FT Domain 89..102 /label= Extracellular_loop_1
 FT Domain 103..124 /label= Transmembrane_domain
 FT /note= "Segment 3"
 FT Domain 125..141 /label= Intracellular_loop_2
 FT Domain 142..166 /label= Transmembrane_domain
 FT /note= "Segment 4"
 FT Domain 167..195 /label= Extracellular_loop_2
 FT Domain 196..223 /label= Transmembrane_domain
 FT /note= "Segment 5"
 FT Domain 224..235 /label= Intracellular_loop_3
 FT Domain 236..260

FT /label= Transmembrane_domain
 FT /note= "Segment 6"
 FT 261..274 /label= Extracellular_loop_3
 FT 287..305 /label= Transmembrane_domain
 FT /note= "Segment 7"
 FT 306..352 /label= Intracellular_domain
 FT
 XX WO200158915-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004152.
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2001-488965/53.
 DR N-PSDB; AAD13181.
 XX
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX
 XX Claim 102; Fig 1; 495pp; English.

XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5
 CC HDGNR10 antibodies are useful for treating, preventing or ameliorating a
 CC disease or disorder associated with inflammation, defective or aberrant
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen
 CC presenting cell interaction. The disease or disorder may also be an
 CC infectious disease (e.g. a viral infection such as an early stage HIV
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative
 CC disorder. The disease or disorder may be associated with aberrant CCR5
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or
 CC lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene
 CC therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists
 CC are also useful in the diagnosis, treatment and prevention of cancer
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis); cardiovascular disorders (myocardial ischaemia) and wound
 CC healing
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
 Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 15
 ID AAE07039 standard; protein; 352 AA.
 XX

AC AAE07039;
 XX 16-OCT-2001. (first entry)
 XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
 DE Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 XX human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytosolic; immunosuppressive; nontropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX Homo sapiens.
 OS WO200158915-A2.
 XX 16-AUG-2001.
 PD 09-FEB-2001; 2001WO-US004152.
 PF 09-FEB-2000; 2000US-0181258P.
 XX 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2001-488965/53.
 XX N-PSDB; AAD13198.
 DR Isolated nucleic acid encoding a human G-protein chemokine receptor
 XX (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 XX diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 XX neurodegenerative disorders.
 XX Example 40; Page 486-487; 495pp; English.
 PS The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 XX protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
 XX ameliorating a disease or disorder associated with inflammation,
 XX defective or aberrant chemotaxis of immune cells, HIV infection (such as
 XX Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
 XX aberrant T-cell antigen presenting cell interaction. The disease or
 XX disorder may also be an infectious disease (e.g. a viral infection such
 XX as an early stage HIV infection, a cytomegalovirus infection, or a
 XX poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
 XX a neurodegenerative disorder. The disease or disorder may be associated
 XX with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
 XX ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
 XX is used as a food additive or preservative to increase or decrease
 XX storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
 XX identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
 XX antibodies, agonists and antagonists are also useful in the diagnosis,
 XX treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
 XX bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
 XX disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
 XX autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 XX sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
 XX disorders (myocardial ischaemias) and wound healing

Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 SQQFWNFQTLKIVILG 18
 ||||||||||||||||

Db 185 SQQFWNFQTLKIVILG 202
 RESULT 16
 AAB46858
 ID AAB46858 standard; protein; 352 AA.
 XX AAB46858;
 AC 16-AUG-2001 (revised)
 DT 02-AUG-2001 (revised)
 DT 04-MAY-2001 (first entry)
 XX Human HDGNR10 protein.
 DE HDGNR10; human; G-protein chemokine receptor; antiinflammatory;
 XX immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
 KW cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;
 KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
 KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
 KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
 KW anaphylaxis; malignancy; inflammation; histamine; IGE; silicosis; shock;
 KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
 KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
 KW hyper-eosinophilic syndrome; vulnery.
 XX Homo sapiens.
 OS US2001000241-A1.
 XX 12-APR-2001.
 PD 29-NOV-2000; 2000US-00725285.
 PF 06-JUN-1995; 95US-00466343.
 PR 18-NOV-1998; 98US-00195662.
 PR 25-JUN-1999; 99US-00339912.
 XX (LIYY/) LI Y.
 XX (RUBE/) RUBEN S M.
 PA Li Y, Ruben SM;
 XX WPI; 2001-226317/23.
 XX N-PSDB; AAF26390.
 DR New human G-protein chemokine receptor polypeptides and polynucleotides,
 XX useful for identifying (ant)agonists to the G-protein chemokine receptor.
 PS Claim 1a; Page 15; 22pp; English.
 CC This invention describes a novel receptor polypeptide (I) selected from
 CC (i) a fully defined 329 amino acid sequence (ii) fully disclosed in the
 CC specification; and (ii) a polypeptide encoded by the cDNA contained in a
 CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
 CC products of the invention have antiinflammatory, immunomodulatory,
 CC anticoagulant, antiallergic, immunosuppressive, vulnery, cytostatic,
 CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic
 CC activity and can be used for gene therapy. The G-protein chemokine
 CC receptors, HDGNR10, (I) are useful for screening for compounds which
 CC activate or inhibit activation of (I). The products of the invention can
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,
 CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and
 CC stimulating growth factor activity. HDGNR10 is useful for treating
 CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and immunoglobulin E (IGE)-mediated allergic
 CC reactions, prostaglandin-independent fever, bone marrow failure,
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. (N.B. this record was resubmitted to correct
 CC errors in the keyword formatting)
 XX Sequence 352 AA;

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Query Match      100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 17
AB856342
ID AB856342 standard; protein; 352 AA.
AC AB856342;
DT 18-FEB-2002 (first entry)
XX Non-endogenous human GPCR protein, SEQ ID NO: 477.
DE Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW constitutively activated GPCR; agonist; disease.
XX Homo sapiens.
OS Synthetic.
XX WO200177172-A2.
XX 18-OCT-2001.
XX 05-APR-2001; 2001WO-US011098.
XX 07-APR-2000; 2000US-0195747P.
XX (AREN-) ARENA PHARM INC.
XX Lehmann-Bruinsma K, Liaw CW, Lin I;
XX WPI; 2001-648759/74.
XX N-PSDB; ABI97978.
XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
XX disease treatment, comprises contacting candidate compounds with versions
XX of GPCRs.
XX Claim 1; Page 277-278; 394pp; English.
XX The invention relates to G protein-coupled receptors (GPCRs) for which
XX the endogenous ligand has been identified. Non-endogenous constitutively
XX activated versions of known GPCRs are used in the invention for the
XX direct identification of candidate compounds as receptor agonists,
XX inverse agonists or partial agonists. Such agonists are useful as
XX therapeutic agents for diseases or disorders associated with GPCRs. The
XX present sequence is a non-endogenous version of a known human GPCR
XX
XX Sequence 352 AA;
Query Match      100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 18
AB833354
ID AB833354 standard; protein; 352 AA.
XX AAB83354;
XX 09-OCT-2001 (first entry)
XX
XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
XX disease treatment, comprises contacting candidate compounds with versions
XX of GPCRs.
XX Claim 1; Page 277-278; 394pp; English.
XX The invention relates to G protein-coupled receptors (GPCRs) for which
XX the endogenous ligand has been identified. Non-endogenous constitutively
XX activated versions of known GPCRs are used in the invention for the
XX direct identification of candidate compounds as receptor agonists,
XX inverse agonists or partial agonists. Such agonists are useful as
XX therapeutic agents for diseases or disorders associated with GPCRs. The
XX present sequence is a non-endogenous version of a known human GPCR
XX
XX Sequence 352 AA;
Query Match      100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 19
AAB82948
ID AAB82948 standard; protein; 352 AA.
XX AAB82948;
XX 21-DEC-2001 (first entry)
XX
XX Human HIV-1 co-receptor CCR5.
XX CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
XX infection; therapy; vaccine; anti-HIV-1.
XX Homo sapiens.
XX

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XX Human CCR5 protein sequence.
DE Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
XX human immunodeficiency virus; anti-inflammatory disease; human.
KW Homo sapiens.
XX EP1118858-A2.
XX 25-JUL-2001.
XX 03-JAN-2001; 2001EP-00300020.
XX 12-JAN-2000; 2000GB-00000659.
XX 12-JAN-2000; 2000GB-00000661.
XX 12-JAN-2000; 2000GB-00000663.
XX (PFIZ ) PFIZER LTD.
XX (PFIZ ) PFIZER INC.
XX Dobbs S, Perros M, Rickett GA;
XX WPI; 2001-477088/52.
XX N-PSDB; AAF87099.
XX Determining if an agent can modulate CCR5-gp120 interaction, comprises
XX incubating the agent with CCR5 and gp120 and determining if the agent
XX modulates the interaction.
XX Claim 1; Page 110; 113pp; English.
XX This sequence represents the human CCR5 protein sequence. The invention
XX relates to a method for determining whether an agent is capable of
XX modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
XX with gp120, comprising incubating the agent with CCR5 and gp120 and
XX determining whether the agent modulates the interaction, where gp120 is
XX associated with CD4, and where the interaction is a low affinity binding.
XX The method is used to identify an agent capable of modulating the
XX interaction of CCR5 with gp120. An agent identified by the method is used
XX to prepare a pharmaceutical composition for the treatment of a disease or
XX condition associated with CCR5 and gp120 interaction, to treat a subject
XX with a disease or condition associated with CCR5 and gp120 interaction,
XX and for preparing a pharmaceutical for treating human immunodeficiency
XX virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
XX is commercially useful, amenable to high throughput screening, and
XX detects interaction of gp120 with cells expressing only CCR5
XX
XX Sequence 352 AA;
Query Match      100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 19
AAB82948
ID AAB82948 standard; protein; 352 AA.
XX AAB82948;
XX 21-DEC-2001 (first entry)
XX
XX Human HIV-1 co-receptor CCR5.
XX CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
XX infection; therapy; vaccine; anti-HIV-1.
XX Homo sapiens.
XX

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XX Key Location/Qualifiers
FT Binding-site 2..18 /note= "binds to HIV-1 gp120"
FT FT
XX WO200164710-A2.
XX 07-SEP-2001.
XX 28-FEB-2001; 2001WO-US006599.
XX 29-FEB-2000; 2000US-01856677.
PR 19-MAY-2000; 2000US-0205839P.
PR 07-FEB-2001; 2001US-0267231P.
XX (PROG-) PROGENICS PHARM INC.
PA (AARO-) AARON DIAMOND AIDS RES CENT.
XX Dragic T, Olson WC;
PI WPI; 2001-611273/70.
DR N-PSDB; AAH26903.
XX Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-receptor) amino terminal domain including negatively charged and two sulfated tyrosine residues is useful for treating HIV infection in humans.
XX Claim 1; Page 30; 163pp; English.
XX The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding site that determines the specificity of the interaction between CCR5 and HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the CCR5 N-terminus is required for gp120 binding and may critically modulate the susceptibility of target cells to HIV-1 infection in vivo. The invention provides claimed sulfated peptides (see AB82947) that are based on the CCR5 N-terminal region and which are effective for inhibiting HIV-1 binding to CCR5. These peptides are used in claimed methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+ cells from becoming infected with HIV, of treating a subject whose CD4+ cells are infected with HIV, and of identifying an agent which inhibits binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried out in a subject, especially a human, infected (therapeutic method), not infected with HIV (prophylactic method), or in a subject who is not infected with, but has been exposed to, HIV
SQ Sequence 352 AA;
Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202
RESULT 20
AAU97150
ID AAU97150 standard; protein; 352 AA.
XX AAU97150;
XX 13-AUG-2002 (first entry)
XX Human G-protein chemokine receptor (CCR5) HDGNNR10 #1.
XX Human; G-protein chemokine receptor; CCR5; HDGNNR10; inflammation;
XX immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
KW hyperproliferative disease; neurological disease; receptor.
XX

OS Homo sapiens.
XX US2002048786-A1.
XX 25-APR-2002.
XX 09-FEB-2001; 2001US-00779879.
XX 09-FEB-2000; 2000US-0181258P.
PR 09-MAR-2000; 2000US-0187999P.
PR 22-SEP-2000; 2000US-0234336P.
XX (ROSE/) ROSEN C A.
PA (ROSC/) ROSCHKE V.
PA (LIYY/) LI Y.
PA (RUBE/) RUBEN S M.
XX Rosen CA, Roschke V, Li Y, Ruben SM;
PI WPI; 2002-434754/46.
DR N-PSDB; ABK51853.
XX New nucleic acid encoding an antibody specific for the G-protein PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g. PT inflammation.
XX Claim 61; Fig 1; 180pp; English.
XX The present invention relates to the isolation of a novel human G-protein CC chemokine receptor (CCR5) designated HDGNNR10, and polynucleotide CC sequences encoding it. The invention also describes antibodies that bind CC human G-protein chemokine receptor (CCR5) HDGNNR10 and polynucleotide CC sequences encoding the antibodies. The antibodies are useful for treating CC or preventing inflammation, defective or aberrant chemotaxis of immune CC cells and T-cell/antigen-presenting cell interactions, infections and CC autoimmune diseases, Rheumatoid arthritis, neurodegeneration, viral CC infections (especially early-stage human immune deficiency virus (HIV), CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions CC associated with aberrant or deficient expression of the CCR5 receptor or CC its ligands. The antibodies are also useful to determine CCR5 expression, CC e.g. for diagnosis, prognosis and monitoring of cancer and other CC hyperproliferative diseases. The polynucleotide sequences encoding human CC G-protein chemokine receptor (CCR5) HDGNNR10 can be used to produce the CC recombinant receptor, and in the treatment of a wide range of diseases CC such as infectious diseases (e.g. influenza), neurological diseases (e.g. CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The CC present sequence represents human G-protein chemokine receptor (CCR5) CC HDGNNR10 #1
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 96; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202
RESULT 21
AAU97152
ID AAU97152 standard; protein; 352 AA.
XX AAU97152;
XX 13-AUG-2002 (first entry)
XX Human G-protein chemokine receptor (CCR5) HDGNNR10 #2.
XX Human; G-protein chemokine receptor; CCR5; HDGNNR10; inflammation;
KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
KW hyperproliferative disease; neurological disease; receptor.
KW

XX KW hyperproliferative disease; neurological disease; receptor.

XX OS Homo sapiens.

XX PN US2002048786-A1.

XX PD 25-APR-2002.

XX PF 09-FEB-2001; 2001US-00779879.

XX PR 09-FEB-2000; 2000US-0181259P.

XX PR 09-MAR-2000; 2000US-0187999P.

XX PR 22-SEP-2000; 2000US-0234336P.

XX PA (ROSE/) ROSEN C A.

XX PA (ROSC/) ROSCHKE V.

XX PA (LIYY/) LI Y.

XX PA (RUBE/) RUBEN S M.

XX PI Rosen CA, Roschke V, Li Y, Ruben SM;

XX DR WPI; 2002-434754/46.

XX DR N-PSDB; ABK51870.

XX PT New nucleic acid encoding an antibody specific for the G-protein

XX PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.

XX PT inflammation.

XX PS Disclosure; Page 165-166; 180pp; English.

XX CC The present invention relates to the isolation of a novel human G-protein

XX CC chemokine receptor (CCR5) designated HDGMR10, and polynucleotide

XX CC sequences encoding it. The invention also describes antibodies that bind

XX CC human G-protein chemokine receptor (CCR5) HDGMR10 and polynucleotide

XX CC sequences encoding the antibodies. The antibodies are useful for treating

XX CC or preventing inflammation, defective or aberrant chemotaxis of immune

XX CC cells and T-cell/antigen-presenting cell interactions, infections and

XX CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral

XX CC infections (especially early-stage human immune deficiency virus (HIV),

XX CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions

XX CC associated with aberrant or deficient expression of the CCR5 receptor or

XX CC its ligands. The antibodies are also useful to determine CCR5 expression,

XX CC e.g. for diagnosis, prognosis and monitoring of cancer and other

XX CC hyperproliferative diseases. The polynucleotide sequences encoding human

XX CC G-protein chemokine receptor (CCR5) HDGMR10 can be used to produce the

XX CC recombinant receptor, and in the treatment of a wide range of diseases

XX CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.

XX CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The

XX CC present sequence represents human G-protein chemokine receptor (CCR5)

XX CC HDGMR10 #2

XX SQ Sequence 352 AA;

XX Query Match 100.0%; Score 96; DB 5; Length 352;

XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18

DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 22

ID AAM52829

XX AAM52829 standard; protein; 352 AA.

XX AC AAM52829;

XX DT 22-FEB-2002 (first entry)

XX DE Human CCR5 Gln 55 variant.

XX CC CCR5; CC chemokine receptor 5; human; HIV infection;

XX KW

XX KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;

XX XX drug screening; identification; variant.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Misc-difference 55

XX FT /note= "Glu replaces wild-type Leu; encoded by CTG"

XX FT Misc-difference 58

XX FT /note= "Encoded by AGC"

XX XX WO200171346-A2.

XX XX 27-SEP-2001.

XX XX 21-MAR-2001; 2001WO-US009155.

XX XX 21-MAR-2000; 2000US-0190946P.

XX PR 21-MAR-2000; 2000US-0190996P.

XX PR 21-MAR-2000; 2000US-0191299P.

XX PR 20-MAR-2001; 2001US-00813448.

XX PR 20-MAR-2001; 2001US-00813651.

XX PR 20-MAR-2001; 2001US-00813653.

XX XX (CONS-) CONSENSUS PHARM INC.

XX PA Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;

XX PI WPI; 2002-010610/01.

XX DR N-PSDB; ABA02318.

XX XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,

XX PT comprises binding a molecule from library to a molecule having binding

XX PT property corresponding to CCR5 and identifying bound molecule.

XX PS Example 3; Fig 4B; 50pp; English.

XX CC The invention relates to a method for identifying a binding compound for

XX CC chemokine receptor 5 (CCR5). The method involves screening a library

XX CC of test molecules (particularly peptides) with immobilised CCR5, and then

XX CC identifying those molecules which bind. The invention also relates to

XX CC CCR5-binding molecules identified using the method of the invention,

XX CC methods for identifying consensus motifs for CCR5-binding peptides, a

XX CC transfer vector encoding tagged CCR5, a computer-aided methods for

XX CC determining the relative binding affinity of a test molecule to CCR5 and

XX CC a computer aided drug screening assay that utilises the three-dimensional

XX CC structure of CCR5. Compounds identified using the methods of the

XX CC invention are useful for treating or preventing HIV (human

XX CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency

XX CC syndrome) in a patient. The methods of the invention may also be used to

XX CC identify agonists or antagonists of the interaction of CCR5 with its

XX CC natural ligand, and to determine a binding motif for CCR5. The present

XX CC sequence represents a naturally occurring variant of human CCR5 in which

XX CC there is a glutamine, rather than a leucine, at position 55

XX SQ Sequence 352 AA;

XX Query Match 100.0%; Score 96; DB 5; Length 352;

XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18

DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 23

ID AAM52828

XX AAM52828 standard; protein; 352 AA.

XX AC AAM52828;

XX DT 22-FEB-2002 (first entry)

XX CC CCR5; CC chemokine receptor 5; human; HIV infection;

XX KW


```

XX DE Human CC chemokine receptor 5 (CCR5).
XX KW CCR5; CC chemokine receptor 5; human; HIV infection;
XX KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
XX KW drug screening; identification.
XX OS Homo sapiens.
XX PN WO200171346-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009155.
XX PR 21-MAR-2000; 2000US-0190946P.
XX PR 21-MAR-2000; 2000US-019096P.
XX PR 21-MAR-2000; 2000US-0191299P.
XX PR 20-MAR-2001; 2001US-00813448.
XX PR 20-MAR-2001; 2001US-00813451.
XX PR 20-MAR-2001; 2001US-00813653.
XX PA (CONS-) CONSENSUS PHARM INC.
XX PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX PT WPI; 2002-010610/01.
XX DR N-PSDB; ABA02317.
XX PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX PT comprises binding a molecule from library to a molecule having binding
XX PT property corresponding to CCR5 and identifying bound molecule.
XX PS Example 3; Fig 4A; 50pp; English.
XX CC The invention relates to a method for identifying a binding compound for
XX CC chemokine receptor 5 (CCR5). The method involves screening a library
XX CC of test molecules (particularly peptides) with immobilised CCR5, and then
XX CC identifying those molecules which bind. The invention also relates to
XX CC CCR5-binding molecules identified using the method of the invention,
XX CC methods for identifying consensus motifs for CCR5-binding peptides, a
XX CC transfer vector encoding tagged CCR5, a computer-aided methods for
XX CC determining the relative binding affinity of a test molecule to CCR5 and
XX CC a computer aided drug screening assay that utilises the three-dimensional
XX CC structure of CCR5. Compounds identified using the methods of the
XX CC invention are useful for treating or preventing HIV (human
XX CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
XX CC syndrome) in a patient. The methods of the invention may also be used to
XX CC identify agonists or antagonists of the interaction of CCR5 with its
XX CC natural ligand, and to determine a binding motif for CCR5. The present
XX CC sequence represents human CCR5
XX SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
Db 185 SOYQFWKNFQTLKIVILG 202

RESULT 24
ABG70597
ID ABG70597 standard; protein; 352 AA.
XX AC ABG70597;
XX DT 03-DEC-2002 (first entry)
XX DE Human G-protein chemokine receptor, HDGNR10.
XX

```

```

KW Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;
KW haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;
KW chronic infection; leukaemia; T-cell mediated autoimmune disease;
KW parasitic infection; psoriasis; growth factor activity; allergy;
KW atherogenesis; anaphylaxis; malignancy; inflammation; histamine;
KW immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;
KW prostaglandin-independent fever; bone marrow failure; shock;
KW rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic;
KW immunosuppressive; antiparasitic; antipsoriatic; antiallergic;
KW antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;
KW antipyretic; receptor.
XX OS Homo sapiens.
XX PN US2002099176-A1.
XX PD 25-JUL-2002.
XX PF 25-JUN-1999; 99US-00339912.
XX PR 06-JUN-1995; 95US-00466343.
XX (LIYY/) LI Y.
XX (RUBS/) RUBEN S M.
XX PI Li Y, Ruben SM;
XX WPI; 2002-690494/74.
XX DR N-PSDB; ABS54272.
XX PT Novel human G-protein chemokine receptor polypeptide useful for
XX PT identifying modulators for stimulating hematopoiesis, wound healing,
XX PT leukemia, for treating allergy, rheumatoid arthritis, shock and as
XX PT research agents.
XX PS Claim 7; Fig 1; 22pp; English.
XX CC The present invention relates to the isolation of human G-protein
XX CC chemokine receptor, HDGNR10 (CCR5 receptor), and the polynucleotide
XX CC sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences
XX CC are useful for diagnosing a disease or a susceptibility to a disease
XX CC related to underexpression of HDGNR10. They are useful for identifying
XX CC modulators for stimulating haematopoiesis, wound healing, coagulation,
XX CC angiogenesis, to treat solid tumours, chronic infections, leukaemia, T-
XX CC cell mediated autoimmune diseases, parasitic infections, psoriasis, or
XX CC for stimulating growth factor activity. The sequences are also useful for
XX CC preventing and/or treating allergy, atherogenesis, anaphylaxis,
XX CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
XX CC E (IgE)-mediated allergic reactions, prostaglandin-independent fever,
XX CC bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-
XX CC eosinophilic syndrome. Polynucleotide sequences encoding HDGNR10 can be
XX CC used in gene therapy to treat conditions related to underexpression of
XX CC HDGNR10. The present sequence represents human G-protein chemokine
XX CC receptor, HDGNR10
XX SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
Db 185 SOYQFWKNFQTLKIVILG 202

RESULT 25
ABG92883
ID ABG92883 standard; protein; 352 AA.
XX AC ABG92883;
XX DT 19-NOV-2002 (first entry)

```

XX DE Human immunoglobulin variable heavy domain #1.

XX

XX Immunoglobulin; variable heavy chain; variable light chain; human;

KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;

KW immunologic deficiency syndrome; blood protein disorder; nephritis;

KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;

KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;

KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;

KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;

KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;

KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;

KW lymphocytopenia.

XX

OS Homo sapiens.

XX

XX WO200264612-A2.

XX

XX 22-AUG-2002.

XX

XX 08-FEB-2002; 2002WO-US003634.

XX

XX 09-FEB-2001; 2001US-00779880.

PR 09-FEB-2001; 2001WO-US004153.

PR 12-JUN-2001; 2001US-0297257P.

PR 08-AUG-2001; 2001US-0310458P.

PR 12-OCT-2001; 2001US-0328447P.

PR 21-DEC-2001; 2001US-0341725P.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

XX

XX Roschke V, Rosen CA, Ruben SM;

XX

XX WPI; 2002-643455/69.

DR N-PSDB; ABS68606.

XX

XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for

PT treating, preventing, ameliorating or monitoring diseases or disorders

PT associated with aberrant expression of HDGNR10 e.g. cancer.

XX

XX Example 55; Fig 4; 562pp; English.

XX

XX The invention describes an isolated polynucleotide encoding a first

CC antibody at least 95-100% identical to a second antibody consisting of an

CC amino acid sequence comprising at least one, two or three CDR regions of

CC a variable heavy (VH) or variable light (VL) domain of the antibody

CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,

CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.18B5,

CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody

CC is useful treating, preventing, ameliorating, prognosing or monitoring

CC cancers or other diseases or disorders e.g. immunologic deficiency

CC syndromes such as blood protein disorders and ataxia telangiectasia,

CC inflammation associated disorders such as endotoxin lethality, nephritis

CC and inflammatory bowel disease, conditions associated with an increase in

CC certain haematopoietic cells such as histiocytosis, defective or aberrant

CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,

CC an infectious disease, an autoimmune disease such as Addison's disease,

CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative

CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or

CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,

CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a

CC disease or disorder associated with aberrant expression of novel human G-

CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid

CC sequence of human immunoglobulin sequence associated with the antibodies

CC against HDGNR10

XX

XX Sequence 352 AA;

SQ

Query Match 100.0%; Score 96; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SQYQFWNFQTLKIVLG 18

Db 185 SQYQFWNFQTLKIVLG 202

RESULT 26

ABG92880

ID ABG92880 standard; protein; 352 AA.

XX

XX ABG92880;

XX

XX 19-NOV-2002 (first entry)

DT

XX

XX Human G-protein chemokine receptor (CCR5) HDGNR10 #1.

XX

XX Immunoglobulin; variable heavy chain; variable light chain; human;

KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;

KW immunologic deficiency syndrome; blood protein disorder; nephritis;

KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;

KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;

KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;

KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;

KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;

KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;

KW lymphocytopenia.

XX

XX Homo sapiens.

XX

XX WO200264612-A2.

XX

XX 22-AUG-2002.

XX

XX 08-FEB-2002; 2002WO-US003634.

XX

XX 09-FEB-2001; 2001US-00779880.

PR 09-FEB-2001; 2001WO-US004153.

PR 12-JUN-2001; 2001US-0297257P.

PR 08-AUG-2001; 2001US-0310458P.

PR 12-OCT-2001; 2001US-0328447P.

PR 21-DEC-2001; 2001US-0341725P.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

XX

XX Roschke V, Rosen CA, Ruben SM;

XX

XX WPI; 2002-643455/69.

DR N-PSDB; ABS68653.

XX

XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for

PT treating, preventing, ameliorating or monitoring diseases or disorders

PT associated with aberrant expression of HDGNR10 e.g. cancer.

XX

XX Disclosure; Fig 1A-B; 562pp; English.

XX

XX The invention describes an isolated polynucleotide encoding a first

CC antibody at least 95-100% identical to a second antibody consisting of an

CC amino acid sequence comprising at least one, two or three CDR regions of

CC a variable heavy (VH) or variable light (VL) domain of the antibody

CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,

CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.18B5,

CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody

CC is useful treating, preventing, ameliorating, prognosing or monitoring

CC cancers or other diseases or disorders e.g. immunologic deficiency

CC syndromes such as blood protein disorders and ataxia telangiectasia,

CC inflammation associated disorders such as endotoxin lethality, nephritis

CC and inflammatory bowel disease, conditions associated with an increase in

CC certain haematopoietic cells such as histiocytosis, defective or aberrant

CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,

CC an infectious disease, an autoimmune disease such as Addison's disease,

CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative

CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or

CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,

CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a

CC disease or disorder associated with aberrant expression of novel human G-

CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid

CC sequence of human immunoglobulin sequence associated with the antibodies

CC against HDGNR10

XX

XX Sequence 352 AA;

SQ

Query Match 100.0%; Score 96; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SQYQFWNFQTLKIVLG 18

CC protein chemokine receptor (CCR5) HDGNR10. This is an amino acid sequence
CC of Human G-protein chemokine receptor (CCR5) HDGNR10 #1
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
|||
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 27
AAE25808
ID AAE25808 standard; protein; 352 AA.
XX
AC AAE25808;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human G-protein chemokine receptor (CCR5), HDGNR10 #1.
XX
KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
KW inflammation; viral infection; autoimmune disease; neurodegeneration;
KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
KW hyperproliferative disease; receptor.
XX
OS Homo sapiens.
XX
PN US2002061834-A1.
XX
PD 23-MAY-2002.
XX
PF 09-FEB-2001; 2001US-00779880.
XX
PR 09-FEB-2000; 2000US-0181258P.
PR 09-MAR-2000; 2000US-0187999P.
PR 22-SEP-2000; 2000US-0234336P.
XX
PA (ROSE/) ROSEN C A.
PA (ROSC/) ROSCHKE V.
PA (LIYY/) LI Y.
PA (RUBE/) RUBEN S M.
XX
PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX
DR WPI; 2002-499674/53.
DR N-PSDB; AAD42409.
XX
PT New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
PT useful for treatment, prevention and diagnosis of e.g. cancer, also
PT related antibodies.
XX
PS Claim 61; Page 163-164; 186pp; English.
XX
CC The invention relates to human G-protein chemokine receptor (CCR5), CCR5
CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
CC antibodies are used for the treatment or prevention of inflammation,
CC defective or aberrant chemotaxis of immune cells or T cell antigen-
CC presenting cell interaction, viral infections (specifically human immune
CC deficiency (including its early stages), cytomegalo or pox viruses),
CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
CC carinii infection, Kaposi's sarcoma or any condition associated with
CC aberrant expression of CCR5 or their ligands. They are also used for the
CC detection, diagnosis, prognosis and monitoring of cancers or other
CC hyperproliferative diseases. The present sequence is human G-protein
CC chemokine receptor (CCR5), HDGNR10 DNA
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
|||
DB 185 SOYQFWKNFQTLKIVILG 202

Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
|||
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 28
AAE25811
ID AAE25811 standard; protein; 352 AA.
XX
AC AAE25811;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human G-protein chemokine receptor (CCR5), HDGNR10 #2.
XX
KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
KW inflammation; viral infection; autoimmune disease; neurodegeneration;
KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
KW hyperproliferative disease; receptor.
XX
OS Homo sapiens.
XX
PN US2002061834-A1.
XX
PD 23-MAY-2002.
XX
PF 09-FEB-2001; 2001US-00779880.
XX
PR 09-FEB-2000; 2000US-0181258P.
PR 09-MAR-2000; 2000US-0187999P.
PR 22-SEP-2000; 2000US-0234336P.
XX
PA (ROSE/) ROSEN C A.
PA (ROSC/) ROSCHKE V.
PA (LIYY/) LI Y.
PA (RUBE/) RUBEN S M.
XX
PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX
DR WPI; 2002-499674/53.
DR N-PSDB; AAD42426.
XX
PT New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
PT useful for treatment, prevention and diagnosis of e.g. cancer, also
PT related antibodies.
XX
PS Disclosure; Page 170; 186pp; English.
XX
CC The invention relates to human G-protein chemokine receptor (CCR5), CCR5
CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
CC antibodies are used for the treatment or prevention of inflammation,
CC defective or aberrant chemotaxis of immune cells or T cell antigen-
CC presenting cell interaction, viral infections (specifically human immune
CC deficiency (including its early stages), cytomegalo or pox viruses),
CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
CC carinii infection, Kaposi's sarcoma or any condition associated with
CC aberrant expression of CCR5 or their ligands. They are also used for the
CC detection, diagnosis, prognosis and monitoring of cancers or other
CC hyperproliferative diseases. The present sequence is human G-protein
CC chemokine receptor (CCR5), HDGNR10 DNA
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
|||
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 29
ABB81054
ID ABB81054 standard; protein; 352 AA.
XX AC ABB81054;
XX DT 05-NOV-2002 (first entry)
XX DE G-protein chemokine receptor, HDGNR10.
XX KW 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;
KW G-protein chemokine receptor; haematopoietic; immunosuppressant;
KW antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic;
KW antirheumatic; antiarthritic; gene therapy; human; receptor.
XX OS Homo sapiens.
XX PN US2002076745-A1.
XX PD 20-JUN-2002.
XX PF 18-NOV-1999; 98US-00195662.
XX PR 06-JUN-1995; 95US-00466343.
XX PA (LIVY/) LI Y.
XX PA (RUBE/) RUBEN S M.
XX PI Li Y, Ruben SM;
XX WPI; 2002-598724/64.
XX DR N-PSDB; ABB86542.
XX PT New polynucleotide encoding a human G protein chemokine receptor HDGNR10,
XX useful e.g. for treating tumors.
XX PS Claim 7; Fig 1; 22pp; English.
XX CC The invention relates to a novel human 7-transmembrane receptor, HDGNR10,
XX which has been identified as a G-protein chemokine receptor. The GPCR
XX HDGNR10 polypeptide can be expressed by standard recombinant methodology.
XX Compounds that activate or inhibit the receptor polypeptide, optionally
XX expressed from DNA in gene therapy vectors, are used to treat diseases
XX that require: (a) activation of the receptor (e.g. stimulation of
XX haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune
XX diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the
XX receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis
XX etc). The present sequence represents the human HDGNR10 receptor
XX polypeptide
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 96; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQYQFWKNFOTLKIVILG 18
DB 185 SQYQFWKNFOTLKIVILG 202
RESULT 30
ABB08343
ID ABB08343 standard; protein; 352 AA.
XX AC ABB08343;
XX DT 18-JUN-2002 (first entry)
XX DE Human chemokine (C-C motif) receptor 5 polypeptide.

KW Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;
KW chromosome 3p21.
XX OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
FH Misc-difference 55 /label= Leu, Gln
FT Misc-difference 182 /label= Phe, Leu
FT Misc-difference 223 /label= Arg, Gln
XX WO200177125-A2.
XX 18-OCT-2001.
XX 04-APR-2001; 2001WO-US010708.
XX 05-APR-2000; 2000US-0194361P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Choi JY, Klem SE, Koshy B;
XX WPI; 2002-041282/05.
XX N-PSDB; ABA97318, ABA97319.
XX New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful
XX to diagnose and treat diseases associated with its abnormal expression or
XX function, including human immunodeficiency virus-1 infection.
XX Claim 29; Fig 3; 61pp; English.
XX The present sequence is that of a polypeptide encoded by the human
XX chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see
XX ABA97318, ABA97319). The specification describes haplotyping the CCR5
XX gene of an individual by determining if the individual has one of the
XX CCR5 haplotypes or haplotype pairs fully defined in the specification.
XX The specification also describes an isolated polynucleotide comprising a
XX nucleotide sequence which is a polymorphic variant of the reference CCR5
XX gene sequence and comprises an isogene defined by a haplotype described
XX in the specification and its encoded polypeptide. The methods of the
XX invention are useful to diagnose and develop treatment for diseases
XX associated with abnormal expression or function of the gene. The CCR5
XX isogenes and the screened compounds are useful for treating human
XX immunodeficiency virus (HIV)-1 infection and the progression to acquired
XX immunodeficiency syndrome (AIDS). The invention has antiviral
XX applications. The specification describes genotyping the CCR5 gene of an
XX individual; predicting a haplotype pair for the CCR5 gene of an
XX haplotype pair of the CCR5 gene. The specification describes a
XX composition comprising a genotyping oligonucleotide for detecting a CCR5
XX polymorphism; a recombinant non-human organism transformed with CCR5
XX polynucleotide expressing a CCR5 protein encoded by the variant sequence;
XX an isolated antibody specific for the CCR5 polypeptide and a method for
XX screening drugs targeting the CCR5 polypeptide
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 96; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQYQFWKNFOTLKIVILG 18
DB 185 SQYQFWKNFOTLKIVILG 202
RESULT 31

ABG75540
ID ABG75540 standard; protein; 352 AA.
XX AC ABG75540;
XX DT 16-APR-2003 (first entry)
XX DE Human G-protein chemokine receptor, HDGMR10, protein.
XX KW Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor;
HDGMR10; signal transduction; gene therapy; haematopoiesis;
wound healing; coagulation; angiogenesis; tumour; chronic infection;
leukaemia; T-cell mediated auto-immune disease; parasitic infection;
psoriasis; growth factor; allergy; atherogenesis; anaphylaxis;
malignancy; inflammation; histamine; Igs-mediated;
prostaglandin-independent fever; bone marrow failure; silicosis;
sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.
XX OS Homo sapiens.
XX PN US2002132269-A1.
XX PD 19-SEP-2002.
XX PF 11-FEB-2000; 2000US-00502783.
XX PR 06-JUN-1995; 95US-00466343.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Li Y, Ruben SM;
XX DR WPI; 2003-208944/20.
XX DR N-PSDB; ABX10635.
XX PT Novel human G-protein chemokine receptor polypeptide useful for
diagnostic purposes and for identifying modulators of the polypeptide
useful for treating leukemia, autoimmune diseases, psoriasis and allergic
reactions.
XX PS Claim 7; Fig 1; 22pp; English.
XX CC The invention discloses a G-protein chemokine receptor (sometimes
referred to as a 7-transmembrane receptor) polypeptide, HDGMR10, and the
polynucleotide encoding it. G-protein chemokine receptors are involved in
signal transduction pathways. The polynucleotide and polypeptide can be
used to identify compounds which activate or inhibit activation of the
protein and these compounds are useful for treating a patient having need
to activate or inhibit a G-protein chemokine receptor. The compound is
administered by providing to the patient DNA encoding the agonist or
antagonist and expressing them in vivo (gene therapy). The
polynucleotides and polypeptide are also useful for diagnosing a
disease or susceptibility to a disease related to an under-expression of
the protein, for chromosome identification or as immunogens for producing
antibodies. Agonists are useful in stimulating haematopoiesis, wound
healing, coagulation, angiogenesis, to treat solid tumours, chronic
infections, leukaemia, T-cell mediated auto-immune diseases, parasitic
infections, psoriasis and to stimulate growth factor activity.
XX CC Antagonists are useful in the prevention and treatment of allergy,
atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation,
histamine and Igs-mediated allergic reactions, prostaglandin-independent
fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis,
shock and hyper-eosinophilic syndrome. The sequence presented is the
human HDGMR10 protein
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 96; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKFNQTLKIVILG 18
|||||

Db 185 SQYQFWKFNQTLKIVILG 202
RESULT 32
ABR58602
ID ABR58602 standard; protein; 352 AA.
XX AC ABR58602;
XX DT 09-JUL-2003 (first entry)
XX DE Human cancer related protein SEQ ID NO:259.
XX KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
heart disease; atherosclerosis; endometriosis.
XX OS Homo sapiens.
XX PN WO2003025138-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-US0295560.
XX PR 17-SEP-2001; 2001US-0323469P.
XX PR 20-SEP-2001; 2001US-0323887P.
XX PR 13-NOV-2001; 2001US-0350666P.
XX PR 08-FEB-2002; 2002US-0355145P.
XX PR 08-FEB-2002; 2002US-0355257P.
XX PR 12-APR-2002; 2002US-0372246P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
Zlotnik A;
XX DR WPI; 2003-354600/33.
XX DR N-PSDB; ACC72740.
XX PT New genes that are up-regulated or down-regulated in cancers, useful as
markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
therapeutic targets for screening drugs for treating these diseases.
XX PS Claim 12; Page 745; 767pp; English.
XX CC The present invention describes an isolated nucleic acid molecule, which
comprises the sequence of any of the genes that are up-regulated or down-
regulated in specific cancers (e.g. about 1031 genes up-regulated in
acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
related gene nucleotide sequences which encode the proteins given in
ABR58521 to ABR58709. Also described: (1) determining the presence or
absence of a pathological cell in a patient; (2) an expression vector
comprising a nucleic acid molecule described above; (3) a host cell
comprising the vector; (4) an isolated polypeptide, which is encoded by
the nucleic acid; (5) an antibody that specifically binds the polypeptide
of (4); (6) specifically targeting a compound to a pathological cell in a
patient by administering to the patient the antibody above; and (7) a
drug screening assay. The nucleic acid is useful as diagnostic markers or
therapeutic targets. In particular, the nucleic acid is useful for
diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
atherosclerosis and endometriosis. The nucleic acid is also useful in
drug screening, particularly for identifying agents for treating these
pathologies
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 96; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKFNQTLKIVILG 18

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Db      185 SQYQFWKNFQTLKIVILG 202
|||||
RESULT 33
AAO29514
ID      AAO29514 standard; protein; 352 AA.
XX
AC      AAO29514;
XX
DT      27-AUG-2003 (first entry)
XX
DE      Human C-C chemokine receptor type 5 (333) protein.
XX
KW      Human; urological disorder; stress urinary incontinence; prostate cancer;
KW      benign prostatic hyperplasia; overactive bladder; oversensitive bladder;
KW      overflow urinary incontinence; gene therapy; nephrotropic; prostatitis;
KW      kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
XX
OS      Homo sapiens.
XX
PN      WO2003039475-A2.
XX
PD      15-MAY-2003.
XX
PF      07-NOV-2002; 2002WO-US035824.
XX
PR      07-NOV-2001; 2001US-0344552P.
XX
PA      (MILL-) MILLENNIUM PHARM INC.
XX
PI      Silos-Santiago I;
XX
DR      WPI; 2003-449396/42.
XX
DR      N-PSDB; AAL59912.
XX
PT      Identifying a compound, capable of treating urological disorder e.g.,
PT      benign prostatic hyperplasia, by assaying the ability of the compound to
PT      modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or
PT      polypeptide activity.
XX
PS      Disclosure; Page 81; 87pp; English.
XX
CC      The invention relates to a method for treating a urological disorder
CC      which comprises assaying the ability of the compound to modulate 313,
CC      333, 5464, 188717 or 33524 nucleic acid expression or polypeptide
CC      activity. The method is useful for identifying a compound for treating an
CC      urological disorder comprising urinary incontinence e.g., overactive/
CC      oversensitive bladder, overflow urinary incontinence, stress urinary
CC      incontinence caused by dysfunction of the bladder, urethra or central/
CC      peripheral nervous system, prostatitis, benign prostatic hyperplasia,
CC      prostate cancer or kidney disorders. It is also used in gene therapy. The
CC      present sequence is human C-C chemokine receptor type 5 (CCR5; 333)
CC      protein. This sequence is used to illustrate the method of the invention
XX
SQ      Sequence 352 AA;

Query Match      100.0%; Score 96; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKNFQTLKIVILG 18
|||||
DB      185 SQYQFWKNFQTLKIVILG 202

RESULT 34
ABU61654
ID      ABU61654 standard; protein; 352 AA.
XX
AC      ABU61654;
XX
DT      08-AUG-2003 (first entry)
XX
DE      Human; chemokine receptor; CCR5; viral infection; surface protein;
DE      respiratory virus infection; respiratory syncytial virus infection;
DE      RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.
XX
OS      Homo sapiens.
XX
PN      WO2003014153-A2.
XX
PD      20-FEB-2003.
XX
PF      12-AUG-2002; 2002WO-CA001248.
XX
PR      10-AUG-2001; 2001US-0311088P.

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XX      Human G-protein chemokine receptor (HDGNR10) polypeptide.
DE
XX
KW      Human; G-protein chemokine receptor; receptor; HDGNR10;
KW      7-transmembrane receptor.
XX
OS      Homo sapiens.
XX
PN      US2003023044-A1.
XX
PD      30-JAN-2003.
XX
PF      03-SEP-2002; 2002US-00232686.
XX
PR      06-JUN-1995; 95US-00466343.
PR      18-NOV-1998; 98US-00195662.
PR      25-JUN-1999; 99US-00339912.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Li Y, Ruben SM;
XX
DR      WPI; 2003-456307/43.
DR      N-PSDB; ACA61721.
XX
PT      Producing an antibody, involves immunizing an animal with a polypeptide
PT      or with a polypeptide encoded by the human G-protein chemokine receptor
PT      clone in ATCC 97183, and recovering the antibody.
XX
PS      Claim 1; Fig 1; 23pp; English.
XX
CC      The invention relates to a method of producing an antibody, involving
CC      immunising an animal with a human G-protein chemokine receptor (HDGNR10)
CC      polypeptide (also referred to as a human 7-transmembrane receptor) and
CC      recovering an antibody which binds the polypeptide. The method is useful
CC      for producing an antibody which binds specifically to the human G-protein
CC      chemokine receptor polypeptide. This sequence represents the HDGNR10
CC      polypeptide of the invention
XX
SQ      Sequence 352 AA;

Query Match      100.0%; Score 96; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKNFQTLKIVILG 18
|||||
DB      185 SQYQFWKNFQTLKIVILG 202

RESULT 35
ABP97728
ID      ABP97728 standard; protein; 352 AA.
XX
AC      ABP97728;
XX
DT      28-MAY-2003 (first entry)
XX
DE      Amino acid sequence of human chemokine receptor CCR5.
XX
KW      Human; chemokine receptor; CCR5; viral infection; surface protein;
KW      respiratory virus infection; respiratory syncytial virus infection;
KW      RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.
XX
OS      Homo sapiens.
XX
PN      WO2003014153-A2.
XX
PD      20-FEB-2003.
XX
PF      12-AUG-2002; 2002WO-CA001248.
XX
PR      10-AUG-2001; 2001US-0311088P.

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XX (TOPI-) TOPIGEN PHARM INC.
XX Renzi P, Zemzoumi K;
XX WPI; 2003-256541/25.
XX N-PSDB; ABZ68881.
XX
XX Modulating viral infection of a cell, for treating or preventing
XX respiratory virus infections, bronchitis, pneumonia or asthma, by
XX modulating a binding interaction between a cell chemokine-receptor and a
XX surface protein of the virus.
XX
XX Disclosure; Page 96-98; 120pp; English.
XX
XX The present sequence represents human chemokine receptor CCR5. The
XX specification describes a method for modulating viral infection of a
XX cell. The method comprises modulating a binding interaction between a
XX cell chemokine-receptor and a surface protein of the virus. The proviso
XX is that the cell chemokine-receptor is not CXCR1 and that the virus is
XX not HIV. The method is useful for treating or preventing respiratory
XX virus infection in vertebrates, more particularly respiratory syncytial
XX virus (RSV) infections, and related diseases, e.g. bronchiolitis,
XX bronchitis, pneumonia or asthma
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 96; DB 6; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SQYQFWKNFQTLKIVILG 18
XX |||||
XX Db 185 SQYQFWKNFQTLKIVILG 202
XX
XX RESULT 36
XX ABP81933
XX ID ABP81933 standard; protein; 352 AA.
XX
XX AC ABP81933;
XX
XX DT 04-MAR-2003. (first entry)
XX
XX DE Human C-C chemokine receptor 5 protein SEQ ID NO:352.
XX
XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related cell proliferative disease; autoimmune disease;
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer.
XX
XX OS Homo sapiens.
XX
XX PN WO200261087-A2.
XX
XX PD 08-AUG-2002.
XX
XX PF 19-DEC-2001; 2001WO-US050107.
XX
XX PR 19-DEC-2000; 2000US-0257144P.
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
XX FI Burmer GC, Roush CL, Brown JP;
XX
XX WPI; 2003-046718/04.

DR N-PSDB; ABZ42781.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
XX
XX Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention
XX
XX Sequence 352 AA;
XX

Query Match 100.0%; Score 96; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
|||
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 37
ADC03341
ID ADC03341 standard; protein; 352 AA.

AC ADC03341;
DT 18-DEC-2003 (first entry)
DE Human chemokine receptor 88-C.

KW receptor; human; anti-HIV; virucide; HIV; SIV; 88-C; 88-2B;
KW chemokine receptor; envelope protein; protein; atherosclerosis;
KW rheumatoid arthritis; tumour growth suppression; asthma; viral infection;
KW AIDS; inflammatory condition.

OS Homo sapiens.

PN US2002150888-A1.

PD 17-OCT-2002.

PF 26-MAR-2002; 2002US-00106623.

PR 20-DEC-1995; 95US-00575967.

PR 07-JUN-1996; 96US-00661393.

PR 20-DEC-1996; 96US-00771276.

[illegible][illegible]

XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9953033-A1.
XX PD 21-OCT-1999.
XX PF 16-APR-1999; 99WO-US008214.
XX PR 16-APR-1998; 98US-0081989P.
XX FA (UYVA-) UNIV VANDERBILT.
XX PI Breyer RM, Ma L, Kennedy C;
XX PT WPI: 1999-620416/53.
XX DR N-PSDB; AAZ24738.
XX PT New nucleic acid constructs for high level expression of eukaryotic
XX PT proteins in bacteria, for producing e.g. chemokine receptor CCR-5 for
XX PT preventing HIV infection.
XX PS Disclosure; Page 49-53; 81pp; English.
XX CC The invention provides isolated nucleic acid sequences that encode rabbit
XX CC prostaglandin (PG) E2EP2 receptor, human PG E2EP2 receptor, human
XX CC chemokine receptor CCR-5, human ss2 adrenergic receptor, rat renal outer
XX CC medullary potassium ion channel protein or human small G-protein rho,
XX CC together with deduced protein sequences. Also provided is a method for
XX CC the production of eukaryotic proteins by culturing bacteria transformed
XX CC with vectors containing the above nucleic acid sequences or a nucleic
XX CC acid (i) that comprises: (i) first sequence that encodes either a
XX CC sequence comprising at least three positively charged amino acids, or a
XX CC DNA-binding protein, or a lambda phage repressor protein, placed upstream
XX CC of, and in frame with, (ii) a sequence encoding a protein. (I) are used
XX CC for recombinant production of eukaryotic proteins, particularly membrane
XX CC proteins, G-protein coupled receptors or ion-channel proteins, in
XX CC bacteria. These proteins are useful for biochemical or structural studies
XX CC ; as therapeutic agents; in diagnostic and screening assays and as
XX CC antigens for use in vaccines, and for raising antibodies that are useful
XX CC as immunohistochemical markers, e.g. for orphan receptors or ion
XX CC channels. Antibodies raised against the chemokine receptor CCR-5 can be
XX CC used (when administered as antiserum or generated in vivo) to prevent
XX CC entry of human immune deficiency virus (HIV) into cells
XX SQ Sequence 439 AA;
Query Match 100.0%; Score 96; DB 2; Length 439;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQYQFWKNFQTLKIVILG 18
Db 263 SQYQFWKNFQTLKIVILG 280
RESULT 40
AAW27125
ID AAW27125 standard; protein; 352 AA.
XX AC AAW27125;
XX DT 14-DEC-1997 (first entry)
XX DE Macaque chemokine receptor 88C.
XX KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
XX KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
XX KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX KW modulator; antibody.
XX OS Macaca sp.

XX PN WO9722698-A2.
XX PD 26-JUN-1997.
XX PF 20-DEC-1996; 96WO-US020759.
XX PR 20-DEC-1995; 95US-00575967.
XX PR 07-JUN-1996; 96US-00661393.
XX PA (ICOS-) ICOS CORP.
XX PI Gray PW, Schweickart VL, Raport CJ;
XX DR WPI: 1997-341689/31.
XX DR N-PSDB; AAT85163.
XX PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX PT tumours, viral infections, auto-immune diseases, etc.
XX PS Claim 36; Page 57-58; 65pp; English.
XX CC This polypeptide sequence comprises macaque chemokine receptor 88C, a G
XX CC protein coupled receptor that is involved in leukocyte trafficking. Its
XX CC amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
XX CC amplification. It shows 97% identity to human 88C (AAW27123). 88C
XX CC receptors and their polypeptide fragments can be produced in transformed
XX CC host cells. The receptors, peptides comprising one or more of the
XX CC extracellular or intracellular domains, and anti-receptor antibodies can
XX CC be used to modulate receptor activities, particularly ligand and G
XX CC protein binding, and are potentially useful in the treatment
XX CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX CC infection, AIDS, inflammatory conditions, pathological immune response,
XX CC abnormal haematopoietic processes etc. A hybridoma that produces an
XX CC antibody that specifically binds to macaque 88C is claimed
XX SQ Sequence 352 AA;
Query Match 96.9%; Score 93; DB 2; Length 352;
Best Local Similarity 94.4%; Pred. No. 2.6e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202
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Job time : 43.975 secs

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OM protein - protein search, using sw model

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(without alignments)
97.074 Million cell updates/sec

Title: US-10-084-813-13

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	96	100.0	49	16	US-10-612-731-11
5	96	100.0	54	9	US-09-938-719-11
6	96	100.0	54	9	US-09-939-226-11
7	96	100.0	54	9	US-09-938-703-11
8	96	100.0	352	9	US-09-725-285-2
9	96	100.0	352	9	US-09-759-841-2
10	96	100.0	352	9	US-09-779-879A-2
11	96	100.0	352	9	US-09-779-879A-22
12	96	100.0	352	9	US-09-779-880A-2
13	96	100.0	352	9	US-09-779-880A-22
14	96	100.0	352	9	US-09-813-653-15
15	96	100.0	352	9	US-09-813-653-17

16	96	100.0	352	9	US-09-796-202-1	Sequence 1, Appli
17	96	100.0	352	9	US-09-195-662A-2	Sequence 2, Appli
18	96	100.0	352	9	US-09-339-912A-2	Sequence 2, Appli
19	96	100.0	352	9	US-09-938-719-5	Sequence 5, Appli
20	96	100.0	352	9	US-09-939-226-5	Sequence 5, Appli
21	96	100.0	352	9	US-09-938-703-5	Sequence 5, Appli
22	96	100.0	352	9	US-09-502-783A-2	Sequence 2, Appli
23	96	100.0	352	9	US-09-734-221A-14	Sequence 14, Appli
24	96	100.0	352	11	US-09-826-509-477	Sequence 477, App
25	96	100.0	352	12	US-10-151-274-5	Sequence 5, Appli
26	96	100.0	352	13	US-10-106-623-2	Sequence 2, Appli
27	96	100.0	352	14	US-10-232-686-2	Sequence 1, Appli
28	96	100.0	352	14	US-10-086-814-1	Sequence 2, Appli
29	96	100.0	352	14	US-10-067-800-2	Sequence 2, Appli
30	96	100.0	352	14	US-10-067-800-22	Sequence 2, Appli
31	96	100.0	352	14	US-10-290-058A-6	Sequence 6, Appli
32	96	100.0	352	14	US-10-225-567A-352	Sequence 352, App
33	96	100.0	352	14	US-10-323-314-1	Sequence 1, Appli
34	96	100.0	352	14	US-10-072-301-1	Sequence 1, Appli
35	96	100.0	352	14	US-10-164-649-52	Sequence 52, Appli
36	96	100.0	352	14	US-10-071-866-1	Sequence 1, Appli
37	96	100.0	352	14	US-10-135-839-2	Sequence 2, Appli
38	96	100.0	352	14	US-10-135-839-22	Sequence 22, Appli
39	96	100.0	352	14	US-10-239-423-67	Sequence 67, Appli
40	96	100.0	352	14	US-10-439-845-2	Sequence 2, Appli
41	96	100.0	352	14	US-10-439-845-4	Sequence 4, Appli
42	96	100.0	352	15	US-10-360-828-1	Sequence 1, Appli
43	96	100.0	352	16	US-10-661-798-5	Sequence 5, Appli
44	96	100.0	352	16	US-10-791-505-2	Sequence 2, Appli
45	96	100.0	352	16	US-10-612-791-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-10-084-813-13

; Sequence 13, Application US/10084813

; Publication No. US20030068615A1

; GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL

; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

; FILE REFERENCE: 215875

; CURRENT APPLICATION NUMBER: US/10/084.813

; CURRENT FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: PCT/US00/23505

; PRIOR FILING DATE: 2000-08-25

; PRIOR APPLICATION NUMBER: US 60/151,270

; PRIOR FILING DATE: 1999-08-27

; NUMBER OF SEQ ID NOS: 1242

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: binding peptide

US-10-084-813-13

Query Match 100.0%; Score 96; DB 14; Length 18;
Best Local Similarity 100.0%; Pred.No. 3e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 SQYQFWKNFQTLKIVLG 18

DB 1 SQYQFWKNFQTLKIVLG 18

RESULT 2

US-10-084-813-77

; Sequence 77, Application US/10084813

; Publication No. US20030068615A1

GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084.813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-77

Query Match 100.0%; Score 96; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
DB 1 SOYQFWKNFQTLKIVILG 18

RESULT 3
US-10-661-798-11
; Sequence 11, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Frederic, Libert
; TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV En

FILE REFERENCE: 9409/2023P
; CURRENT APPLICATION NUMBER: US/10/661,798
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: 09/938,703
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: 08/810,028
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: EP 96870021.1
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: EP 96870102.9
; PRIOR FILING DATE: 1996-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-798-11

Query Match 100.0%; Score 96; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
DB 4 SOYQFWKNFQTLKIVILG 21

RESULT 4
US-10-612-791-11
; Sequence 11, Application US/10612791
; Publication No. US20040161739A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Vassart, Gilbert
; TITLE OF INVENTION: HIV Diagnostic Methods
; FILE REFERENCE: 9409/2023E
; CURRENT APPLICATION NUMBER: US/10/612,791
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/938,703
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: 08/810,028
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: EP 96870021.1
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: EP 96870102.9
; PRIOR FILING DATE: 1996-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-791-11

Query Match 100.0%; Score 96; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
DB 4 SOYQFWKNFQTLKIVILG 21

RESULT 5
US-09-938-719-11
; Sequence 11, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-938-719-11
Query Match 100.0%; Score 96; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 9 SQYQFWKNFQTLKIVILG 26

RESULT 6
US-09-939-226-11
; Sequence 11, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-938-703-11
Query Match 100.0%; Score 96; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 9 SQYQFWKNFQTLKIVILG 26

RESULT 7
US-09-938-703-11
; Sequence 11, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-938-703-11
Query Match 100.0%; Score 96; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 9 SQYQFWKNFQTLKIVILG 26

RESULT 8
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

Query Match      100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKNFQTLKIVILG 18
Db      185 SQYQFWKNFQTLKIVILG 202

RESULT 9
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Perros, Manoussos
; APPLICANT: Dobbs, Susan
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: FC10348PME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-841-2

Query Match      100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKNFQTLKIVILG 18
Db      185 SQYQFWKNFQTLKIVILG 202

RESULT 10
US-09-779-879A-2
; Sequence 2, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
US-09-779-879A-2

Query Match      100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKNFQTLKIVILG 18
Db      185 SQYQFWKNFQTLKIVILG 202

RESULT 11
US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
US-09-779-879A-22

Query Match      100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKNFQTLKIVILG 18
Db      185 SQYQFWKNFQTLKIVILG 202

RESULT 12
US-09-779-880A-2
; Sequence 2, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
US-09-779-880A-2

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; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-2

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 13

US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 14

US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15

; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 15

US-09-813-653-17
; Sequence 17, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-17

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 16

US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US2002006813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

RESULT 17
US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGRR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2
Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

RESULT 18
US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGRR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2
Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

RESULT 19
US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGRR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2
Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

RESULT 20
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMONTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5
Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SOYQFWKNFQTLKIVILG 18
Db      185 SOYQFWKNFQTLKIVILG 202

RESULT 20
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMONTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 21
US-09-938-703-5
; Sequence 5, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 22
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. US2002013246A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
; FILE REFERENCE: HDGRL10
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 23
US-09-734-221A-14
; Sequence 14, Application US/09734221A
; Publication No. US20030096221A1
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; DENG, HONGKUI
; ELLMEIER, WILFRIED
; LANDAU, NATHANIEL R.
; LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,221A
; FILING DATE: 11-Dec-2000

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;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14
Query Match 100.0%; Score 96; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 24
US-09-826-509-477
; Sequence 477, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 477
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-477
Query Match 100.0%; Score 96; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 25
US-10-151-274-5
; Sequence 5, Application US/10151274
; Publication No. US20030064071A1
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Xwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeek, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
; TITLE OF INVENTION: INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/10/151,274
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/09/517,605
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-274-5
Query Match 100.0%; Score 96; DB 12; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 26
US-10-106-623-2
; Sequence 2, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
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; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2

Query Match 100.0%; Score 96; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 27
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 28
US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

Db 185 SQYQFWKNFQTLKIVILG 202
RESULT 29
US-10-067-800-2
; Sequence 2, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000I
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-2

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 30
US-10-067-800-22
; Sequence 22, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000I
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-067-800-22

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
   |||||
Db 185 SOYQFWKNFQTLKIVILG 202

RESULT 31
US-10-290-058A-6
; Sequence 6, Application US/10290058A
; Publication No. US20030104455A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; FILE REFERENCE: MPI01-289P1RM
; CURRENT APPLICATION NUMBER: US/10/290,058A
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/344,552
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-290-058A-6

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
   |||||
Db 185 SOYQFWKNFQTLKIVILG 202

RESULT 32
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-352

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
   |||||
Db 185 SOYQFWKNFQTLKIVILG 202
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RESULT 33
US-10-323-314-1
; Sequence 1, Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JPW/MAF/DJK
; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-10-323-314-1

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
   |||||
Db 185 SOYQFWKNFQTLKIVILG 202

RESULT 34
US-10-072-301-1
; Sequence 1, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-301-1

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
   |||||
Db 185 SOYQFWKNFQTLKIVILG 202

RESULT 35
US-10-164-649-52
; Sequence 52, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
```

```
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/164,649
; FILING DATE: 07-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MMI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-164-649-52

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 36
US-10-071-866-1
; Sequence 1, Application US/10071866
; Publication No. US2003016598A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST P
; TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-866-1

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 37
US-10-135-839-2
; Sequence 2, Application US/10135839
; Publication No. US2003016602A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-2

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 39
US-10-239-423-67
; Sequence 67, Application US/10239423
; Publication No. US2003018689A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-22
```

```
;
;
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-2

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 38
US-10-135-839-22
; Sequence 22, Application US/10135839
; Publication No. US2003016602A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-22

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 39
US-10-239-423-67
; Sequence 67, Application US/10239423
; Publication No. US2003018689A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-22
```

APPLICANT: FORSMANN, Wolf-Georg; FORSMANN, Ulf; ADERMAN, Knut;
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
FILE REFERENCE: 022217us
CURRENT APPLICATION NUMBER: US/10/239,423
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: DE10016013.1
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 67
LENGTH: 352
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-67

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKMFQTLKIVILG 18
DB 185 SOYQFWKMFQTLKIVILG 202

RESULT 40
US-10-439-845-2
Sequence 2, Application US/10439845
Publication NO. US20030195348A1
GENERAL INFORMATION:
APPLICANT: Combadiere et al.,
TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/439,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,458
FILING DATE: May 28, 1997
APPLICATION NUMBER: Provisional 60/018,508
FILING DATE: May 28, 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08830/030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-10-439-845-2
Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKMFQTLKIVILG 18
DB 185 SOYQFWKMFQTLKIVILG 202
Search completed: September 28, 2004, 09:44:41
Job time : 59.625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:57:36 ; Search time 9.675 Seconds
(without alignments)
178.961 Million cell updates/sec

Title: US-10-084-813-13
Perfect score: 96
Sequence: 1 SQQFVKNFQTLKIVILG 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	352	2 A43113	chemokine (C-C) re
2	47	49.0	355	2 I49339	macrophage inflam
3	46	47.9	196	2 T22609	hypothetical prote
4	45	46.9	177	2 S34499	hypothetical prote
5	45	46.9	302	2 A75203	2-phosphoglycerate
6	45	46.9	314	2 G85575	hypothetical prote
7	45	46.9	314	2 G90724	hypothetical prote
8	45	46.9	1289	2 S67200	hypothetical prote
9	44.5	46.4	301	2 C71236	probable 2-phospho
10	44	45.8	467	2 A81263	probable integral
11	44	45.8	616	1 I64056	secretion protein
12	43	44.8	237	2 C95199	nitroreductase fam
13	43	44.8	237	2 A98066	NADPH-flavin oxido
14	43	44.8	242	2 A86719	oxidoreductase yng
15	43	44.8	344	2 JCS942	chemokine receptor
16	43	44.8	475	2 G98183	periplasmic sorbit
17	43	44.8	3587	2 I40486	surfactin syntheta
18	42	43.8	241	2 S30843	UTR4 protein - yea
19	42	43.8	350	2 E81303	probable branched-
20	42	43.8	383	2 D90528	hypothetical prote
21	42	43.8	421	2 AB2915	PAD-dependent mono
22	42	43.8	421	2 E97889	hypothetical prote
23	42	43.8	496	2 C84678	hypothetical prote
24	41.5	43.2	159	2 H81442	hypothetical prote
25	41.5	43.2	334	2 S16296	hypothetical prote
26	41.5	43.2	334	2 A85558	ferric enterobacti
27	41.5	43.2	334	2 E90707	ferric enterobacti
28	41	42.7	46	2 I37047	NADH2 dehydrogenas
29	41	42.7	118	2 H83734	hypothetical prote

RESULT 1

A43113

Chemokine (C-C) receptor 5 - human

N/Alternate names: C-C CR-5; CCR5

C/Species: Homo sapiens (man)

C/Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000

C/Accession: A43113; S71808; A58834; A58832; G02653; A58833

R/Samson: M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochemistry 35, 3362-3367, 1996

A/Title: Molecular cloning and functional expression of a new human CC-chemokine receptor

A/Reference number: A43113; MUID:96241590; PMID:8639485

A/Accession: A43113

A/Molecule type: mRNA

A/Residues: 1-352 <SAM1>

A/Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811

R/Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti

M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Par

Nature 382, 722-725, 1996

A/Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of

A/Reference number: S71808; MUID:96345670; PMID:8751444

A/Accession: S71808

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 182-206;207-230 <SAM2>

A/Accession: A58834

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-184, 'IKDSHLGAPARACHGHLILGNPKNSASYSK' <SAM3>

A/Cross-references: GB:X93939; NID:g1524062; PIDN:CAA67767.1; PID:g1524063

A/Note: This frameshift mutation results in a non-functional receptor but confers a degree

nd may have had a selective advantage by conferring resistance to Yersinia plague infecti

R/Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.

J. Leukoc. Biol. 60, 147-152, 1996

A/Title: Cloning and functional expression of CC CK5, a human monocyte CC chemokine rec

A/Reference number: A58832; MUID:96295970; PMID:8699119

A/Accession: A58832

A/Molecule type: mRNA

A/Residues: 1-352 <COM1>

A/Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409

A/Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes

R/Combadiere, C.

submitted to the EMBL Data Library, May 1996

A/Reference number: H01541

A/Accession: G02653

A/Status: translated from GB/EMBL/DBDJ

A/Molecule type: mRNA

A/Residues: 1-89, 'L', '91-352 <COM2>

A/Cross-references: EMBL:U57840

R/Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.

J. Biol. Chem. 271, 17161-17166, 1996

A/Title: Molecular cloning and functional characterization of a novel human CC chemokine

A/Reference number: A58833; MUID:96291862; PMID:8663314

A;Gene: PAB2253
C;Superfamily: 2-phosphoglycerate kinase

Query Match 46.9%; Score 45; DB 2; Length 302;
Best Local Similarity 37.5%; Pred. No. 10;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 QYQFWKNFQTLKIVIL 17
: |||: ||: ||:
Db 77 RYLFRFRFRKKKVPLL 92

RESULT 6
G85575
hypothetical protein Z0898 [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85575
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85575
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <STO>
A;Cross-references: GB:AE005174; NID:g125113664; PIDN:AA055067.1; GSPDB:GN00145; UWGP:Z08
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0898

Query Match 46.9%; Score 45; DB 2; Length 314;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVI 16
|||: |||: ||:
Db 289 SQYRFFKMTNLALVI 304

RESULT 7
G90724
hypothetical protein ECs0767 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: G90724
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90724
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA034190.1; PID:g13360226; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain R1MD 050952
C;Genetics:
A;Gene: ECs0767

Query Match 46.9%; Score 45; DB 2; Length 314;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVI 16
|||: |||: ||:
Db 289 SQYRFFKMTNLALVI 304

RESULT 8
S67200
hypothetical protein YOR296w - yeast (Saccharomyces cerevisiae)

A;Cross-references: GB:AL139079; GB:AL111168; NID:G6968971; PIDN:CAB73647.1; PID:G696907
 A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:
 A;Gene: Cj1660

Query Match 45.8%; Score 44; DB 2; Length 467;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 YQFWKFNQTLKIVILG 18
 : ||||| : |||||
 Db 77 FYFWKTEILNFILLG 92

RESULT 11

I64056
 secretion protein secD - Haemophilus influenzae (strain Rd KW20)
 C;Species: Haemophilus influenzae
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000

C;Accession: I64056
 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
 R;Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman,
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: I64056

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-616 <TIGR>

A;Cross-references: GB:U22710; GB:L42023; NID:G1573200; PIDN:AAC21908.1; PID:G1573205; T

C;Genetics:

A;Gene: secD

C;Superfamily: protein export membrane protein secD

C;Keywords: inner membrane; protein export; transmembrane protein

F;10-30/Domain: transmembrane #status predicted <TM1>

F;457-473/Domain: transmembrane #status predicted <TM2>

F;478-498/Domain: transmembrane #status predicted <TM3>

F;503-519/Domain: transmembrane #status predicted <TM4>

F;565-581/Domain: transmembrane #status predicted <TM5>

F;587-606/Domain: transmembrane #status predicted <TM6>

Query Match 45.8%; Score 44; DB 1; Length 616;

Best Local Similarity 38.9%; Pred. No. 30;

Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQYQFWKFNQTLKIVILG 18
 : ||||| : |||||
 Db 3 NRYPLKMLWIFIVAIG 20

RESULT 12

C95199
 nitroreductase family protein [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001

C;Accession: C95199

R;Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A;Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: C95199

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-237 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75788.1; PID:G14973205; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

C;Genetics:
 A;Gene: SP1710

C;Superfamily: NADPH-flavin oxidoreductase homolog

Query Match 44.8%; Score 43; DB 2; Length 237;

Best Local Similarity 41.7%; Pred. No. 17;

Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17
 : ||||| : |||||
 Db 40 WKNFQSYVIVV 51

RESULT 13

A98066
 NADPH-flavin oxidoreductase (EC 1.6.99.-) homolog [imported] - Streptococcus pneumoniae

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001

C;Accession: A98066

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Es

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M

y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: A98066

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-237 <KUR>

A;Cross-references: GB:AE007317; PIDN:AAL00358.1; PID:G15459219; GSPDB:GN00174

C;Genetics:

A;Gene: frp

C;Superfamily: NADPH-flavin oxidoreductase homolog

C;Keywords: oxidoreductase

Query Match 44.8%; Score 43; DB 2; Length 237;

Best Local Similarity 41.7%; Pred. No. 17;

Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17
 : ||||| : |||||
 Db 40 WKNFQSYVIVV 51

RESULT 14

A86719
 oxidoreductase yhgA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C;Accession: A86719

R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlic

Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: A86719

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-242 <STO>

A;Cross-references: GB:AE005476; PID:G12723669; PIDN:AAK04851.1; GSPDB:GN00146

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: yhgA

C;Superfamily: NADPH-flavin oxidoreductase homolog

Query Match 44.8%; Score 43; DB 2; Length 242;

Best Local Similarity 41.7%; Pred. No. 17;

Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17
 : ||||| : |||||
 Db 43 WKNFQSYVIVV 54

RESULT 15

Matches 6; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
: : | | | : : : : :
Db 1751 ASFAFDANFESLRILVIG 1768

RESULT 18

UTR4 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YEL038W
C:Species: Saccharomyces cerevisiae
C>Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 18-Aug-2000
C:Accession: S30843; S50506; S38544
R:Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, submitted to the EMBL Data Library, February 1993
A:Reference number: S30812
A:Accession: S30843
A:Molecule type: DNA
A:Residues: 1-241 <MUL>
A:Cross-references: GB:U18779; EMBL:L10830; NID:g603625; PIDN:AA65004.1; PID:g603641
R:Dietrich, F.S.
Submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmids 8199, 8334, and 9871.
A:Reference number: S50491
A:Accession: S50506
A:Molecule type: DNA
A:Residues: 1-241 <DIB>
A:Cross-references: EMBL:U18779; NID:g603625; PIDN:AA65004.1; PID:g603641; MIPS:YEL038W
R:Meinick, L.; Sherman, F.
J. Mol. Biol. 233, 372-388, 1993
A:Title: The gene clusters ARC and COR on chromosomes 5 and 10, respectively, of Sacchar
A:Reference number: S38543; MUID:94016558; PMID:8411151
A:Accession: S38544
A:Molecule type: DNA
A:Residues: 1-69, 'MH', 72-152, 'GMIRWT', <MEL>
A:Cross-references: EMBL:S66121; NID:g430827; PIDN:AA628443.1; PID:g430828
C:Genetics:
A:Gene: SGD:UTR4
A:Cross-references: SGD:S0000764; MIPS:YEL038W
A:Map position: 5L
C:Superfamily: Klebsiella oxytoca methionine salvage pathway enzyme E-1

Query Match 43.8%; Score 42; DB 2; Length 241;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYQFWKNFQTL 12
: : | | | : : : : :
Db 231 KQYVKNFETL 241

RESULT 19

E81303
Probable branched-chain amino-acid ABC transport system permease protein Cj1016c [import
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C:Accession: E81303
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10698204
A:Accession: E81303
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <PAR>
A:Cross-references: GB:AL111168; NID:g6968444; PIDN:CAB73272.1; PID:g696845
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: livM; Cj1016c

Query Match 43.8%; Score 42; DB 2; Length 350;

Best Local Similarity 44.4%; Pred. No. 36;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
: : | | | : : : : :
Db 246 TQDFLLTQQLLIIVLG 263

RESULT 20

D90528
hypothetical protein MYPU_1320 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: D90528
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A95512; MUID:21267165; PMID:11353084
A:Accession: D90528
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <KUR>
A:Cross-references: GB:AL445566; PID:g14089545; PIDN:CAC13305.1; GSPDB:GN00153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU_1320
A:Genetic code: SGC3

Query Match 43.8%; Score 42; DB 2; Length 383;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 QYQFWKNFQTLKIVIL 17
: : | | | : : : : :
Db 202 KFWKFKKQKLTIL 215

RESULT 21

AB2915
FAD-dependent monooxygenase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AB2915
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.;
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F
ster, B.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AB2915
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-421 <KUR>
A:Cross-references: GB:AE008688; PIDN:AAL43736.1; PID:g17741269; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu2755
A:Map position: circular chromosome
C:Superfamily: ubiH protein

Query Match 43.8%; Score 42; DB 2; Length 421;
Best Local Similarity 46.2%; Pred. No. 44;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 QYQFWKNFQTLKI 14
: : | | | : : : : :
Db 349 RYOSWERFDTLRM 361

RESULT 22

E97689

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A;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB72717.1; PID:g6967722
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj0249
C;Superfamily: Campylobacter jejuni hypothetical protein Cj0249

Query Match      43.2%; Score 41.5; DB 2; Length 159;
Best Local Similarity 40.0%; Pred. No. 20;
Matches 8; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

QY    3 YQFWK-----FQTLLKIVIL 17
       |||||.....:|||||
Db     33 YKFWNAEIGRYQGTRIFL 52

RESULT 25
SI6296
ferric enterobactin transport protein fepD - Escherichia coli (strain K-12)
N;Alternate names: ferricenterobactin permease fepD
C;Species: Escherichia coli
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 01-Mar-2002
C;Accession: SI6296; SI6305; D64792; S14841
R;Shea, C.M.; McIntosh, M.A.
Mol. Microbiol. 5, 1415-1428, 1991
A;Title: Nucleotide sequence and genetic organization of the ferric enterobactin transporter gene from Escherichia coli K-12
A;Reference number: SI6295; MUID:92157868; PMID:1838574
A;Accession: SI6296
A;Molecule type: DNA
A;Residues: 1-334 <SHE>
A;Cross-references: EMBL:X57471; NID:G41429; PIDN:CAA40707.1; PID:G41430
R;Chenault, S.S.; Eachart, C.F.
Mol. Microbiol. 5, 1405-1413, 1991
A;Title: Organization of genes encoding membrane proteins of the Escherichia coli ferrier operon
A;Reference number: SI6305; MUID:92157867; PMID:1787794
A;Accession: SI6305
A;Molecule type: DNA
A;Residues: 1-232, 'AL', 235-334 <CHE>
A;Cross-references: EMBL:X59402; NID:G41433; PIDN:CAA42043.1; PID:G41434
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collier, R.C.; Rose, D.J.; Mau, B.; Shaoh, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D64792
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-334 <BLAT>
A;Cross-references: GB:AE000164; GB:U000096; NID:g1786800; PIDN:AAC73691.1; PID:g1786805;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: fepD
A;Map position: 14 min
C;Superfamily: vitamin B12 transport protein btuC
C;Keywords: transmembrane protein
F;16-32/Domain: transmembrane #status predicted <TM1>
F;65-81/Domain: transmembrane #status predicted <TM2>
F;94-110/Domain: transmembrane #status predicted <TM3>
F;121-137/Domain: transmembrane #status predicted <TM4>
F;156-172/Domain: transmembrane #status predicted <TM5>
F;198-214/Domain: transmembrane #status predicted <TM6>
F;240-256/Domain: transmembrane #status predicted <TM7>
F;284-300/Domain: transmembrane #status predicted <TM8>
F;310-326/Domain: transmembrane #status predicted <TM9>

Query Match      43.2%; Score 41.5; DB 2; Length 334;
Best Local Similarity 34.8%; Pred. No. 42;
Matches 8; Conservative 5; Mismatches 3; Indels 7; Gaps 1;

QY    2 QYQFW-----KNFQTLKIVIL 17
       |||||.....:|||||
Db     179 QLRFWQAGSLDIRNLTKVLI 201

```


C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C/Accession: A84494
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umavam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.
Nature 402, 763-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: A84494
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-285 <STO>
A:Cross-references: GB:AE002093; NID:g4733967; PIDN:AAD28650.1; GSPDB:GN00139
C/Genetics:
A:Gene: At5g10850
A:Map position: 2

Query Match 42.7%; Score 41; DB 2; Length 285;
Best Local Similarity 41.7%; Pred. No. 43;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 YQFWNFQTLKI 14
:|:|:|:|:
Db 173 PEFWANLPTMKV 184

RESULT 32
I40547
oligopeptide ABC transporter (permease) appC - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 20-Jun-2000
C/Accession: I40547; E69586
R/Koide, A.; Hoch, J.A.
Mol Microbiol 13, 417-426, 1994
A>Title: Identification of a second oligopeptide transport system in Bacillus subtilis
A/Reference number: I40543; MUID:95089678; PMID:7997159
A/Accession: I40547
A>Status: preliminary; translated from GB/EMBL/DBRJ
A:Molecule type: DNA
A:Residues: 1-303 <RES>
A:Cross-references: EMBL:U20909; NID:g677942; PIDN:AAA62360.1; PID:g677947
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kuno, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terfstta, P.; Tognoni, A.; Tosa, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: E69586
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-303 <KIN>
A:Cross-references: GB:299110; GB:AL009126; NID:g2633472; PIDN:CAB12997.1; PID:g2633494
A/Experimental source: strain 168
C/Genetics:
A:Gene: appC
C/Superfamily: oligopeptide permease protein oppB

Query Match 42.7%; Score 41; DB 2; Length 303;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 5 FWKNFQTLKIVLG 18

Db || : | |||
 29 FWEKFSKNLAILG 42

RESULT 33
T22197
Hypothetical protein F44G3.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T22197
R/McMurray, A.
submitted to the EMBL Data Library, November 1996
A/reference number: Z19529
A/accession: T22197
A/status: preliminary; translated from GB/EMBL/DDBJ
A/molecule type: DNA
A/residues: 1-316 <WIL>
A/cross-references: EMBL:Z83109; PIDN:CAB05515.1; GSPDB:GN00023; CBSP:F44G3
C/genetics:
A/gene: CESP:F44G3.5
A/map position: 5
A/introns: 142/3; 185/3; 256/3

Query Match 42.7%; Score 41; DB 2; Length 316;
Best Local Similarity 57.1%; Pred. No. 48;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps

Qy 4 QPWKFQTLLKVIL 17
 |||||
Db 36 QFFKYFNLIKPVL 49
 |||||

RESULT 34
TL1833
NADH2 dehydrogenase (ubiquinone) [EC 1.6.5.3] chain 1 - common gibbon mitochondrion
C/Species: Mitochondrion Hylobates lar (common gibbon, white-handed gibbon)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C/Acession: TL1833
R/Aranson, U.; Gullberg, A.; Xu, X.
Hereditas 124, 185-189, 1996
A/title: A complete mitochondrial DNA molecule of the white-handed gibbon,
F.A reference number: Z17353
A/accession: TL1833
A/status: preliminary; translated from GB/EMBL/DDBJ
A/molecule type: DNA
A/residues: 1-318 <ARN>
A/cross-references: EMBL:X99256; PIDN:CAA67628.1
A/experimental source: isolate Ester
C/genetics:
A/genome: mitochondrion
A/genetic code: SGC1
A/note: NADH1
C/superfamily: NADH dehydrogenase (ubiquinone) chain 1
C/key words: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match 42.7%; Score 41; DB 2; Length 318;
Best Local Similarity 46.7%; Pred. No. 48;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps

Qy 3 YQFWNFQTLLKVIL 17
 |||||
Db 287 YLLMKNFLPLITLLS 301
 |||||

RESULT 35
D83385
Hypothetical protein PA2090 [imported] - Pseudomonas aeruginosa (strain PAO1)
C/Species: Pseudomonas aeruginosa
C/Date: 13-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Acession: D83385
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickman, J.C.; Yuan, Y.; Brody, L.L.; Coulter, K.R.; Folger, K.R.; Kas, A.; Larson, S.; Adams, R.J.
adman, S.

```

.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83385
A:Molecule type: DNA
A>Status: preliminary
A:Cross-references: GB:AE004636; GB:AE004091; NID:59948093; PIDN:AG05478.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2090

Query Match 42.7%; Score 41; DB 2; Length 359;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 9; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 4 QPWNFQTLKIVILG 18
DB 233 KFWKHFQ-----VILG 243

RESULT 36
E42594
hypothetical protein ORF5 hycC 3'-region, hycE 5'-region - Pseudomonas sp. plasmid pHN67
C:Species: Pseudomonas sp.
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: E42594; A41895
R:Watabe, K.; Ishikawa, T.; Mukohara, Y.; Nakamura, H.
J. Bacteriol. 174, 962-969, 1992
A:Title: Cloning and sequencing of the genes involved in the conversion of 5-substituted
A:Reference number: A42594; MUID:92121137; PMID:1732229
A:Accession: E42594
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <WAT>
A:Cross-references: GB:D10494; GB:D90469; NID:G216829; PIDN:BAA01380.1; PID:G216834
A:Note: sequence extracted from NCBI backbone (NCBIN:77753, NCBI:77764)
R:Watabe, K.; Ishikawa, T.; Mukohara, Y.; Nakamura, H.
J. Bacteriol. 174, 3461-3466, 1992
A:Title: Identification and sequencing of a gene encoding a hydantoin racemase from the
A:Reference number: A41895; MUID:92276321; PMID:1339422
A:Accession: A41895
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 244-456 <WAT>
A:Experimental source: strain NS671
A:Note: sequence extracted from NCBI backbone (NCBIN:104597, NCBIP:104598)
C:Genetics:
A:Genome: plasmid
C:Superfamily: Escherichia coli probable transport protein b0511

Query Match 42.7%; Score 41; DB 1; Length 456;
Best Local Similarity 42.9%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 QYQFKNFQTLKIV 15
DB 382 QYKWNVNPAAII 395

RESULT 37
S47920
pre-mRNA splicing factor PRP39 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YM9827.06; protein YML046w
C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C:Accession: S47920; S50946
R:Lockhart, S.R.; Rymond, B.C.
Mol. Cell. Biol. 14, 3623-3633, 1994
A:Title: Commitment of yeast pre-mRNA to the splicing pathway requires a novel U1 small
A:Reference number: S47920; MUID:94254821; PMID:8196508
A:Accession: S47920

```

```

A:Molecule type: DNA
A:Residues: 1-629 <LOC>
A:Cross-references: EMBL:129224; NID:G460045; PIDN:AAA20131.1; PID:G460046
A:Note: the authors translated the codon GAC for residue 29 as Ala
R:Odell, C.; Bowman, S.
submitted to the EMBL Data Library, January 1995
A:Reference number: S50941
A:Accession: S50946
A:Molecule type: DNA
A:Residues: 1-629 <CODE>
A:Cross-references: EMBL:Z47816; NID:G642303; PID:G642309; MIPS:YML046w
C:Genetics:
A:Gene: SGD:PRP39
A:Cross-references: SGD:S0004509; MIPS:YML046w
A:Map position: 13L
C:Function:
A:Description: pre-mRNA splicing
A:Note: necessary for the stable interaction of mRNA precursors with the snRNP components
C:Keywords: nucleus; pre-mRNA splicing; transmembrane protein
F:429-445/Domain: transmembrane #status predicted <TMM>

```

```

Query Match 42.7%; Score 41; DB 2; Length 629;
Best Local Similarity 37.5%; Pred. No. 96;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 3 YQFKNFQTLKIVILG 18
DB 88 FGFWRKFAIIEYQLFG 103

```

RESULT 38

```

T48016
Probable zinc-finger protein - Arabidopsis thaliana
N:Alternate names: protein T17J13.200
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48016
R:Riegler, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, P.
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24482
A:Accession: T48016
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-812 <RIE>
A:Cross-references: EMBL:AL138651
A:Experimental source: cultivar Columbia; BAC clone T17J13
C:Genetics:
A:Map position: 3
A:Introns: 56/3; 159/3; 229/2; 245/3; 275/3; 296/3
A:Note: T17J13.200

```

```

Query Match 42.7%; Score 41; DB 2; Length 812;
Best Local Similarity 46.2%; Pred. No. 1.2e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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```

QY 2 QYQFKNFQTLKIV 14
DB 234 QYEYKNYDDLEI 246

```

RESULT 39

```

T49799
related to TOM1 protein [imported] - Neurospora crassa
N:Alternate names: protein B1B22.10
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49799
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49799
A>Status: preliminary
A:Molecule type: DNA

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Search completed: September 28, 2004, 09:07:09
Job time : 11.925 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:55:11 ; Search time 5.625 Seconds
(without alignments)
166.624 Million cell updates/sec

Title: US-10-084-813-13
Perfect score: 96
Sequence: 1 SQYQFWKNFQTLKIVILG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	96	100.0	352	1 CCR5_CERAE	P56493 cercoptithec
2	96	100.0	352	1 CCR5_CERP	Q9tv42 cercoptithec
3	96	100.0	352	1 CCR5_CERTO	O62743 cercocebub
4	96	100.0	352	1 CCR5_GORGO	P56439 gorilla gor
5	96	100.0	352	1 CCR5_HUMAN	P51681 homo sapien
6	96	100.0	352	1 CCR5_HYLLE	O97883 hyllobates l
7	96	100.0	352	1 CCR5_HYLMJ	Q95nc0 hyllobates m
8	96	100.0	352	1 CCR5_HYLSY	Q95nc5 hyllobates s
9	96	100.0	352	1 CCR5_PANTR	P56440 pan troglod
10	96	100.0	352	1 CCR5_PAPHA	P56441 papio hamad
11	96	100.0	352	1 CCR5_PONPY	O97881 pongo pygma
12	96	100.0	352	1 CCR5_PYGBI	O97880 pygathrix b
13	96	100.0	352	1 CCR5_PYGNE	O97882 pygathrix n
14	96	100.0	352	1 CCR5_TRAPR	O97878 trachypithe
15	96	100.0	352	1 CCR5_TRAPH	O97879 trachypithe
16	93	96.9	352	1 CCR5_MACMU	P79436 macaca mula
17	74	77.1	354	1 CCR5_MOUSE	P51682 mus musculus
18	74	77.1	354	1 CCR5_RAT	O08556 rattus norv
19	47	49.0	355	1 CCR1_MOUSE	P51675 mus musculus
20	46	47.9	373	1 CCR2_MOUSE	P51683 mus musculus
21	45	46.9	355	1 CCR1_MACMU	P56482 macaca mula
22	45	46.9	634	1 DYXB_HUMAN	P31516 euglena gra
23	45	46.9	4523	1 YHXB_HUMAN	Q96dt5 homo sapien
24	44	45.8	616	1 SECD_HAEN	O44591 haemophilus
25	43	44.8	300	1 PYRB_MYCPE	O8eux9 mycoplasma
26	43	44.8	355	1 CCR3_CERAE	P56492 cercoptithec
27	43	44.8	355	1 CCR3_MACMU	P56483 macaca mula
28	43	44.8	373	1 VIO3_CHRVO	Q983u8 chromobacte
29	43	44.8	3587	1 SRF2_BACSU	Q04747 bacillus su
30	42	43.8	241	1 UTR4_YEAST	P23626 saccharomyc
31	41.5	43.2	334	1 FEPD_ECOLI	P23876 escherichia
32	41	42.7	244	1 Y28K_SSV1	P20213 sulfolobus
33	41	42.7	303	1 APPC_BACSU	P42063 bacillus su

34	41	42.7	318	1 NUIM_HYLLA	Q96126 hyllobates l
35	41	42.7	358	1 CCR3_CAVPO	Q92d13 cavia porce
36	41	42.7	373	1 CCR2_RAT	O52193 rattus norv
37	41	42.7	397	1 O22B_DROME	P81910 drosophila
38	41	42.7	461	1 FCMD_HUMAN	O75072 homo sapien
39	41	42.7	629	1 PR39_YEAST	P39682 saccharomyc
40	40	41.7	284	1 SUHA_HUMAN	Q06520 homo sapien
41	40	41.7	309	1 YBCK_HAEN	P44298 haemophilus
42	40	41.7	355	1 CCR1_HUMAN	P32246 homo sapien
43	40	41.7	371	1 Y180_CLOAB	Q04354 clostridium
44	40	41.7	437	1 ARLY_CLOAB	Q97ke5 clostridium
45	40	41.7	501	1 AMPA_BUCBP	Q89ag2 buchnera ap

ALIGNMENTS

RESULT 1
CKR5_CERAE
ID CKR5_CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
[2]
SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; U83324; AAC51795.1; -;
DR EMBL; U83325; AAC51796.1; -;
DR EMBL; AB015944; BAA31328.1; -;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00003; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
Polymorphism.
DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT

us-10-084-813-13.rsp

Tue Sep 28 15:49:57 2004

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DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECP F1.1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1.2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 15 15
FT VARIANT 14 14
FT VARIANT 352 352
SQ SEQUENCE 352 AA; 40561 MW; 7F52E690C72EC29A CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKQFQTLKIVILG 18
    |||||
DB 185 SOYQFWKQFQTLKIVILG 202

RESULT 2
CKR5_CERP
ID CKR5_CERP STANDARD; PRT; 352 AA.
AC Q9TV42;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS).
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS).
GN CCR5 OR CCR5R5.
OS Cercopithecus pygmychrys (Vervet monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=100;
RX MEDLINE=99335215; PubMed=10408730;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
RA Diop O., Rigoulet J., Barre-Sinoussi F., Ponsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with HIV
RT carrier status in African nonhuman primates."
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL; AF035222; AAD44015.1;
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECP F1.1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1.2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 15 15
FT VARIANT 14 14
FT VARIANT 352 352
SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKQFQTLKIVILG 18
    |||||
DB 185 SOYQFWKQFQTLKIVILG 202

RESULT 3
CKR5_CERTO
ID CKR5_CERTO STANDARD; PRT; 352 AA.
AC Q62743; Q62744; Q62745; Q62746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS).
DE CCR5 OR CCR5R5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate 079, 085, 087, and 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gattie A., Ho D.D., Marx P.A.;
RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of primary SIVsm, HIV-2, and SIVmac."
RL Virology 246:113-124(1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL; AF035222; AAD44015.1;
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.

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DR EMBL; AF051902; AAC39830.1; -
DR EMBL; AF051903; AAC39831.1; -
DR EMBL; AF051904; AAC39832.1; -
DR EMBL; AF051905; AAC39833.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 88
FT DOMAIN 90 102
FT TRANSMEM 103 124
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RP SULFATION.
RX MEDLINE=99189752; PubMed=10089882;
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RP FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and rantes and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation. Acts as co-receptor with CD4 for primary non-
CC syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1
CC virus. It promotes Env-mediated fusion of the virus.
CC [14]
RP SUBCELLULAR LOCATION: Integral membrane protein.
CC [15]
RP TISSUE SPECIFICITY: Found in promyelocytic cells.
CC [16]
RP PTM: Sulfation contributes to the efficiency of HIV-1 entry.
CC [17]
RP PTM: Modified by O-linked glycosylation, but not by N-linked
CC glycosylation.
CC [18]
RP SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC [19]
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DR EMBL; U95626; AAB57793.1; -
DR EMBL; U83326; AAC51797.1; -
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CC -----
 CC EMBL; AF177899; AAK43382.1; -;
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 CC DOMAIN 1 30
 CC TRANSMEM 1 30
 CC DOMAIN 31 58
 CC TRANSMEM 31 58
 CC DOMAIN 59 68
 CC TRANSMEM 59 68
 CC DOMAIN 69 89
 CC TRANSMEM 69 89
 CC DOMAIN 90 102
 CC TRANSMEM 90 102
 CC DOMAIN 103 124
 CC TRANSMEM 103 124
 CC DOMAIN 125 141
 CC TRANSMEM 125 141
 CC DOMAIN 142 166
 CC TRANSMEM 142 166
 CC DOMAIN 167 198
 CC TRANSMEM 167 198
 CC DOMAIN 199 218
 CC TRANSMEM 199 218
 CC DOMAIN 219 235
 CC TRANSMEM 219 235
 CC DOMAIN 236 260
 CC TRANSMEM 236 260
 CC DOMAIN 261 277
 CC TRANSMEM 261 277
 CC DOMAIN 278 301
 CC TRANSMEM 278 301
 CC DOMAIN 302 352
 CC TRANSMEM 302 352
 CC DISULFID 101 178
 CC MOD_RES 3 3
 CC MOD_RES 10 10
 CC MOD_RES 14 14
 CC SQU SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SOYQFWKFNQTLKIVILG 18
 |||||
 DB 185 SOYQFWKFNQTLKIVILG 202

RESULT 8
 CKR5_HYLSY STANDARD; PRT; 352 AA.
 ID CKR5_HYLSY STANDARD; PRT; 352 AA.
 AC Q95NC5;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKBR5.
 OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=9590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC -----
 CC EMBL; AF177884; AAK43367.1; -;
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 CC DOMAIN 1 30
 CC TRANSMEM 1 30
 CC DOMAIN 31 58
 CC TRANSMEM 31 58
 CC DOMAIN 59 68
 CC TRANSMEM 59 68
 CC DOMAIN 69 89
 CC TRANSMEM 69 89
 CC DOMAIN 90 102
 CC TRANSMEM 90 102
 CC DOMAIN 103 124
 CC TRANSMEM 103 124
 CC DOMAIN 125 141
 CC TRANSMEM 125 141
 CC DOMAIN 142 166
 CC TRANSMEM 142 166
 CC DOMAIN 167 198
 CC TRANSMEM 167 198
 CC DOMAIN 199 218
 CC TRANSMEM 199 218
 CC DOMAIN 219 235
 CC TRANSMEM 219 235
 CC DOMAIN 236 260
 CC TRANSMEM 236 260
 CC DOMAIN 261 277
 CC TRANSMEM 261 277
 CC DOMAIN 278 301
 CC TRANSMEM 278 301
 CC DOMAIN 302 352
 CC TRANSMEM 302 352
 CC DISULFID 101 178
 CC MOD_RES 3 3
 CC MOD_RES 10 10
 CC MOD_RES 14 14
 CC SQU SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SOYQFWKFNQTLKIVILG 18
 |||||
 DB 185 SOYQFWKFNQTLKIVILG 202

RESULT 9
 CKR5_PANTR STANDARD; PRT; 352 AA.
 ID CKR5_PANTR STANDARD; PRT; 352 AA.
 AC P564Z0; Q02778;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKBR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharzon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RL simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Zimmerman P.A., Buckler-White A., Alkhatib G.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98022612; PubMed=9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;

RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=97426118; PubMed=9282822;
RX Zacharova V., Zachar V., Goustin A.S.;
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
RL HIV type 1 host.";
RN AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
RP SEQUENCE FROM N.A.
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
RN AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RP SEQUENCE FROM N.A.
RX Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RL phylogeny.";
RN Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC
CC EMBL; AF005663; AAB62557.1; -
CC EMBL; U94329; AAB58446.1; -
CC EMBL; AF011542; AAB65742.1; -
CC EMBL; U97666; AAC51670.1; -
CC EMBL; AF011540; AAB65740.1; -
CC EMBL; U89797; AAC03717.1; -
CC EMBL; AF177894; AAK43377.1; -
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
CC PROSITE; PS00237; G PROTEIN RECP FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT CARBOHYD 268 268
FT CONFLICT 123 123
FT SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQYQFWNQTILKIVILG 18
DB 185 SQYQFWNQTILKIVILG 202
RESULT 10
CKR5_PAPHA STANDARD; PRT; 352 AA.
AC P56441;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CXCR5.
OS Papio hamadryas (Hamadryas baboon), and
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557, 9555;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains".
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RX MEDLINE=99210133; PubMed=10195758;
RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
RT nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=P.anubis;
RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC
CC EMBL; AF005658; AAB62552.1; -
CC EMBL; AF105287; AAD20556.1; -
CC EMBL; AF105288; AAD20557.1; -
CC EMBL; AF105289; AAD20558.1; -
CC EMBL; AF105290; AAD20559.1; -
CC EMBL; AF023452; AAC63830.1; -
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.

Tue Sep 28 15:49:57 2004

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DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 4 (POTENTIAL).
FT TRANSMEM 142 166 5 (POTENTIAL).
FT DOMAIN 167 198 6 (POTENTIAL).
FT TRANSMEM 199 218 7 (POTENTIAL).
FT DOMAIN 219 235 8 (POTENTIAL).
FT TRANSMEM 236 260 9 (POTENTIAL).
FT DOMAIN 261 277 10 (POTENTIAL).
FT TRANSMEM 278 301 11 (POTENTIAL).
FT DOMAIN 302 352 12 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 352 AA; 40489 MW; 521504A9B1FE8B2 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKQFQTLKIVILG 18
DB 185 SOYQFWKQFQTLKIVILG 202

RESULT 11
CKRS_PONPY
ID CKRS_PONPY STANDARD; PRT; 352 AA.
AC 097881;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKBR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OC Pygathrix.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokines. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075446; AAD19858.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PS00237; GPCR_HODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 4 (POTENTIAL).
FT TRANSMEM 142 166 5 (POTENTIAL).
FT DOMAIN 167 198 6 (POTENTIAL).
FT TRANSMEM 199 218 7 (POTENTIAL).
FT DOMAIN 219 235 8 (POTENTIAL).
FT TRANSMEM 236 260 9 (POTENTIAL).
FT DOMAIN 261 277 10 (POTENTIAL).
FT TRANSMEM 278 301 11 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKQFQTLKIVILG 18
DB 185 SOYQFWKQFQTLKIVILG 202

RESULT 12
CKRS_PYGBI
ID CKRS_PYGBI STANDARD; PRT; 352 AA.
AC 097880;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKBR5.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075445; AAD19857.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.

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DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE; PS00237; G_PROTEIN_REC_F1_2; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | |
DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 13
CKRS_PYGNE
ID CKRS PYGNE STANDARD; PRT; 352 AA.
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CKR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
CC EMBL; AF075448; AAD19860.1; -

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DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE; PS00237; G_PROTEIN_REC_F1_2; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3E861 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | |
DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 14
CKRS_TRAFR
ID CKRS TRAFR STANDARD; PRT; 352 AA.
AC O97878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CKR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF075448; AAD19860.1; -

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[3] SEQUENCE FROM N.A.
RP SPECIES=M.mulatta; PubMed=11461684;
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
receptors.";
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [4]
[4] SEQUENCE FROM N.A.
RP SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX MEDLINE=97269687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parnett M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [5]
[5] MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U77672; AAC51109.1; -;
DR EMBL; U73739; AAC51158.1; -;
DR EMBL; U97672; AAC3432.1; -;
DR EMBL; AF005660; AAB62554.1; -;
DR EMBL; AF005661; AAB62555.1; -;
DR EMBL; AF005662; AAB62556.1; -;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECPT_F2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 241 241 M -> I (IN REF. 3).
FT CONFLICT 292 292 I -> M (IN REF. 3).
SQ SEQUENCE 352 AA; 40507 MW; 58B96C85903FACB2 CRC64;

Query Match 96.9%; Score 93; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 2e-07;

Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKNFQTLKIVILG 18
DB 185 SOYQFWKNFQTLKIVILG 202
RESULT 17
CKR5_MOUSE
ID CKR5_MOUSE STANDARD; PRT; 354 AA.
AC P51682; O35313; O35891; P97308; P97405; Q61867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (MIP-1
alpha receptor).
OS CCR5 OR CMKR5.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Spleen;
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
chemoattractant protein 1) and murine macrophage inflammatory protein
1alpha receptors: evidence for two closely linked C-C chemokine
receptors on chromosome 9.";
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96278910; PubMed=8662890;
RA Meyer A., Coyle A.J., Froufoot A.E.I., Wells T.N.C., Power C.A.;
RT "Cloning and characterization of a novel murine macrophage
inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 271:14445-14451(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Ola;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=97404635; PubMed=9261347;
RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
RT "Two distinct CCR5 domains can mediate coreceptor usage by human
immunodeficiency virus type 1.";
RL J. Virol. 71:6305-6314(1997).
RN [6]
RP SEQUENCE FROM N.A.
RA Guo B., Kuno K., Harada A., Matsushima K.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
but not in nonhematopoietic cell lines.


```

QY      2 QYQFQKQFQTLKIVIL 17
DB      188 QYRFQKHFQTLKIVIL 203

RESULT 19
CKR1 MOUSE
ID CKR1 MOUSE STANDARD; PRT; 355 AA.
AC P51675; Q91VP9;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)
DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
DE (RANTES-R).
GN CCR1 OR CMKCR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv; TISSUE=Pitotoneal macrophage;
RX MEDLINE=96072806; PubMed=7594543;
RA Gerard C.;
RA Post T.W.; Bozic C.R.; Rothenberg M.E.; Luster A.D.; Gerard N.,
RT "Molecular characterization of two murine eosinophil beta chemokine
RT receptors.";
RL J. Immunol. 155:5299-5305 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L.; Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a
RT functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501 (1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.,
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.,
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.,
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.,
RA Datchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.,
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.,
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.,
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.,
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.,
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.,
RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.,
RA Faney J.; Helton E.; Kettman M.; Madan A.; Rodrigues S.; Sanchez A.,
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.,
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickinson M.C.,
RA Rodriguez A.C.; Grimwood J.C.; Schmutz J.; Myers R.M.,
RA Butlerfield Y.S.N.; Krzywinski M.I.; Skaleka U.; Smailus D.E.,
RA Schnerch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC RANTES, AND LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC PROLIFERATION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in the heart, spleen, lung,
CC peritoneal exudate cells and leukocytes.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; U29678; AAA86119.1; -;
EMBL; U28404; AAA89153.1; -;
EMBL; BC011092; AAH11092.1; -;
PIR; I49339; I49339;
MGD; MGI:104618; Ccr1.
GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0030595; P:immune cell chemotaxis; IDA.
GO; GO:0006954; P:inflammatory response; IMP.
GO; GO:0030099; P:myeloid blood cell differentiation; IMP.
InterPro: IPR000276; GPCR_Rhodopsin.
Pfam: PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHOPOPSN.
PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
G-protein coupled receptor; Transmembrane.
DOMAIN 1 34
TRANSMEM 35 60
DOMAIN 61 64
TRANSMEM 65 91
DOMAIN 92 107
TRANSMEM 108 129
DOMAIN 130 146
TRANSMEM 147 171
DOMAIN 172 197
TRANSMEM 198 223
DOMAIN 224 239
TRANSMEM 240 264
DOMAIN 265 281
TRANSMEM 282 305
DOMAIN 306 355
DISULFID 106 183
CONFLICT 55 55
CONFLICT 149 149
CONFLICT 278 278
SEQUENCE 355 AA; 40901 MW; FCE9FF70E6F38B1 CRC64;

Query Match 49.0%; Score 47; DB 1; Length 355;
Best Local Similarity 61.5%; Pred. No. 3.9; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 3;

QY 6 WKNFQTLKIVILG 18
DB 195 WKRFQALXNLIG 207

RESULT 20
CKR2 MOUSE
ID CKR2 MOUSE STANDARD; PRT; 373 AA.
AC P51683; Q61172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (JE/FIC receptor) (MCP-1 receptor).
GN CCR2 OR CMKCR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L.; Gosling J.; Montecclaro F.S.; Lusis A.J.; Tsou C.-L.,
RA Charo I.F.

RT Molecular cloning and functional expression of murine JE (monocyte
 RT chemoattractant protein 1) and murine macrophage inflammatory protein
 RT alpha receptors: evidence for two closely linked C-C chemokine
 RT receptors on chromosome 9.;
 RL J. Biol. Chem. 271:7551-7558(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=94216064; PubMed=8662823;
 RA Kurihara T., Bravo R.;
 RT "Cloning and functional expression of mCCR2, a murine receptor for
 RT the C-C chemokines JE and FIC.";
 RL J. Biol. Chem. 271:11603-11606(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97026720; PubMed=8872898;
 RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
 RA Post T.W., Gerard C., Dorf M.E.;
 RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
 RT transcriptase-polymerase chain reaction does not detect mRNA for the
 RT KC or new MCP-1 receptor.";
 RL J. Neurosci. Res. 45:382-391(1996).
 CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
 CC chemokines. Transduces a signal by increasing the intracellular
 CC calcium ions level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
 CC but not in nonhematopoietic cell lines.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC
 CC EMBL; U47035; AAC52453.1; -;
 CC EMBL; U51717; AAC52557.1; -;
 CC EMBL; U56819; AAC52784.1; -;
 CC MGD; MGI:106185; Ccr2.
 CC GO; GO:0016493; P:C-C chemokine receptor activity; IDA.
 CC GO; GO:0019955; P:cytokine binding; IPI.
 CC GO; GO:0046066; P:cellular defense response (sensu Vertebrata); IMP.
 CC GO; GO:0030097; P:hemoiesis; IMP.
 CC GO; GO:0006959; P:humoral immune response; IMP.
 CC GO; GO:0006954; P:inflammatory response; IMP.
 CC GO; GO:0030334; P:regulation of cell migration; IMP.
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm.1.1;
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
 CC G-protein coupled receptor; Transmembrane.
 KW DOMAIN 1 55 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1 55
 FT TRANSMEM 56 83
 FT DOMAIN 84 93
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 94 93
 FT TRANSMEM 94 114
 FT DOMAIN 115 127
 FT TRANSMEM 128 149
 FT DOMAIN 150 166
 FT TRANSMEM 167 191
 FT DOMAIN 192 219
 FT TRANSMEM 220 239
 FT DOMAIN 240 256
 FT TRANSMEM 257 281
 FT DOMAIN 282 298
 FT TRANSMEM 299 322
 FT DOMAIN 323 373
 FT CYTOPLASMIC (POTENTIAL).
 FT DISULFID 126 203
 FT CONFLICT 39 39
 FT Y -> H (IN REF. 1).
 FT A -> G (IN REF. 1).
 FT CONFLICT 184 184

FT CONFLICT 264 264 V -> G (IN REF. 1).
 SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;
 Query Match 47.9%; Score 46; DB 1; Length 373;
 Best Local Similarity 64.3%; Pred. No. 5.8;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 4 QFQKNFQTLKIVIL 17
 DB 209 QLWKNFQIMRNIL 222
 RESULT 21
 CKR1_MACMU
 ID CKR1_MACMU STANDARD; PRT; 355 AA.
 AC P56482;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1).
 GN CCR1 OR CCR1.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9544;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC RANTES, MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
 CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
 CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
 CC PROLIFERATION
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC
 CC EMBL; AF017282; AAB70526.1; -;
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm.1.1;
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1 34
 FT TRANSMEM 35 60
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 61 64
 FT TRANSMEM 65 91
 FT DOMAIN 92 107
 FT TRANSMEM 108 129
 FT DOMAIN 130 146
 FT TRANSMEM 147 171
 FT DOMAIN 172 197
 FT TRANSMEM 198 223
 FT DOMAIN 224 239
 FT TRANSMEM 240 264
 FT DOMAIN 265 281
 FT TRANSMEM 282 305
 FT DOMAIN 306 355
 FT CARBOHYD 5 5
 FT BY SIMILARITY.
 FT DISULFID 106 183


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SQ SEQUENCE 355 AA; 41198 MW; 41CAEA7CC19D23D4 CRC64;
Query Match 46.9%; Score 45; DB 1; Length 355;
Best Local Similarity 50.0%; Pred. No. 8;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 YQFWNFKQTLKIVILG 18
Db 192 FQWKLFOALKINLFG 207

RESULT 22
YCX3_EUGGR STANDARD; PRT; 634 AA.
AC P31916; P31917;
DT 01-JUN-1993 (Rel. 26, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 78.0 kDa protein in PBBC intron 2 (ORF635).
OS Euglena gracilis.
OG Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3039;
RN [1]
SEQUENCE FROM N.A.
STRAIN=Z / UTEX 753;
MEDLINE=93347989; PubMed=8346031;
RA Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A.,
Orsat B., Spielmann A., Stutz E.;
RT "Complete sequence of Euglena gracilis chloroplast DNA.";
RL Nucleic Acids Res. 21:3537-3544(1993).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z11874; -; NOT ANNOTATED_CDS.
DR EMBL; X70810; CAA50080.1; -.
DR PIR; S34499; S34499.
DR PIR; S34500; S34500.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 634 AA; 78049 MW; D966B8864519E334 CRC64;

Query Match 46.9%; Score 45; DB 1; Length 634;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

Qy 4 QFW----KNFQTLKIVIL 17
Db 60 KFWDSQIKNFQTLKIVIL 77

RESULT 23
DYHB_HUMAN STANDARD; PRT; 4523 AA.
AC Q96DT5; Q9UJ82;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ciliary dynein heavy chain 11 (Axonemal beta dynein heavy chain 11).
GN DNAB11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A., VARIANT PCD GLN-3004, AND VARIANTS LEU-34;
RP ARG-639; CYS-654; ALA-1023; THR-1038; GLY-1640; ASN-2641; THR-3474;
RP VAL-3715; PRO-3765 AND ILE-4177.
```

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RC TISSUE=Nasal epithelium, and Testis;
RX MEDLINE=22155903; PubMed=12142464;
RA Rossioni L., Blouin J.L., Pan Y., Gehrig C., Maiti A.K., Scamuffa N.,
RA Rossier C., Jorissen M., Armengot M., Meeks M., Mitchison H.M.,
RA Chung E.M., Delozier-Blanchet C.D., Craigen W.J., Antonarakis S.E.;
RT "Mutations in the DNAB11 (axonemal heavy chain dynein type 11) gene
RT cause one form of situs inversus totalis and most likely primary
RT ciliary dyskinesia.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10282-10286(2002).
RN [2]
SEQUENCE OF 1904-2004 FROM N.A.
RC TISSUE=Nasal polyps;
RA Maiti A.K., Mattai M.-G., Jorissen M., Volz A., Ziegler A.,
RA Bouvagnet P.;
RT "Chromosomal localization of human dynein heavy chain genes.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Force generating protein of respiratory cilia. Produces
CC force towards the minus ends of microtubules. Dynein has ATPase
CC activity; the force-producing power stroke is thought to occur on
CC release of ADP.
CC -!- SUBUNIT: Consists of at least two heavy chains and a number of
CC intermediate and light chains.
CC -!- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem
CC (which binds cargo and interacts with other dynein components),
CC and the head or motor domain. The motor contains six tandemly-
CC linked AAA domains in the head, which form a ring. A stalk-like
CC structure (formed by two of the coiled coil domains) protrudes
CC between AAA 4 and AAA 5 and terminates in a microtubule-binding
CC site. A seventh domain may also contribute to this ring; it is not
CC clear whether the N-terminus or the C-terminus forms this extra
CC domain. There are four well-conserved and two non-conserved ATPase
CC sites, one per AAA domain. Probably only one of these (within AAA
CC 1) actually hydrolyzes ATP, the others may serve a regulatory
CC function.
CC -!- DISEASE: Defects in DNAB11 are a cause of primary ciliary
CC dyskinesia (PCD) [MIM:242850]; also known as immotile cilia
CC syndrome 1 (ICSI). The phenotype of this autosomal recessive
CC disease is characterized by axonemal abnormalities of respiratory
CC cilia and sperm tails leading to bronchiectasis and sinusitis,
CC which are sometimes associated with situs inversus (Kartagener
CC syndrome) and male sterility.
CC -!- SIMILARITY: Belongs to the dynein heavy chain family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ320497; CAC60121.1; -.
DR EMBL; AJ132087; CAA10560.1; -.
DR Genew; HGNC:2942; DNAB11.
DR MIM; 603339; -.
DR MIM; 242650; -.
DR GO; GO:0005858; C:axonemal dynein complex; NAS.
DR GO; GO:0003775; F:axonemal motor activity; NAS.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR004273; Dynein_heavy.
DR Pfam; PF03028; Dynein_heavy; 1.
DR SMART; SM00382; AAA; 4.
KW Motor protein; Dynein; Microtubule; ATP-binding; Repeat; Coiled coil;
KW Polymorphism; Disease mutation.
FT DOMAIN 1 1861 STEM (BY SIMILARITY).
FT DOMAIN 1862 2083 AAA 1 (BY SIMILARITY).
FT DOMAIN 2143 2373 AAA 2 (BY SIMILARITY).
FT DOMAIN 2479 2726 AAA 3 (BY SIMILARITY).
FT DOMAIN 2824 3073 AAA 4 (BY SIMILARITY).
FT DOMAIN 3079 3410 STALK (BY SIMILARITY).
FT DOMAIN 3466 3693 AAA 5 (BY SIMILARITY).
FT DOMAIN 3903 4129 AAA 6 (BY SIMILARITY).
FT DOMAIN 1274 1327 COILED COIL (POTENTIAL).
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FT DOMAIN 3079 3143 COILED COIL (POTENTIAL).
FT DOMAIN 3319 3410 COILED COIL (POTENTIAL).
FT DOMAIN 3675 3710 COILED COIL (POTENTIAL).
FT NP_BIND 1900 1907 ATP (POTENTIAL).
FT NP_BIND 2181 2188 ATP (POTENTIAL).
FT NP_BIND 2517 2524 ATP (POTENTIAL).
FT NP_BIND 2862 2869 ATP (POTENTIAL).
FT VARIANT 34 34 E -> L (requires 2 nucleotide
FT VARIANT 34 34 substitutions).
FT VARIANT 639 639 /FTid=VAR_013851.
FT VARIANT 654 654 Q -> R.
FT VARIANT 654 654 S -> C.
FT VARIANT 1023 1023 /FTid=VAR_013852.
FT VARIANT 1023 1023 /FTid=VAR_013853.
FT VARIANT 1038 1038 V -> A.
FT VARIANT 1038 1038 /FTid=VAR_013854.
FT VARIANT 1038 1038 A -> T.
FT VARIANT 1640 1640 /FTid=VAR_013855.
FT VARIANT 1640 1640 D -> G.
FT VARIANT 2641 2641 /FTid=VAR_013856.
FT VARIANT 2682 2682 S -> N.
FT VARIANT 2682 2682 I -> V.
FT VARIANT 3004 3004 /FTid=VAR_013857.
FT VARIANT 3004 3004 R -> Q (in PC; not proven to be
FT VARIANT 3004 3004 pathogenic).
FT VARIANT 3474 3474 /FTid=VAR_013858.
FT VARIANT 3474 3474 A -> T.
FT VARIANT 3715 3715 /FTid=VAR_013859.
FT VARIANT 3715 3715 L -> V.
FT VARIANT 3765 3765 /FTid=VAR_013860.
FT VARIANT 3765 3765 S -> P.
FT VARIANT 4177 4177 /FTid=VAR_013861.
FT VARIANT 4177 4177 T -> I.
FT VARIANT 4177 4177 /FTid=VAR_013862.
FT SEQUENCE 4523 AA; 520969 MW; 7C9A71C95B296889 CRC64;

Query Match 46.9%; Score 45; DB 1; Length 4523;
Best Local Similarity 50.0%; Pred. No. 97;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 FWNQFQTLKIVILG 18
DB 648 FWSNFASLRYLFLG 661

RESULT 24
SECD_HAEIN
ID SECD_HAEIN STANDARD; PRT; 616 AA.
AC P44591;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein-export membrane protein secD.
GN SECD OR HI0240.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RA MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McInerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae

FT RD";
FT Science 269:496-512(1995).
FT -!- FUNCTION: Involved in protein export (By similarity).
FT -!- SUBUNIT: Part of the prokaryotic protein translocation apparatus
FT which comprise secA, secB, secD, secE, secF, secG and secY (By
FT similarity).
FT -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
FT (By similarity).
FT -!- SIMILARITY: Belongs to the secD/secF family. SecD family.
FT
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FT between the Swiss Institute of Bioinformatics and the EMBL Outstation
FT the European Bioinformatics Institute. There are no restrictions on its
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FT or send an email to license@isb-sib.ch).
FT
FT EMBL; U32710; AAC21908.1; -.
FT TIGR; HI0240; -.
FT InterPro; IPR005791; SecD.
FT InterPro; IPR003335; SecD_SecF.
FT Pfam; PF02355; SecD_SecF; 1.
FT PRINTS; PR01755; SECFTNLKASE.
FT TIGRFAMs; TIGR00916; 2A0604s01; 1.
FT TIGRFAMs; TIGR01129; secD; 1.
FT Protein transport; Translocation; Transmembrane; Inner membrane;
FT Complete proteome. 31 POTENTIAL.
FT TRANSMEM 11 473 POTENTIAL.
FT TRANSMEM 453 495 POTENTIAL.
FT TRANSMEM 475 517 POTENTIAL.
FT TRANSMEM 497 582 POTENTIAL.
FT TRANSMEM 562 605 POTENTIAL.
FT TRANSMEM 585 605 POTENTIAL.
FT SEQUENCE 616 AA; 66986 MW; 7D51E4B085065F8F CRC64;

Query Match 45.8%; Score 44; DB 1; Length 616;
Best Local Similarity 38.9%; Pred. No. 20;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 SOYQWKNFQTLKIVILG 18
DB 3 NRYPLWKLWIFIVAIG 20

RESULT 25
PYRB_MYCPE
ID PYRB_MYCPE STANDARD; PRT; 300 AA.
AC Q8EUX9;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
DE transcarbamylase) (AtCase).
GN PYRB OR MYPE7890.
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HF-2;
RA MEDLINE=22354719; PubMed=12466555;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RA "The complete genomic sequence of Mycoplasma penetrans, an
RA intracellular bacterial pathogen in humans.";
RA Nucleic Acids Res. 30:5293-5300(2002).
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
CC + N-carbamoyl-L-aspartate.
CC -!- PATHWAY: Pyrimidine biosynthesis; second step.
CC -!- SIMILARITY: Belongs to the ATCase/OTCase family.
CC

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```

ENBL; AP0C4173; BAC44582.1; -.
HAMAP; MF_00001; -.
InterPro; IPR006130; Asp/Orn_Cotransf.
InterPro; IPR002082; Asp_carbMalttransf.
InterPro; IPR006131; OTCace_O.
InterPro; IPR006132; OTCace_P.
Pfam; PF00155; OTCace; 1.
Pfam; PF02729; OTCace_N; 1.
PRINTS; PR00100; ACTCACE.
TIGRGRAMS; TIGR00670; asp_carb tr; 1.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
Pyridine biosynthesis; Transferase; Complete proteome.
SEQUENCE 300 AA; 34532 MW; 9F9200EEED298E2
CRG54;

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      100% Match      44.8%; Score 43; DB 1; Length 300;
      100% Local Similarity 50.0%; Pred. No. 14;
      100% Conses 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

3 YQFWKFNQTLKIVILG 18
| : | : | | | : |
143 YEKFKSEGLKIAVG 158

T. 26
CERAE
CKR3 CERAE
P56432;
15-JUL-1998 (rel. 36; Created)
15-JUL-1998 (rel. 36; Last sequence update)
30-MAY-2000 (rel. 39; Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR3)
STANDARD; PRT; 355 AA.
CCR3-3 (CC-CKR-3) (CCR3)

CCR3 OR CMKBR3.
Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecoidea; Cercopithecinae; Cercopithecus.
NCBI_TaxID=9534;
[1]
SEQUENCE FROM N.A.
Sol N., Treboute C., Gomas E., Ferchal F., Alison M.;
Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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ENBL, Y13775; CAA74106.1; -
interpro: IPR000276; GPCR_Rhodopsn.
Pfam, PF00001; 7tm1; 1.
PRINTS; P00237; GPCRHHODPSN.
PROSITE; PS00337; G_PROTEIN_REC_F1_1; 1.
PROSITE; PS0362; G_PROTEIN_REC_F1_2; 1.
G-protein coupled receptor; Transmembrane.
DOMAIN 1 34
TRANSMEM 35 62
1 (POTENTIAL).
1 (POTENTIAL).

[illegible]

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RESULT 27
CCR3_MACMU
ID CCR3 MACMU STANDARD; PRT; 355 AA.
AC P56483;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CCR-3) (CCR-3) (CCR3)
DE (CCR3).
GN CCR3 OR CMKBR3.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
NCBI_TaxID=9544;
OX [1]_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RL receptors.";
RL Aids Res. Hum. Retroviruses 17:981-986(2001).
RN [2]
RP SEQUENCE FROM N.A.
RP MEDLINE=98118446; PubMed=9454594;
RA Sol N., Treboute C., Gomas E., Ferchal F., Shacklett B., Alizon M.;
RT "The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor
RL for HIV-2, but not for HIV-1.";
RL Virology 240:213-220(1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to ectatin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF017283; AAB70527.1; -.
CC EMBL; Y13776; CAA74107.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHOODPSN.

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DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; transmembrane.
FT DOMAIN 1 34
FT TRANSMEM 35 62
FT DOMAIN 63 72
FT TRANSMEM 73 93
FT DOMAIN 94 107
FT TRANSMEM 108 129
FT DOMAIN 130 146
FT TRANSMEM 147 171
FT DOMAIN 172 203
FT TRANSMEM 204 223
FT DOMAIN 224 239
FT TRANSMEM 240 264
FT DOMAIN 265 281
FT TRANSMEM 282 305
FT DOMAIN 306 355
FT DISULFID 106 183
FT CONFLICT 180 180
FT CONFLICT 202 202
SQ SEQUENCE 355 AA; 40805 MW; E271F1E694970D9F CRC64;

Query Match 44.8%; Score 43; DB 1; Length 355;
Best Local Similarity 58.3%; Pred. No. 17;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17
DB 195 WRHFTLKWTL 206

RESULT 28
VTOD CHRVQ
ID VTOD CHRVQ STANDARD; PRT; 373 AA.
AC Q983U8; Q980N2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable tryptophan hydroxylase viod (EC 1.-.-.-).
GN VIOD OR CV3271.
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UQM51;
RX MEDLINE=20525185; PubMed=11075927;
RA August P.R., Grossman T.H., Minor C., Draper M.P., MacNeil I.A.,
RA Pemberton J.M., Call K.M., Holt D., Osburne M.S.;
RA "Sequence analysis and functional characterization of the violacein
RT biosynthetic pathway from Chromobacterium violaceum.";
RL J. Mol. Microbiol. Biotechnol. 2:513-519(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 1249;
RX Hoshino T.;
RA "Biosynthetic gene cluster for violacein pigment.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22582880; PubMed=14500782;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Arraiza J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Beio A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso J.C.M., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
```

STRAIN=168;
 MEDLINE=93181186; PubMed=8441623;
 Fuma S., Fujishina Y., Corbell N., D'Souza C., Nakano M.M.,
 Zuber P., Yamane K.;
 "Nucleotide sequence of 5' portion of srfA that contains the region
 required for competence establishment in *Bacillus subtilis*.";
 Nucleic Acids Res. 21:93-97(1993).
 [2]
 SEQUENCE FROM N.A.
 RC STRAIN=168; / JH642;
 RX MEDLINE=93360813; PubMed=8955609;
 RA Cosmina P., Rodriguez F., de Ferra F., Grandi G., Perego M.,
 Venema G., van Sinderen D.;
 "Sequence and analysis of the genetic locus responsible for surfactin
 synthesis in *Bacillus subtilis*.";
 Mol. Microbiol. 8:821-831(1993).
 [3]
 SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=97124189; PubMed=8969502;
 RA Yamane K., Kumano M., Kurita K.;
 "The 25 degrees-36 degrees region of the *Bacillus subtilis*
 chromosome: determination of the sequence of a 146 kb segment and
 identification of 113 genes.";
 Microbiology 142:3047-3056(1996).
 [4]
 SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 Brouillet S., Bruschini C., Brans A., Braun M., Brignell S.C., Bron S.,
 Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 Enrian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
 Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut L.,
 Hilbert H., Holst S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 Lee S.M., Levine A., Liu H., Masuda S., Maestl D., Nakai S., Noback M.,
 Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 Presecan E., Pujic P., Puxnelle B., Rapoport G., Rey M., Reynolds S.,
 Rieger M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y.,
 Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 Takeuchi M., Tamakoshi A., Tanaka T., Terpestra P., Tognoni A.,
 Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 Yoshida K., Yoshikawa H.F., Zmstein E., Yoshikawa H., Danchin A.;
 "The complete genome sequence of the Gram-positive bacterium *Bacillus*
subtilis.";
 Nature 390:249-256(1997).
 [5]
 SEQUENCE OF 514-800 FROM N.A.
 RC STRAIN=ATCC 21332;
 RX MEDLINE=92290255; PubMed=1601288;
 RA Borchert S., Paill S.S., Marandiel M.A.;
 "Identification of putative multifunctional peptide synthetase genes
 using highly conserved oligonucleotide sequences derived from known
 synthetases.";
 FEMS Microbiol. Lett. 71:175-180(1992).
 RL FEMS Microbiol. Lett. 71:175-180(1992).
 CC -!- FUNCTION: THIS PROTEIN IS A MULTIFUNCTIONAL ENZYME ABLE TO
 CC ACTIVATE AND POLYMERIZE THE AMINO ACIDS LEU, GLU, ASP AND VAL.
 CC ACTIVATION SITES FOR THESE AA CONSIST OF INDIVIDUAL DOMAINS.
 CC -!- COFACTOR: Contains 3 covalently bound phosphopantetheines.

-!- PATHWAY: Cyclic peptide antibiotic surfactin biosynthesis.
 -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
 family.
 -!- SIMILARITY: Contains 3 acyl carrier domains.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR ENBL; D13262; BAA02533.1; -;
 DR ENBL; X70356; CAA49817.1; -;
 DR ENBL; D50453; BAA08983.1; -;
 DR ENBL; Z99105; CAB12143.1; -;
 DR ENBL; X65835; CAA46678.1; -;
 DR PIR; I40486; I40496.
 DR HSSP; P14687; 1AMU
 DR Subtilist; BG10169; srfAB.
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR001242; Condensatr.
 DR InterPro; IPR006163; Pp-bind.
 DR InterPro; IPR006162; Ppantne S.
 DR Pfam; PF00501; AMP-binding; 3.
 DR Pfam; PF00668; Condensation; 4.
 DR Pfam; PF00550; Pp-binding; 3.
 DR PRINTS; PRO0154; AMPBINDING.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 3.
 DR PROSITE; PS00455; AMP BINDING; 3.
 DR PROSITE; PS0075; ACP DOMAIN; 3.
 KW Ligase; Antibiotic biosynthesis; Phosphopantetheine; Sporulation;
 KW Multifunctional enzyme; Repeat; Complete proteome
 FT REPEAT ? 1040 DOMAIN 1 (VAL-ACTIVATING).
 FT REPEAT ? 2036 DOMAIN 2 (ASP-ACTIVATING).
 FT REPEAT ? 3114 DOMAIN 3 (D-LEU-ACTIVATING).
 FT DOMAIN 970 1036 ACYL CARRIER (ACP) 1.
 FT DOMAIN 2015 2082 ACYL CARRIER (ACP) 2.
 FT DOMAIN 3043 3109 ACYL CARRIER (ACP) 3.
 FT BINDING 999 999 PHOSPHOPANTHETHEINE (POTENTIAL).
 FT BINDING 2045 2045 PHOSPHOPANTHETHEINE (POTENTIAL).
 FT BINDING 3073 3073 PHOSPHOPANTHETHEINE (POTENTIAL).
 FT CONFLICT 33 33 S -> F (IN REF. 1).
 FT CONFLICT 42 42 A -> G (IN REF. 1).
 FT CONFLICT 110 110 Q -> D (IN REF. 1).
 FT CONFLICT 113 115 RQA -> AQG (IN REF. 1).
 FT CONFLICT 139 139 A -> V (IN REF. 1).
 FT CONFLICT 239 259 L -> W (IN REF. 1).
 FT CONFLICT 309 309 R -> A (IN REF. 1).
 FT CONFLICT 478 480 TPA -> SRP (IN REF. 1).
 FT CONFLICT 596 596 MISSING (IN REF. 5).
 FT CONFLICT 648 648 A -> R (IN REF. 1).
 FT CONFLICT 680 682 RHV -> ETL (IN REF. 1).
 FT CONFLICT 694 698 EQSIT -> DKRIS (IN REF. 5).
 FT CONFLICT 788 788 M -> L (IN REF. 5).
 FT CONFLICT 939 940 PL -> LV (IN REF. 1).
 FT CONFLICT 1038 1038 N -> I (IN REF. 1).
 FT CONFLICT 1133 1133 H -> Q (IN REF. 1).
 FT CONFLICT 1310 1310 V -> C (IN REF. 1).
 FT CONFLICT 1333 1333 G -> V (IN REF. 1).
 FT CONFLICT 1384 1384 P -> R (IN REF. 1).
 FT CONFLICT 1582 1582 G -> E (IN REF. 1).
 FT CONFLICT 1677 1682 KRRADG -> E (IN REF. 1).
 FT CONFLICT 1700 1700 C -> S (IN REF. 1).
 FT CONFLICT 1755 1755 F -> K (IN REF. 1).
 FT CONFLICT 1787 1787 T -> S (IN REF. 1).
 FT CONFLICT 1801 1822 GAIAGRVDLPDAFAKPTIG -> APSPOGLICMSRCIC
 FT ETDPNR (IN REF. 1).
 FT LG -> PK (IN REF. 1).
 FT R -> C (IN REF. 1).
 FT A -> V (IN REF. 1).
 FT ARLTP -> LRDSLN (IN REF. 1).
 FT CONFLICT 2141 2145

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FT CONFLICT 2445 2445 E -> Q (IN REF. 1).
FT CONFLICT 2485 2489 ATDLF -> ROICS (IN REF. 1).
FT CONFLICT 2546 2566 TVHOLFETVORHKRDPAVY -> DGCISYKRLSSATKT
FT CONFLICT 2608 2615 ARLSHT (IN REF. 1).
FT CONFLICT 2644 2645 KLA -> NV (IN REF. 1).
FT CONFLICT 2645 2645 D -> H (IN REF. 1).
FT CONFLICT 2713 2713 D -> H (IN REF. 1).
FT CONFLICT 2723 2723 GELCVA -> RALRG (IN REF. 1).
FT CONFLICT 2876 2881 RF -> L (IN REF. 1).
FT CONFLICT 2899 2900 EDR -> QDA (IN REF. 1).
FT CONFLICT 2958 2960 R -> A (IN REF. 1).
FT CONFLICT 2964 2964
SQ SEQUENCE 3587 AA; 401248 MW; 6B0B05A9FF32054D CRC64;

Query Match 44.8%; Score 43; DB 1; Length 3587;
Best Local Similarity 33.3%; Pred. No. 1.6e+02;
Matches 6; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 SQYQFWKFNQTLKIVLG 18
: | | | | | | | | | | | | | | | | | | | |
Db 1751 ASFAFDANFESLRILVLG 1768

RESULT 30
UTR4_YEAST STANDARD; PRT; 241 AA.
AC P32626;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UTR4 protein (Unknown transcript 4 protein).
GN UTR4 OR YEL038W OR SXGP-ORE20.
OS Saccharomyces cerevisiae (baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313264; PubMed=9169858;
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
RA Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RA "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
RN Nature 367:78-81(1997).
[2]
RC SEQUENCE OF 1-158 FROM N.A.
RX STRAIN=B-6441;
RX MEDLINE=94016558; PubMed=6411151;
RA Melnick L., Sherman F.;
RT "The gene clusters ARC and COR on chromosomes 5 and 10, respectively,
RT of Saccharomyces cerevisiae share a common ancestry.";
RN J. Mol. Biol. 233:372-388(1993).
[3]
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DR EMBL; L22173; AAA34939.1; -
DR EMBL; S65964; RAD13973.1; -
DR EMBL; S66121; AAB28443.1; -
DR EMBL; U18779; AAB65004.1; -
DR PIR; S30843; S30843.
DR Germline; 139042; -.
DR SCD; S0000764; UTR4.

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DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1. ID -> MH (IN REF. 2).
FT CONFLICT 70 71 AHDSLD -> GNIRMI (IN REF. 2).
FT CONFLICT 153 158 BF6FBEC7FEL14B5AD CRC64;
SQ SEQUENCE 241 AA; 26735 MW; 6F6FBEC7FEL14B5AD CRC64;

Query Match 43.8%; Score 42; DB 1; Length 241;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYQFWKFNQTL 12
: | | | | | | | | | | | | | | | | | | | |
Db 231 KYQVKNFETL 241

RESULT 31
FECD_ECOLI STANDARD; PRT; 334 AA.
AC P23876; P77097;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ferric enterobactin transport system permease protein fepd.
GN FECD OR B0590.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92157868; PubMed=1838574;
RA Shea C.M., McIntosh M.A.;
RT "Nucleotide sequence and genetic organization of the ferric
RT enterobactin transport system: homology to other periplasmic binding
RT protein-dependent systems in Escherichia coli.";
RL Mol. Microbiol. 5:1415-1428(1991).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92157867; PubMed=1787794;
RA Chenault S.S., Earhart C.F.;
RT "Organization of genes encoding membrane proteins of the Escherichia
RT coli ferric enterobactin permease.";
RL Mol. Microbiol. 5:1405-1413(1991).
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RN Science 277:12453-1474(1997).
[4]
RN SEQUENCE FROM N.A.
RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA Federspiel N., Hyman R., Kaiman S., Komp C., Kurdi O., Lew H.,
RA Lin D., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR FERRIC ENTEROACTIN. PROBABLY RESPONSIBLE FOR THE
CC TRANSLUCULAR LOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- INDUCTION: Controlled in part by the amount of available iron.
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family. FeCD subfamily.
-----
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-----
DR EMBL; L22173; AAA34939.1; -
DR EMBL; S65964; RAD13973.1; -
DR EMBL; S66121; AAB28443.1; -
DR EMBL; U18779; AAB65004.1; -
DR PIR; S30843; S30843.
DR Germline; 139042; -.
DR SCD; S0000764; UTR4.

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Best Local Similarity 53.8%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 WNFQTLKIVILG 18
   |||||:|
DB 199 WKRFQALRMNIFG 211

RESULT 16
CKR2_RAT
ID CKR2_RAT STANDARD; PRT; 373 AA.
AC O55193;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2).
GN CKR2 OR CCR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA deGiebrie C.M., Pennell N.A., Strait W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis";
RL J. Neuroimmunol. 86:11-12(1998).
CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
CC macrophages.
CC -!- INDUCTION: In animals in which experimental allergic
CC encephalomyelitis (EAE) has been induced.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC -----
CC EMBL: U77349; AAC03242.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR00237; GPCRHHODOPSN.
CC PROSITE: PS00237; G.PROTEIN RECP FL 1; 1.
CC PROSITE: PS0262; G.PROTEIN RECP FL 2; 1.
CC KW G-protein coupled receptor; Transmembrane.
CC DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 61 81 POTENTIAL.
CC DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 92 112 POTENTIAL.
CC DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 129 149 POTENTIAL.
CC DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 171 191 POTENTIAL.
CC DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 221 241 POTENTIAL.
CC DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 257 277 POTENTIAL.
CC DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 302 322 POTENTIAL.
CC DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
CC DISULFID 126 203 BY SIMILARITY.
CC SEQUENCE 373 AA; 42763 MW; 2E7B012F5D6FD09 CRC64;
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Query Match 42.7%; Score 41; DB 1; Length 373;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 WNFQTLKIVIL 17
   |||||:|
DB 211 WNFQTLINRIL 222

RESULT 37
O22B_DROME
ID O22B_DROME STANDARD; PRT; 397 AA.
AC P81910; Q9U6X6; Q9VQ19;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Odorant receptor 22B.
GN OR22B OR OR22A.2 OR DOR22A.2 OR DOR67 OR ANI2 OR CG4231.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RC STRAIN=Oregon-R; Tissue=Antenna;
RX MEDLINE=99189757; PubMed=10089887;
RA Vosehall L.B., Amrein H., Morozov P.S., Rzhetsky A., Axel R.;
RT "A spatial map of olfactory receptor expression in the Drosophila
RT antenna";
RL Cell 96:725-736(1999).
RN [2]
RP REVISION TO 58.
RA Vosehall L.B., Amrein H., Morozov P.S., Rzhetsky A., Axel R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99389723; PubMed=10458908;
RA Gao Q., Chess A.;
RT "Identification of candidate Drosophila olfactory receptors from
RT genomic DNA sequence.";
RL Genomics 60:31-39(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Calinkner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiheu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de la Chapelle A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flosser C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mileshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [5]
RP IDENTIFICATION, AND TISSUE SPECIFICITY.
RC TISSUE=Antenna;
RX MEDLINE=99166868; PubMed=10069338;
RA Clyne P.J., Warr C.G., Freeman M.R., Lessing D., Kim J., Carlson J.R.;
RT "A novel family of divergent seven-transmembrane proteins: candidate
RT odorant receptors in Drosophila.";
RL Neuron 22:327-338(1999).
CC -!- FUNCTION: Probable role in the odorant response, being an odorant
CC receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN 20-22 SENSORY NEURONS ON THE
CC MEDIAL-PROXIMAL EDGE OF THE ANTENNA. THIS EXPRESSION PATTERN
CC MATCHES THE DISTRIBUTION OF THE LARGE SENSILLA BASICONICA.
CC EXPRESSION IS FIRST SEEN AT 60 HOURS APF IN A SUBSET OF CELLS
CC RESTRICTED TO A SUBREGION OF THE DEVELOPING ANTENNA. EXPRESSION
CC CONTINUES THROUGHOUT ANTENNAL DEVELOPMENT.
CC -!- SIMILARITY: Belongs to family Dr-or of G-protein coupled
CC receptors.
CC
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CC
CC -----
CC EMBL; AF127924; RAD26359.2; -;
CC EMBL; AB003586; RAF51363.1; -;
CC Flybase; FBgn0026397; Or22b.
CC GO; GO:0016021; C:integral to membrane; NAS.
CC GO; GO:0004984; F:olfactory receptor activity; NAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; NAS.
CC GO; GO:0007608; P:olfaction; NAS.
CC InterPro; IPR004117; 7tm_6.
CC Pfam; PF02949; 7tm_6; 1.
CC Transmembrane; G-protein coupled receptor; Olfaction;
KW Multigene family.
FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 50 70 1 (POTENTIAL).
FT DOMAIN 71 85 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 86 105 2 (POTENTIAL).
FT DOMAIN 106 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 164 3 (POTENTIAL).
FT DOMAIN 165 194 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 195 215 4 (POTENTIAL).
FT DOMAIN 216 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 269 289 5 (POTENTIAL).
FT DOMAIN 290 295 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 296 316 6 (POTENTIAL).
FT DOMAIN 317 347 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 348 368 7 (POTENTIAL).
FT DOMAIN 369 397 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 58 58 V -> L (IN REF. 3, 4 AND 5).
FT CONFLICT 256 256 D -> TICDFKFFVLPYFFS (IN REF. 3).
FT CONFLICT 376 397 MYKLAFTVTVIKVFNLAQKQ -> VSIHQVEL (IN
FT REF. 3).
FT SEQUENCE 397 AA; 46387 MW; EB76169D0A13E50 CRC64;

Query Match

Best Local Similarity 53.3%; Score 41; DB 1; Length 397;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 3 YQFMKNFQTLKIVIL 17
Db 48 YKLWSTFVTLVIFIL 62
RESULT 38
FCMD HUMAN STANDARD; PRT; 461 AA.
ID FCMD_HUMAN
AC Q75072; Q96TE1; Q9P295;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fukutin precursor (Fukuyama-type congenital muscular dystrophy
DE protein).
GN FCMD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98952786; PubMed=9690476;
RA Kobayashi K., Nakahori Y., Miyake M., Matsumura K., Kondo-Iida E.,
RA Nomura Y., Segawa M., Yoshioka M., Saito K., Osawa M., Hamano K.,
RA Sakakihara Y., Nonaka I., Nakagome Y., Kanazawa I., Nakamura Y.,
RA Tokunaga K., Toda T.;
RA "An ancient retrotransposal insertion causes Fukuyama-type congenital
RA muscular dystrophy.";
RT Nature 394:388-392(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21099876; PubMed=11165248;
RA Kobayashi K., Sasaki J., Kondo-Iida E., Fukuda Y., Kinoshita M.,
RA Sunada Y., Nakamura Y., Toda T.;
RA "Structural organization, complete genomic sequences and mutational
RA analyses of the Fukuyama-type congenital muscular dystrophy gene,
RA fukutin.";
RT FEBS Lett. 489:192-196(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Babbage A.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May interact with and reinforce a large complex
CC encompassing the outside and inside of muscle membranes. May also
CC be involved in brain development.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable). May be located in the
CC extracellular matrix.
CC -!- TISSUE SPECIFICITY: Widely expressed with highest expression in
CC brain, heart, pancreas and skeletal muscle.
CC -!- DISEASE: Defects in FCMD is the cause of Fukuyama-type congenital
CC dystrophy (FCMD) [MIM:253800]. FCMD is an autosomal recessive
CC disorder characterized by congenital muscular dystrophy associated
CC with brain malformation due to a defect in the migration of
CC neurons. The disease is often due to a retrotransposal insertion
CC of tandemly repeated sequences in the 3'-UTR of FCMD.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AB008226; BAA32000.1; -;
CC EMBL; AB038490; BAA94082.1; -;
CC EMBL; AL158070; CAC22162.1; -;
CC GenBank; HGNC:3622; FCMD.
CC MIM; 607440; -;
CC MIM; 253800; -;

DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0007517; P:muscle development; TAS.
DR GO: GO:0007399; P:neurogenesis; TAS.
KW Glycoprotein; Signal.
FT SIGNAL 21 POTENTIAL.
FT CHAIN 22 461 FUKUTIN.
FT CARBOHYD 92 92 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 203 203 R -> Q (IN REF. 1).
SQ SEQUENCE 461 AA; 53724 MW; 2D11F2BE4BCDD858 CRC64;

Query Match 42.7%; Score 41; DB 1; Length 461;
Best Local Similarity 40.0%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 3; Indels 12; Gaps 1;

QY 2 QYQWKN-----FQTLKI 14
DB 116 QYHLKNEGCFRIENMGFQCLKI 140

RESULT 39
PR39 YEAST
ID PR39 YEAST STANDARD; PRT; 629 AA.
AC P396B2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pre-mRNA processing protein PRP39.
GN PRP39 OR YML046W OR YN9827.06.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GRF88;
RX MEDLINE=94254821; PubMed=8196608;
RA Lockhart S.R., Rymond B.C.;
RT "Commitment of yeast pre-mRNA to the splicing pathway requires a novel U1 small nuclear ribonucleoprotein polypeptide, Prp39p.";
RL Mol. Cell. Biol. 14:3623-3633(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churche C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.";
RL Nature 387:90-93(1997).
RN [3]
RP PARTIAL SEQUENCE.
RX MEDLINE=97165029; PubMed=9012791;
RA Neubauer G., Gottschalk A., Fabrizio P., Seraphin B., Luehrmann R., Mann M.;
RT "Identification of the proteins of the yeast U1 small nuclear ribonucleoprotein complex by mass spectrometry.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3385-3390(1997).
CC -1- FUNCTION: FUNCTION PRIOR TO STABLE BRANCH POINT RECOGNITION BY THE U1 SNRNP PARTICLE TO FACILITATE OR STABILIZE THE U1 SNRNP/5' SPLICE SITE INTERACTION. HAS A DIRECT ROLE IN THE ASSEMBLY OR FUNCTION OF A CATALYTICALLY ACTIVE SPLICEOSOME.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Contains 7 HAT repeats.

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CC EMBL; L29224; AAA20131.1; --
DR EMBL; Z47816; CAA87828.1; --
DR PIR; S47920; S47920.
DR Germline; 142575; --
DR SGB; S0004509; FAP39.
DR GO: GO:0000243; C:commitment complex; IPI.
DR GO: GO:0005685; C:snrnp U1; IDA.
DR GO: GO:0003723; P:RNA binding; IPI.
DR GO: GO:0006371; P:mRNA splicing; IMP.
DR InterPro; IPR003107; HAT.
DR SMART; SM00386; HAT; 2.
KW mRNA processing; mRNA splicing; Nuclear protein; Repeat.
FT REPEAT 68 100 HAT 1.
FT REPEAT 102 134 HAT 2.
FT REPEAT 138 173 HAT 3.
FT REPEAT 175 208 HAT 4.
FT REPEAT 233 265 HAT 5.
FT REPEAT 270 302 HAT 6.
FT REPEAT 446 480 HAT 7.
SQ SEQUENCE 629 AA; 74748 MW; 67480ED01347B6AB CRC64;

Query Match 42.7%; Score 41; DB 1; Length 629;
Best Local Similarity 37.5%; Pred. No. 60;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 QYQWKNFQTLKIVILG 18
DB 88 FGFKRFATIEYQLFG 103

RESULT 40
SUHA HUMAN
ID SUHA HUMAN STANDARD; PRT; 284 AA.
AC Q06520;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alcohol sulfotransferase (SC 2.8.2.2) (Hydroxysteroid Sulfotransferase) (HST) (Dehydroepiandrosterone sulfotransferase) (DHEA-ST) (ST2) (ST2A3).
GN SUL2A1 OR STD OR HST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 60-64; 104-119 AND 273-284.
RC TISSUE=Liver;
RX MEDLINE=93143674; PubMed=7678732;
RA Comer K.A., Falany J.L., Falany C.N.;
RT "Cloning and expression of human liver dehydroepiandrosterone sulfotransferase.";
RL Biochem. J. 289:233-240(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 80-107 AND 176-198.
RC TISSUE=Liver;
RX MEDLINE=92269778; PubMed=1588921;
RA Ottensm F.D., Wieben E.D., Wood T.C., Watson R.W.G., Madden B.J., McCormick D.J., Weishilboum R.M.;
RT "Human liver dehydroepiandrosterone sulfotransferase: molecular cloning and expression of cDNA.";
RL Mol. Pharmacol. 41:865-872(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RX MEDLINE=96034512; PubMed=7589785;
RA Forbes K.J., Hagen M., Coughtrie M.W.H., Glatt H.R., Hume R.;
RT "Human fetal adrenal hydroxysteroid sulphotransferase: cDNA cloning, stable expression in V79 cells and functional characterisation of the expressed enzyme.";
RL Mol. Cell. Endocrinol. 112:53-60(1995).
RN [4]

SEQUENCE FROM N.A.
 RX MEDLINE=95322029; PubMed=759806;
 RA Luu-The V., Dufort I., Paquet N., Reimnitz G., Labrie F.,
 RT "Structural characterization and expression of the human
 RT dehydroepiandrosterone sulfotransferase gene.";
 RL DNA Cell Biol. 14:511-518(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95225980; PubMed=7710689;
 RA Ohteress D.M., Her C., Aksoy S., Kimura S., Wieben E.D.,
 RA Weinschilboum R.M.;
 RT "Human dehydroepiandrosterone sulfotransferase gene: molecular
 RT cloning and structural characterization.";
 RL DNA Cell Biol. 14:331-341(1995).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92392364; PubMed=1520333;
 RA Kong A.-N.T., Yang L., Ma M., Tao D., Bjornsson T.D.;
 RT "Molecular cloning of the alcohol/hydroxysteroid form (hSta) of
 RT sulfotransferase from human liver.";
 RL Biochem. Biophys. Res. Commun. 187:448-454(1992).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Casavant P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Catalyzes the sulfation of steroids and bile acids in
 CC the liver and adrenal glands.
 CC -!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + an alcohol =
 CC adenosine 3',5'-bisphosphate + an alkyl sulfate.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Liver, adrenal and at lower level in the
 CC kidney. Is present in human fetus in higher level in the adrenal
 CC than the liver and the kidney.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Estrogens present in maternal circulation is
 CC predominantly derived from fetal dehydroepiandrosterone sulfate
 CC which is hydrolyzed and metabolized to estrogens in placenta.
 CC -!- SIMILARITY: Belongs to the sulfotransferase family.
 CC -----
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 CC -----
 DR EMBL; L20000; AAA35758.1; -;
 DR EMBL; X70222; CAA49755.1; -;
 DR EMBL; U08024; AAA17749.1; -;
 DR EMBL; U08025; AAA17750.1; -;

DR EMBL; X84816; CAA59274.1; -;
 DR EMBL; L36196; AAA75491.1; -;
 DR EMBL; L36191; AAA75491.1; JOINED.
 DR EMBL; L36192; AAA75491.1; JOINED.
 DR EMBL; L36193; AAA75491.1; JOINED.
 DR EMBL; L36194; AAA75491.1; JOINED.
 DR EMBL; L36195; AAA75491.1; JOINED.
 DR EMBL; U13061; AAC51353.1; -;
 DR EMBL; U13056; AAC51353.1; JOINED.
 DR EMBL; U13057; AAC51353.1; JOINED.
 DR EMBL; U13058; AAC51353.1; JOINED.
 DR EMBL; U13059; AAC51353.1; JOINED.
 DR EMBL; U13060; AAC51353.1; JOINED.
 DR EMBL; S43859; AAB23169.2; -;
 DR EMBL; BC020755; AAH20755.1; -;
 DR PIR; I53037; I38548.
 DR PDB; 1J99; 19-JUN-02.
 DR Genew; HGNC:11458; SULT2A1.
 DR MIM; 125263; -;
 DR GO; GO:0008146; F:sulfotransferase activity; TAS.
 DR GO; GO:0008202; P:steroid metabolism; TAS.
 DR InterPro; IPR000863; Sulfotransferase.
 DR Pfam; PF00685; Sulfotransfer; 1.
 DR ProDom; PD001218; Sulfotransferase; 1.
 DR Bile acid catabolism; Steroid metabolism; Transferase; 3D-structure.
 KW INIT_MET 0 BY SIMILARITY 0
 FT BINDING 248 254 PAPS BINDING SITE (POTENTIAL).
 FT CONFLICT 62 62 A -> P (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 89 89 T -> S (IN REF. 1).
 FT CONFLICT 118 118 L -> D (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 158 158 L -> V (IN REF. 6).
 SQ SEQUENCE 284 AA; 33648 MW; 3C89C7597833EBA1 CRC64;
 Query Match 41.7%; Score 40; DB 1; Length 284;
 Best Local Similarity 53.8%; Pred. No. 40;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SOYQWKNFQTLK 13
 DB 128 SOYFFWKNMKPIK 140
 Search completed: September 28, 2004, 09:04:06
 Job time : 6.625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:56:16 ; Search time 28.8 Seconds
(without alignments)
197.199 Million cell updates/sec

Title: US-10-084-813-13
Perfect score: 96
Sequence: 1 SQYQFWKNFQTLKIVILG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREML_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	52	4 Q9PIT5	Q9PIT5 homo sapien
2	96	100.0	60	4 Q9PIT4	Q9PIT4 homo sapien
3	96	100.0	333	4 O14694	O14694 homo sapien
4	96	100.0	334	5 Q9TUQ7	Q9TUQ7 erythrocebu
5	96	100.0	339	4 Q9UN24	Q9UN24 homo sapien
6	96	100.0	339	4 Q9UN26	Q9UN26 homo sapien
7	96	100.0	339	4 Q9UN23	Q9UN23 homo sapien
8	96	100.0	339	4 Q9UBJ7	Q9UBJ7 homo sapien
9	96	100.0	339	4 Q9UN25	Q9UN25 homo sapien
10	96	100.0	339	4 Q9UN27	Q9UN27 homo sapien
11	96	100.0	339	4 Q9UBT9	Q9UBT9 homo sapien
12	96	100.0	339	4 Q9UN28	Q9UN28 homo sapien
13	96	100.0	339	6 Q9TUQ0	Q9TUQ0 hylobates c
14	96	100.0	339	6 Q9TUX1	Q9TUX1 hylobates c
15	96	100.0	339	6 Q9TUU9	Q9TUU9 cercopithec
16	96	100.0	339	6 Q9TUW9	Q9TUW9 hylobates c

ALIGNMENTS

RESULT 1

Q9PIT5
ID Q9PIT5 PRELIMINARY; PRT; 52 AA.
AC Q9PIT5; TREMBLrel. 15, Created
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Mutant chemokine receptor CCR5 (Fragment).
GN CCR5.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9392755; PubMed=10465086;
RA Aikionbare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,
Bond V.C.;
RT "Characterization of a third CCR5 amplicon from CCR5-delta32-
RT heterozygous HIV-1-infected individuals.";
RL AIDS 13:1585-1586(1999).
DR EMBL; AF056019; AAF65578.1; -;
DR GO; GO:0004872; F:receptor activity; IEA.

KW Receptor.

FT NON TER 1 41 P -> S.

FT VARIANT 41 41

SQ SEQUENCE 52 AA; 5962 MW; DAEB2A5A9529C3A9 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 52;

Best Local Similarity 100.0%; Pred. No. 3.2e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18

Db 11 SQYQFWKNFQTLKIVILG 28

RESULT 2

Q9PIT4

Q9TSQ1 cercopithec
Q9TUU8 cercopithec
Q9TQW4 pan troglod
Q9TUW4 pan troglod
Q9TUW7 cercopithec
Q9TUR6 cercopithec
Q9TQV6 colobus gue
Q9TUW6 pan troglod
Q9TUW9 cercopithec
Q9TUR2 erythrocebu
Q9TQV0 papio papio
Q9TQV5 cercopithec
Q9TUS7 papio papio
Q9TUW3 pongo pygma
Q9TUS5 papio papio
Q9TQV2 papio papio
Q9TQV3 cercopithec
Q9TUR3 cercopithec
Q9TUR3 erythrocebu
Q9TQW2 pongo pygma
Q9TQX2 erythrocebu
Q9TSQ4 cercopithec
Q9TQW2 gorilla gor
Q9TSQ3 cercopithec
Q9TUR0 cercopithec
Q9TUW5 pan troglod
Q9TUQ4 erythrocebu
Q9TUQ6 erythrocebu
Q9TUW8 papio papio

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ID Q9PIT4 PRELIMINARY; PRT; 60 AA.
AC Q9PIT4;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Chemokine receptor CCR5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9932755; PubMed=10465086;
RA Aikihonbare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,
RT Bond V.C.;
RL "Characterization of a third CCR5 amplicon from CCR5-delta32-
heterozygous HIV-1-infected individuals.";
RL AIDS 13:1585-1586(1999).
DR EMBL; AF056020; AAF65579.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR KW Receptor.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 7156 MW; AFF4B9CAPB80AFB CRC64;

Query Match 100.0%; Score 96; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DQ 11 SOYQFWKNFQTLKIVILG 28

RESULT 3
ID Q14694 PRELIMINARY; PRT; 333 AA.
AC Q14694;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RT Ho D.D.;
RL "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011504; AAB65704.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR KW Receptor.
FT NON_TER 333 333
SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

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Query Match 100.0%; Score 96; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DQ 166 SOYQFWKNFQTLKIVILG 183

RESULT 4
ID Q9TUQ7 PRELIMINARY; PRT; 334 AA.
AC Q9TUQ7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162049; AAD47804.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR KW Receptor.
FT NON_TER 1 334
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 334;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
DQ 173 SOYQFWKNFQTLKIVILG 190

RESULT 5
ID Q9UN24 PRELIMINARY; PRT; 339 AA.
AC Q9UN24;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian

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RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161919; AAD47676.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 6
Q9UN26 PRELIMINARY; PRT; 339 AA.
ID Q9UN26
AC Q9UN26;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SE SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161916; AAD47673.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 7
Q9UN23 PRELIMINARY; PRT; 339 AA.
ID Q9UN23
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AC Q9UN23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SE SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 8
Q9UBJ7 PRELIMINARY; PRT; 339 AA.
ID Q9UBJ7
AC Q9UBJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SE SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR EMBL; AF161917; AAD47674.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
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FT  NON TER      1
FT  NON TER    339
SQ  SEQUENCE    339 AA; 39128 MW;  9C3369FF1F2F27A CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SOYQFWKNFQTLKIVILG 18
DB  178 SQYQFWKNFQTLKIVILG 195

RESULT 9
Q9UN25
ID  Q9UN25      PRELIMINARY;      PRT;      339 AA.
AC  Q9UN25
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  C-C chemokine receptor 5 (Fragment).
GN  CCR5.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RT  species.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF161918; AAD47675.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
FT  NON TER      1
FT  NON TER    339
SQ  SEQUENCE    339 AA; 39146 MW;  10FE05FE5371D4B3 CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SOYQFWKNFQTLKIVILG 18
DB  178 SQYQFWKNFQTLKIVILG 195

RESULT 10
Q9UN27
ID  Q9UN27      PRELIMINARY;      PRT;      339 AA.
AC  Q9UN27
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  C-C chemokine receptor 5 (Fragment).
GN  CCR5.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RT  species.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF161918; AAD47675.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
FT  NON TER      1
FT  NON TER    339
SQ  SEQUENCE    339 AA; 39146 MW;  10FE05FE5371D4B3 CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SOYQFWKNFQTLKIVILG 18
DB  178 SQYQFWKNFQTLKIVILG 195

RESULT 11
Q9UBT9
ID  Q9UBT9      PRELIMINARY;      PRT;      339 AA.
AC  Q9UBT9
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  C-C chemokine receptor 5 (Fragment).
GN  CCR5.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RT  species.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF161915; AAD47672.1; -.
DR  EMBL; AF161909; AAD47666.1; -.
DR  EMBL; AF161910; AAD47667.1; -.
DR  EMBL; AF161911; AAD47668.1; -.
DR  EMBL; AF161912; AAD47669.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
FT  NON TER      1
FT  NON TER    339
SQ  SEQUENCE    339 AA; 39114 MW;  3C6369F92C29F4A7 CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SOYQFWKNFQTLKIVILG 18
DB  178 SQYQFWKNFQTLKIVILG 195

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RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RT  species.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF161914; AAD47671.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
FT  NON TER      1
FT  NON TER    339
SQ  SEQUENCE    339 AA; 39086 MW;  88AD8B44E2CB4EC2 CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SOYQFWKNFQTLKIVILG 18
DB  178 SQYQFWKNFQTLKIVILG 195

RESULT 11
Q9UBT9
ID  Q9UBT9      PRELIMINARY;      PRT;      339 AA.
AC  Q9UBT9
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  C-C chemokine receptor 5 (Fragment).
GN  CCR5.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RT  species.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF161915; AAD47672.1; -.
DR  EMBL; AF161909; AAD47666.1; -.
DR  EMBL; AF161910; AAD47667.1; -.
DR  EMBL; AF161911; AAD47668.1; -.
DR  EMBL; AF161912; AAD47669.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRHHODPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
FT  NON TER      1
FT  NON TER    339
SQ  SEQUENCE    339 AA; 39114 MW;  3C6369F92C29F4A7 CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SOYQFWKNFQTLKIVILG 18
DB  178 SQYQFWKNFQTLKIVILG 195

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Db 178 SQYQFWKNFQTLKIVILG 195
RESULT 12
Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
|||||
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 13
Q9TQW0 PRELIMINARY; PRT; 339 AA.
AC Q9TQW0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

Db 178 SQYQFWKNFQTLKIVILG 195
|||||
Qy 1 SQYQFWKNFQTLKIVILG 18
|||||
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 14
Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257F8B834C4AE CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
|||||
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 15
Q9TUU9 PRELIMINARY; PRT; 339 AA.
AC Q9TUU9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Cercopithecus.

OX NCBI_TaxID=36224;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161949; AAD47704.1; -;
 DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0004872; F: receptor activity; IEA.

DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm 1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON TER 1 1

FT NON TER 339 339

SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18

|||||

178 SOYQFWKNFQTLKIVILG 195

RESULT 16

Q9TUW9 PRELIMINARY; PRT; 339 AA.

AC Q9TUW9;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

CCRS.

OS Hylobates concolor (crested gibbon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.

OX NCBI_TaxID=29089;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

species.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161890; AAD47647.1; -;

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0004872; F: receptor activity; IEA.

DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm 1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON TER 1 1

FT NON TER 339 339

SQ SEQUENCE 339 AA; 39024 MW; EC4CE48DEEF107E CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18

|||||

178 SOYQFWKNFQTLKIVILG 195

RESULT 17

Q9TSQ1

ID Q9TSQ1 PRELIMINARY; PRT; 339 AA.

AC Q9TSQ1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

CCRS.

OS Cercopithecus aethiops (Green monkey) (Grivet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

OC Cercopitheciinae; Cercopithecus.

OX NCBI_TaxID=9534;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

species.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF162023; AAD47778.1; -;

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0004872; F: receptor activity; IEA.

DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm 1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

FT NON TER 1 1

FT NON TER 339 339

SQ SEQUENCE 339 AA; 39216 MW; 847E935FA403E52D CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18

|||||

178 SOYQFWKNFQTLKIVILG 195

RESULT 18

Q9TUW8

ID Q9TUW8 PRELIMINARY; PRT; 339 AA.

AC Q9TUW8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

CCRS.

OS Cercopithecus diana (Diana monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

OC Cercopitheciinae; Cercopithecus.

OX NCBI_TaxID=36224;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

species.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161949; AAD47705.1; -;

DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 33049 MW; 6D1A93F66270F3ED CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 19
Q9TUW4 PRELIMINARY; PRT; 339 AA.
AC Q9TUW4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39159 MW; 85699B882BAC0E84 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 21
Q9TUW7 PRELIMINARY; PRT; 339 AA.
AC Q9TUW7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.
DR EMBL; AF162044; AAD47799.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39129 MW; 4A88F8B601D46A4 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 20
Q9TUW4 PRELIMINARY; PRT; 339 AA.
ID Q9TUW4

Q9TUW4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39159 MW; 85699B882BAC0E84 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 21
Q9TUW7 PRELIMINARY; PRT; 339 AA.
AC Q9TUW7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.
DR EMBL; AF162044; AAD47799.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39129 MW; 4A88F8B601D46A4 CRC64;

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DR PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 339 AA; 39150 MW; 847D5F92BB03E6E2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 96; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 22
Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=100936;
RN RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162001; AAD47756.1; -
DR EMBL; AF162001; AAD47756.1; -
DR EMBL; AF162002; AAD47757.1; -
DR EMBL; AF162003; AAD47758.1; -
DR EMBL; AF162004; AAD47759.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1.1
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 339 AA; 39168 MW; 6A4BF72FBFF566F CRC64;

Query Match
Best Local Similarity 100.0%; Score 96; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 24
Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161900; AAD47657.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1.1
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 339 AA; 39103 MW; 4038C132D024C5A4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 96; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 23
Q9TQV6 PRELIMINARY; PRT; 339 AA.
AC Q9TQV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Colobus quereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae;
OC Colobus.

```

Best Local Similarity 100.0%; Pred. No. 2e-07;		
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 SQYQFWKNFQTLKIVILG 18	
DB	178 SQYQFWKNFQTLKIVILG 195	
<p>RESULT 25</p> <p>Q9TUQ9 PRELIMINARY; PRT; 339 AA.</p> <p>AC Q9TUQ9; (13, Created)</p> <p>DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)</p> <p>DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)</p> <p>DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)</p> <p>DE C-C chemokine receptor 5 (Fragment).</p> <p>GN CCR5.</p> <p>OS Cercopithecus mona.</p> <p>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p> <p>OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;</p> <p>OC Cercopithecinae; Cercopithecus.</p> <p>NCBI_TaxID=36226;</p> <p>OX [1]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,</p> <p>RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;</p> <p>RT "Sequences of the CCR5 genes from diverse simian and prosimian</p> <p>RT species";</p> <p>RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.</p> <p>DR EMBL; AF162041; AAD47796.1; -.</p> <p>DR GO; GO:0016021; C:integral to membrane; IEA.</p> <p>DR GO; GO:0004872; F:receptor activity; IEA.</p> <p>DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.</p> <p>DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.</p> <p>DR InterPro; IPR000276; GPCR_Rhodpsn.</p> <p>DR Pfam; PF00001; 7tm_1; 1.</p> <p>DR PRINTS; PR0237; GPCR_RHODOPS.</p> <p>DR PROSITE; PS00237; G PROTEIN RECEPT FL 1; 1.</p> <p>DR PROSITE; PS0262; G_PROTEIN_RECEP_FL 2; 1.</p> <p>KW Receptor.</p> <p>FT NON_TER 1 1</p> <p>FT NON_TER 339 339</p> <p>SQ SEQUENCE 339 AA; 39019 MW; 7176F940AF11F3ED CRC64;</p> <p>Query Match 100.0%; Score 96; DB 6; Length 339;</p> <p>Best Local Similarity 100.0%; Pred. No. 2e-07;</p> <p>Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>		
QY	1 SQYQFWKNFQTLKIVILG 18	
DB	178 SQYQFWKNFQTLKIVILG 195	
<p>RESULT 26</p> <p>Q9TUR2 PRELIMINARY; PRT; 339 AA.</p> <p>AC Q9TUR2; (13, Created)</p> <p>DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)</p> <p>DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)</p> <p>DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)</p> <p>DE C-C chemokine receptor 5 (Fragment).</p> <p>GN CCR5.</p> <p>OS Erythrocybus patas (Red guenon) (Hussar).</p> <p>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p> <p>OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;</p> <p>OC Cercopithecinae; Erythrocybus.</p> <p>NCBI_TaxID=9538;</p> <p>OX [1]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,</p> <p>RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;</p> <p>RT "Sequences of the CCR5 genes from diverse simian and prosimian</p> <p>RT species";</p>		

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ID Q9TQUS PRELIMINARY; PRT; 339 AA.
AC Q9TQUS;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162046; AAD47801.1; -.
DR EMBL; AF162043; AAD47798.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39178 MW; 847F8F936B00E6E2 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
Db 178 SOYQFWKNFQTLKIVILG 195

RESULT 29
Q9TUS7 PRELIMINARY; PRT; 339 AA.
ID Q9TUS7;
AC Q9TUS7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161995; AAD47750.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.

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ID Q9TQUS PRELIMINARY; PRT; 339 AA.
AC Q9TQUS;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161908; AAD47665.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39103 MW; 4350C4625FB0657C CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
Db 178 SOYQFWKNFQTLKIVILG 195

RESULT 31
Q9TUS5 PRELIMINARY; PRT; 339 AA.
ID Q9TUS5;
AC Q9TUS5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=100937;

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[1]
SEQUENCE FROM N.A.
Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF161997; AAD47752.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39028 MW; 8C9C978FD880B936 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. NO. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 32
Q9TQV2 PRELIMINARY; PRT; 339 AA.
AC Q9TQV2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=100937;
[1]
SEQUENCE FROM N.A.
Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF161993; AAD47748.1; -.
EMBL; AF161987; AAD47742.1; -.
EMBL; AF161990; AAD47745.1; -.
EMBL; AF161991; AAD47746.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39079 MW; 7176E3EA0E00F3ED CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. NO. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 33
Q9TQV3 PRELIMINARY; PRT; 339 AA.
AC Q9TQV3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Cercopithecus mona.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=36226;
[1]
SEQUENCE FROM N.A.
Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF162040; AAD47795.1; -.
EMBL; AF162038; AAD47793.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39079 MW; 7176E3EA0E00F3ED CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. NO. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 34
Q9TUQ8 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=36228;
[1]
SEQUENCE FROM N.A.
Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 33
Q9TQV3 PRELIMINARY; PRT; 339 AA.
AC Q9TQV3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Cercopithecus mona.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=36226;
[1]
SEQUENCE FROM N.A.
Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF162040; AAD47795.1; -.
EMBL; AF162038; AAD47793.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39079 MW; 7176E3EA0E00F3ED CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. NO. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 34
Q9TUQ8 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=36228;
[1]
SEQUENCE FROM N.A.
Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF162045; AAD47800.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; -.
DR PRINTS; PS00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39148 MW; 0CA289CDEDEDE831 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred.No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 35
Q9TUR3 PRELIMINARY; PRT; 339 AA.
AC Q9TUR3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CC5.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161907; AAD47664.1; -.
DR EMBL; AF161906; AAD47663.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39117 MW; 4C4E35825BD54E9C CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred.No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 37
Q9TQX2 PRELIMINARY; PRT; 339 AA.
AC Q9TQX2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CC5.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162053; AAD47808.1; -.
DR EMBL; AF162035; AAD47790.1; -.
DR EMBL; AF162036; AAD47791.1; -.
DR EMBL; AF162048; AAD47803.1; -.
DR EMBL; AF162050; AAD47805.1; -.
DR EMBL; AF162052; AAD47807.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.

RESULT 36
Q9TQW2 PRELIMINARY; PRT; 339 AA.
AC Q9TQW2

```



```

DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39154 MW; 09715882A6074884 CRC64;

Query Match
Best Local Similarity 100.0%; Score 96; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 38
Q9TSQ4 PRELIMINARY; PRT; 339 AA.
AC Q9TSQ4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciniae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162006; AAD47761.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciniae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162006; AAD47761.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161897; AAD47654.1; -
DR EMBL; AF161891; AAD47648.1; -
DR EMBL; AF161892; AAD47649.1; -
DR EMBL; AF161893; AAD47650.1; -
DR EMBL; AF161895; AAD47652.1; -
DR EMBL; AF161896; AAD47653.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DE C-C chemokine receptor 5 (Fragment).
GN Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39105 MW; F5400A7AB6FF7AB9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 96; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 40
Q9TSQ3 PRELIMINARY; PRT; 339 AA.
AC Q9TSQ3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciniae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162007; AAD47762.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DE C-C chemokine receptor 5 (Fragment).
GN Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39219 MW; BFFE9138E82933D0 CRC64;

```

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 178 SOYQFWKNFQTLKIVILG 195

Search completed: September 28, 2004, 09:06:19
Job time : 29.8 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:51:21 ; Search time 52.525 Seconds
(without alignments)
118.345 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYNIVLLNTFQEFFGLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1950s:*
2: Geneseqp1950s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	22	4 AAB88996	Aab88996 HIV gp120
2	118	100.0	268	7 ADC10142	Adc10142 Human NOV
3	118	100.0	268	7 ADC10144	Adc10144 Human NOV
4	118	100.0	332	2 AAW25765	Aaw25765 Human che
5	118	100.0	352	2 AAW27407	Aaw27407 Human CCR
6	118	100.0	352	2 AAW27123	Aaw27123 Human che
7	118	100.0	352	2 AAW27125	Aaw27125 Macaque c
8	118	100.0	352	2 AAW07602	Aaw07602 Human G-p
9	118	100.0	352	2 AAW23835	Aaw23835 Human CC
10	118	100.0	352	2 AAW8232	Aaw8232 HIV-1 co-
11	118	100.0	352	3 AAY80128	Aay80128 Human G-p
12	118	100.0	352	4 AAG79089	Aag79089 Amino aci
13	118	100.0	352	4 AAE07046	Aae07046 Human G-p
14	118	100.0	352	4 AAE07048	Aae07048 Human G-p
15	118	100.0	352	4 AAG80111	Aag80111 Human CCR
16	118	100.0	352	4 AAE04321	Aae04321 Human che
17	118	100.0	352	4 AAE07037	Aae07037 Human G-p
18	118	100.0	352	4 AAE07039	Aae07039 Human G-p
19	118	100.0	352	4 AAB46858	Aab46858 Human HDG
20	118	100.0	352	4 AAB56342	Aab56342 Non-endog
21	118	100.0	352	4 AAB83354	Aab83354 Human CCR
22	118	100.0	352	4 AAB82948	Aab82948 Human HIV
23	118	100.0	352	5 AAU97150	Aau97150 Human G-p
24	118	100.0	352	5 AAU97152	Aau97152 Human G-p
25	118	100.0	352	5 AAM52829	Aam52829 Human CCR

26	118	100.0	352	5 AAM52828	Aam52828 Human CC
27	118	100.0	352	5 ABG70597	Abg70597 Human G-p
28	118	100.0	352	5 ABG92883	Abg92883 Human Imm
29	118	100.0	352	5 ABG92880	Abg92880 Human G-p
30	118	100.0	352	5 AAE25808	Aae25808 Human G-p
31	118	100.0	352	5 AAE25811	Aae25811 Human G-p
32	118	100.0	352	5 ABB81054	Abb81054 G-protein
33	118	100.0	352	5 ABB81054	Abb81054 Human che
34	118	100.0	352	5 ABB08343	Abb08343 Human G-p
35	118	100.0	352	6 ABG75540	Abg75540 Human can
36	118	100.0	352	6 ABR58602	Abf58602 Human C-C
37	118	100.0	352	6 AAO29514	Aao29514 Human G-p
38	118	100.0	352	6 ABU61654	Abu61654 Human G-p
39	118	100.0	352	6 ABP97728	Abp97728 Amino aci
40	118	100.0	352	7 ABP81933	Abp81933 Human C-C
41	118	100.0	352	7 ADC03341	Adc03341 Human che
42	118	100.0	371	2 ADC03359	Adc03359 Macaque c
43	118	100.0	439	2 AAW23834	Aaw23834 Human CC
44	108	91.5	354	2 AAY41280	Aay41280 Fusion pr
45	105	89.0	354	7 AAW54037	Aaw54037 Mouse CC-
					Add44859 Rat Prote

ALIGNMENTS

RESULT 1

AAB88996
ID AAB88996 standard; peptide; 22 AA.

XX
AC AAB88996;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #89.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.

XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.
XX
PR 27-AUG-1999; 99US-0151270P.

XX
(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
Saxinger C;
XX
WPI; 2001-244398/25.

XX
Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions.
XX
Claim 21; Page 38; 114pp; English.
XX
The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus.
XX
The present sequence is an example of a peptide of the invention

SQ Sequence 22 AA;

Query Match 100.0%; Score 118; DB 4; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.1e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22


```

PR 26-JUN-2001; 2001US-0300893P.
PR 28-JUN-2001; 2001US-0301530P.
PR 28-JUN-2001; 2001US-0301550P.
PR 03-JUL-2001; 2001US-0302951P.
PR 31-JUL-2001; 2001US-0308990P.
PR 14-SEP-2001; 2001US-0322297P.
PR 25-SEP-2001; 2001US-0324659P.
PR 03-DEC-2001; 2001US-0337477P.
PR 14-DEC-2001; 2001US-0341562P.
PR 21-FEB-2002; 2002US-0358565P.
PR 21-FEB-2002; 2002US-0359122P.
PR 22-FEB-2002; 2002US-0358978P.
PR 22-FEB-2002; 2002US-0359034P.
PR 22-FEB-2002; 2002US-0359035P.
PR 27-FEB-2002; 2002US-0359121P.
PR 27-FEB-2002; 2002US-0359964P.
PR 12-MAR-2002; 2002US-0360858P.
PR 12-MAR-2002; 2002US-0363430P.
PR 12-MAR-2002; 2002US-0363676P.
PR 10-APR-2002; 2002US-0371346P.
PR 10-MAY-2002; 2002US-0379444P.
PR 04-JUN-2002; 2002US-00379444.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Agee MJ, Anderson DW, Berghs C, Casman SJ, Catterton B,
PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA,
PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R,
PI Kuratsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I,
PI Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK,
PI Rothenberg ME, Shenoy SG, Shinkens RA, Smithson G, Spaderna SK,
PI Spytak KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP,
PI Burgess CE, Lepley DM;
XX
XX WPI; 2003-210149/20.
DR N-PSDB; ADC10143.
XX
XX New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.
XX
XX Claim 1; SEQ ID NO 164; 772pp; English.
XX
XX The invention relates to novel isolated polypeptides, mature form of the
CC polypeptide, a sequence that is 95% identical to the polypeptide or the
CC polypeptide comprising one or more conservative substitutions. The NOVX
CC polypeptide is useful for treating or preventing a pathology associated
CC with the polypeptide e.g. disorders associated with aberrant expression
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
CC endocrine, CNS and inflammatory disorders. They can also be used in
CC various detection and screening assays, chromosome mapping, tissue typing
CC and predictive medicine. This sequence corresponds to one of the
CC polypeptides of the invention.
XX
SQ Sequence 268 AA;
Query Match 100.0%; Score 118; DB 7; Length 268;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIIVLLNTFOEFFGLNCS 22
DB 165 APYNIIVLLNTFOEFFGLNCS 186
RESULT 4
AAW26766
ID AAW26766 standard; protein; 332 AA.
XX
XX AAW26766;
XX
XX 21-MAY-1998 (first entry)
DT

```

```

XX Human chemokine receptor MMLR-CCR.
DE
XX Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human;
KW monocyte; macrophage; chemotaxis; haematopoiesis; infection; tumour;
KW inflammation; proliferative disease; cardiovascular disease; tumour;
KW rheumatoid arthritis; alveolitis; atherosclerosis;
KW chronic granulomatous disease; asthma; myasthenia gravis; diabetes;
KW inflammatory bowel disease; toxic shock syndrome; septic shock;
KW Chediak-Higashi syndrome; therapy; diagnosis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 107..128
FT /note= "conserved peptide"
FT Misc-difference 121
FT /note= "a claimed polypeptide has isoleucine at residue
FT 121"
XX
XX WO9741225-A2.
XX
XX 06-NOV-1997.
XX
XX 25-APR-1997; 97WO-US006993.
XX
XX 26-APR-1996; 96US-00638081.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Au-Young J, Bandman O, Coleman R, Wilde CG;
XX
XX WPI; 1997-549729/50.
DR N-PSDB; AAT99542.
XX
XX Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful
PT to study, diagnose and treat, e.g. infection, inflammation, solid tumour
PT and proliferative and cardiovascular disease.
XX
XX Claim 8; Page 37-38; 59pp; English.
XX
XX This protein comprises human MMLR-CCR, a novel C-C chemokine receptor
CC associated with monocyte/macrophage infiltration and chemotaxis and
CC haematopoiesis. The amino acid sequence was deduced from a cDNA clone
CC (see AAT99542) obtained from a cDNA library made from mononuclear cells
CC collected on day 2 of a mixed lymphocyte culture, i.e. cells associated
CC with inflammation and immunomodulation. Another novel chemokine receptor,
CC MPHG-CCR (see AAW36767), is also claimed. MMLR-CCR contains 7
CC transmembrane spanning segments connected by a series of intracellular
CC and extracellular loops. MMLR-CCR and MPHG-CCR can be used to study,
CC diagnose and treat disease states in which normal leukocyte function is
CC perturbed by normal leukopoiesis or inappropriate activation via
CC chemokine agonists or antagonists, such as infection, inflammation,
CC proliferative disease, tumorigenesis, autoimmune disease, abnormal cell
CC proliferation, solid tumours, cardiovascular disease, rheumatoid
CC arthritis, alveolitis, atherosclerosis, chronic granulomatous disease,
CC asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic
CC shock syndrome, septic shock and Chediak-Higashi syndrome
XX
XX Sequence 332 AA;
Query Match 100.0%; Score 118; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIIVLLNTFOEFFGLNCS 22
DB 229 APYNIIVLLNTFOEFFGLNCS 250
RESULT 5
AAW27407
ID AAW27407 standard; protein; 352 AA.

```



```

XX 14-DEC-1997 (first entry)
XX Macaque chemokine receptor 88C.
XX
XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
XX asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
XX diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX modulator; antibody.
XX
XX Macaca sp.
XX
XX WO9722698-A2.
XX
XX 26-JUN-1997.
XX
XX 20-DEC-1996; 96WO-US020759.
XX
XX 20-DEC-1995; 95US-00575967.
XX
XX 07-JUN-1996; 96US-00661393.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX
XX WPI; 1997-341689/31.
XX
XX N-PSDB; AAT85163.
XX
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX tumours, viral infections, auto-immune diseases, etc.
XX
XX Claim 36; Page 57-58; 65pp; English.
XX
XX This polypeptide sequence comprises macaque chemokine receptor 88C, a G
XX protein coupled receptor that is involved in leukocyte trafficking. Its
XX amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
XX amplification. It shows 97% identity to human 88C (AAW27123). 88C
XX receptors and their polypeptide fragments can be produced in transformed
XX host cells. The receptors, peptides comprising one or more of the
XX extracellular or intracellular domains, and anti-receptor antibodies can
XX be used to modulate receptor activities, particularly ligand and G
XX protein binding, and are potentially useful in the treatment
XX of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX infection, AIDS, inflammatory conditions, pathological immune response,
XX abnormal haematopoietic processes etc. A hybridoma that produces an
XX antibody that specifically binds to macaque 88C is claimed
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 118; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 APYNIVLLNTFQFFGLNCS 22
XX |||||
XX Db 249 APYNIVLLNTFQFFGLNCS 270
XX
XX RESULT 8
XX AAW07602
XX ID AAW07602 standard; protein; 352 AA.
XX
XX AC AAW07602;
XX
XX 26-FEB-1997 (first entry)
XX
XX Human G-protein chemokine receptor HDGNR10.
XX
XX G-protein chemokine receptor; HDGNR10; signal transduction;
XX haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
XX therapy.
XX

```

```

OS Homo sapiens.
XX
XX WO9639437-A1.
XX
XX 12-DEC-1996.
XX
XX 06-JUN-1995; 95WO-US007173.
XX
XX 06-JUN-1995; 95WO-US007173.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Li Y, Ruben SM;
XX
XX WPI; 1997-043072/04.
XX
XX N-PSDB; AAT44042.
XX
XX Human G-protein chemokine receptor, HDGNR10 - useful to identify
XX PT (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and
XX PT acute inflammation, rheumatoid arthritis, etc.
XX
XX Claim 1; Page 44-46; 61pp; English.
XX
XX Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7
XX -transmembrane protein involved in signal transduction. Its amino acid
XX sequence was deduced from a cDNA clone (AAT44042) isolated from a human
XX monocyte library. Isolation of the cDNA allows prodn. of recombinant
XX HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant
XX receptor can be used to identify agonists or antagonists of the receptor;
XX such cpds. can be used to treat conditions related to the under- and over
XX -expression of G-protein chemokine receptors
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 118; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 APYNIVLLNTFQFFGLNCS 22
XX |||||
XX Db 249 APYNIVLLNTFQFFGLNCS 270
XX
XX RESULT 9
XX AAW23835
XX ID AAW23835 standard; protein; 352 AA.
XX
XX AC AAW23835;
XX
XX 08-JUN-1998 (first entry)
XX
XX Human CC chemokine receptor 5 (CCR5).
XX
XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;
XX KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 29..55
XX FT /label= I
XX FT /note= "transmembrane domain"
XX FT 104..126
XX FT /label= III
XX FT /note= "transmembrane domain"
XX FT 109..120
XX FT /note= "extracellular loop-1 (Claim 19)"
XX FT 143..171
XX FT /label= IV
XX FT /note= "transmembrane domain"
XX FT 187..210
XX FT /note= "extracellular loop-2 (Claim 19)"
XX FT 194..219
XX

```

```

FT FT /label= V
FT FT /note= "transmembrane domain"
FT FT 238..258
FT FT /label= VI
FT FT /note= "transmembrane domain"
FT FT 261..276
FT FT /note= "extracellular loop-3 (Claim 19)"
FT FT 277..300
FT FT /label= VII
FT FT /note= "transmembrane domain"
FT FT
XX XX WO9745543-A2.
XX XX 04-DEC-1997.
XX XX
XX XX 28-MAY-1997; 97WO-US009586.
XX XX 28-MAY-1996; 96US-0018508P.
XX XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
XX XX Broder CC, Kennedy PE;
XX XX WPI; 1998-032650/03.
XX XX N-PSDB; AAT76920.
XX XX
XX XX CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
XX XX between HIV and a target cell.
XX XX
XX XX Claim 68; Fig 1C; 70pp; English.
XX XX
XX XX This protein sequence comprises of a novel human macrophage-selective CC
XX XX chemokine receptor that has been designated CCR5. The sequence was
XX XX deduced from an isolated cDNA clone (see AAT76920). An Ala127Leu variant
XX XX (see W238340 of CCR5 was also identified. The susceptibility of human
XX XX macrophages to HIV infection depends on cell surface expression of CD4
XX XX and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
XX XX protein coupled cell surface molecules. It plays an essential role in the
XX XX membrane fusion step of infection by some HIV isolates. The establishment
XX XX of stable, non-human cell lines and transgenic mammals having cells that
XX XX coexpress human CD4 and CCR5 provides valuable tools for research of HIV
XX XX infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
XX XX agents capable of blocking membrane fusion between HIV and target cells
XX XX represent potential anti-HIV therapeutics for macrophage tropic strains
XX XX of HIV
XX XX
XX XX Sequence 352 AA;
XX XX
XX XX Query Match 100.0%; Score 118; DB 2; Length 352;
XX XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX 1 APYNIIVLLNTFQEPFGLNCS 22
XX XX |||||
XX XX 249 APYNIIVLLNTFQEPFGLNCS 270
XX XX
XX XX RESULT 10
XX XX AAW88232
XX XX ID AAW88232 standard; protein; 352 AA.
XX XX
XX XX AAW88232;
XX XX 15-MAR-1999 (first entry)
XX XX
XX XX HIV-1 co-receptor CCR5.
XX XX
XX XX HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
XX XX gene therapy; human.
XX XX
XX XX Homo sapiens.
XX XX

```

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FH Key Location/Qualifiers
FT Domain 32..56
FT /note= "transmembrane domain 1"
FT Domain 67..87
FT /note= "transmembrane domain 2"
FT Misc-difference 101
FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA
FT (stop) in CCR5m303"
FT Domain 103..124
FT /note= "transmembrane domain 3"
FT Domain 142..167
FT /note= "transmembrane domain 4"
FT Domain 200..223
FT /note= "transmembrane domain 5"
FT Domain 236..260
FT /note= "transmembrane domain 6"
FT Domain 275..301
FT /note= "transmembrane domain 7"
XX
XX WO9854317-A1.
XX
XX 03-DEC-1998.
XX
XX 29-MAY-1998; 98WO-EP003437.
XX
XX 30-MAY-1997; 97US-0048057P.
XX
XX (WOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX
XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
XX
XX WPI; 1999-059835/05.
XX
XX N-PSDB; AAV84126.
XX
XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
XX PT resistance of CCR5-expressing cells to HIV-1 infection.
XX
XX Disclosure; Page 34-35; 55pp; English.
XX
XX This is the amino acid sequence of wild-type human CCR5, which serves as
XX CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
XX CC HIV-1. The invention relates to the identification of a CCR5 variant (see
XX CC AAW8231), designated CCR5m303, comprising the first two transmembrane
XX CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
XX CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a
XX CC positive correlation with resistance to infection with M-tropic HIV-1
XX CC strains, and may indicate slower progression of the disease. The
XX CC detection of CCR5 variants may be used to identify individuals at lower
XX CC risk of infection relative to the general population who, if infected,
XX CC may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
XX CC 36) are provided for use in diagnostic methods for detecting the presence
XX CC of such variants. A method is provided for inhibiting HIV-1 infection of
XX CC a cell expressing the CCR5 receptor. This involves introducing a nucleic
XX CC acid encoding a CCR5 variant into the cell, thereby reducing the number
XX CC of functional CCR5 molecules present on the cell surface
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 118; DB 2; Length 352;
XX XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX 1 APYNIIVLLNTFQEPFGLNCS 22
XX XX |||||
XX XX 249 APYNIIVLLNTFQEPFGLNCS 270
XX XX
XX XX RESULT 11
XX XX AAY80128
XX XX ID AAY80128 standard; protein; 352 AA.
XX XX
XX XX AAY80128;
XX XX
XX XX Homo sapiens.
XX XX

```


DT 19-MAY-2000 (first entry)
 XX Human G-protein chemokine receptor HDGFR10 SEQ ID NO:2.
 DE Human; G-protein coupled receptor; G-protein chemokine receptor; HDGFR10;
 XX diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
 KW tumour; infection; leukaemia; psoriasis; allergy;
 KW T-cell mediated autoimmune disease; atherosclerosis; anaphylaxis;
 KW inflammation; allergic reaction; silicosis; sarcoidosis;
 KW rheumatoid arthritis; hyper-eosinophilia syndrome.
 XX Homo sapiens.
 XX US6025154-A.
 XX 15-FEB-2000.
 XX 06-JUN-1995; 95US-00466343.
 XX 06-JUN-1995; 95US-00466343.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Li Y, Ruben SM;
 XX WPI; 2000-181807/16.
 XX N-PSDB; AAZ91481.
 XX Isolated nucleic acid encoding human G-protein chemokine receptor useful
 PT for diagnostic assays, scientific research and screening for compounds
 PT which bind to and activate or inhibit activation of the receptor
 PT polypeptides.
 XX Claim 1; Fig 1; 22pp; English.
 XX The present sequence represents a human G-protein chemokine receptor
 CC designated HDGFR10. HDGFR10 polynucleotides are useful in methods of
 CC screening for compounds which bind to and either: (1) activate the
 CC HDGFR10 polypeptides causing stimulation of haematopoiesis, wound
 CC healing, coagulation, and angiogenesis; treatment of solid tumours,
 CC chronic infections, leukaemia, T-cell mediated autoimmune diseases,
 CC parasitic infections, psoriasis, and to stimulate growth factor activity;
 CC or (2) inhibit activation of the HDGFR10 polypeptides which is useful for
 CC preventing and/or treating allergy, atherosclerosis, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 CC E-mediated allergic reactions, prostaglandin-independent fever, bone
 CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
 CC hyper-eosinophilia syndrome. The polynucleotides are also useful for
 CC diagnostic assays for detecting diseases related to mutations in the
 CC nucleic acid sequences encoding the polypeptides and for detecting an
 CC altered level of the soluble form of the receptor polypeptides. The
 CC polynucleotides are also useful for in vitro purposes related to
 CC scientific research, synthesis of DNA and manufacture of DNA vectors
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFQBFGLNCS 22
 |||||
 Db 249 APYNIVLLNTFQBFGLNCS 270
 |||||
 RESULT 12
 AAG79089
 ID AAG79089 standard; protein; 352 AA.
 AC AAG79089;
 XX 10-DEC-2001 (first entry)
 DT 10-DEC-2001 (first entry)
 XX

DE Amino acid sequence of human CCR5 protein.
 XX Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
 KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
 XX Homo sapiens.
 XX WO200164752-A2.
 XX 07-SEP-2001.
 XX 28-FEB-2001; 2001WO-US006322.
 XX 02-MAR-2000; 2000US-00517605.
 XX (UYNV) UNIV NEW YORK STATE.
 XX (UYNV-) UNIV NIJMEGEN.
 XX Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
 XX WPI; 2001-602565/68.
 XX An antibody for the treatment or prevention of HIV-infection comprises a
 PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
 PT DC-SIGN due to concomitant conformational change.
 XX Disclosure; Page 118-119; 131pp; English.
 XX The specification describes an antibody which is specific for an
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
 CC is exposed upon gp120 binding of DC-SIGN due to concomitant
 CC conformational change. DC-SIGN is a receptor that is specifically
 CC expressed on dendritic cells and facilitates infection of T lymphocytes
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
 CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 CC with high affinity. The antibody of the invention inhibits the trans
 CC enhancement of HIV entry into a T cell or macrophage facilitated by
 CC dendritic cells. The antibody is useful to treat or prevent HIV
 CC infection. The present sequence represents a human CCR5 protein, which is
 CC a translocation promoting agent that interacts with CD4. This receptor
 CC functions in HIV-1 entry into cells
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFQBFGLNCS 22
 |||||
 Db 249 APYNIVLLNTFQBFGLNCS 270
 |||||
 RESULT 13
 AAE07046
 ID AAE07046 standard; protein; 352 AA.
 XX AAE07046;
 XX 16-OCT-2001 (first entry)
 DT 16-OCT-2001 (first entry)
 XX Human G-protein chemokine receptor (CCR5) HDGFR10 protein #1.
 XX Human; G-protein chemokine receptor; CCR5; HDGFR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; neurotropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; immune disorder; Addison's disease;
 KW gastrointestinal tract; lung; liver; diabetes mellitus; allergy;
 KW haemolytic anaemia; autoimmune thyroiditis; Crohn's disease; wound healing;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX

OS XX Homo sapiens.

FT FH Key Location/Qualifiers

FT FT Domain 1..36 /label= Extracellular_domain

FT FT Domain 37..305 /label= Transmembrane_domain

FT FT Domain 37..58 /label= Transmembrane_domain

FT FT Domain 59..67 /label= Transmembrane_domain

FT FT Domain 68..88 /label= Intracellular_loop_1

FT FT Domain 89..102 /label= Transmembrane_domain

FT FT Domain 103..124 /label= Transmembrane_domain

FT FT Domain 125..141 /label= Transmembrane_domain

FT FT Domain 142..166 /label= Transmembrane_domain

FT FT Domain 167..195 /label= Transmembrane_domain

FT FT Domain 196..223 /label= Transmembrane_domain

FT FT Domain 224..235 /label= Transmembrane_domain

FT FT Domain 236..260 /label= Transmembrane_domain

FT FT Domain 261..274 /label= Transmembrane_domain

FT FT Domain 287..305 /label= Transmembrane_domain

FT FT Domain 306..352 /label= Transmembrane_domain

FT FT Domain 306..352 /label= Intracellular_domain

XX WO200158916-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US004153.

XX PR 09-FEB-2000; 2000US-0181258P.

XX PR 09-MAR-2000; 2000US-0187999P.

XX PR 22-SEP-2000; 2000US-0234336P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Roschke V, Li Y, Ruben SM;

XX DR WPI; 2001-488966/53.

XX DR N-PSDB; AAD13282.

XX FT Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

XX PS Claim 102; Fig 1; 518pp; English.

XX CC The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemia) and wound healing. The present sequence is human CCR5 HDGNR10 protein

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLNLTQPEFFGLNCS 22
|||||

DB 249 APYNIVLNLTQPEFFGLNCS 270
|||||

RESULT 14

AAE07048

ID AAE07048 standard; protein; 352 AA.

XX AAE07048;

XX 16-OCT-2001 (first entry)

XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnary;

XX cytostatic; immunosuppressive; neutropenic; neuroprotective; gene therapy;

XX neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;

XX rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;

XX gastrointestinal tract; lung; liver; immune disorder; Addison's disease;

XX haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;

XX multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;

XX cardiovascular disorder; myocardial ischaemia.

XX OS Homo sapiens.

XX WO200158916-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US004153.

XX PR 09-FEB-2000; 2000US-0181258P.

XX PR 09-MAR-2000; 2000US-0187999P.

XX PR 22-SEP-2000; 2000US-0234336P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Roschke V, Li Y, Ruben SM;

XX DR WPI; 2001-488966/53.

XX DR N-PSDB; AAD13299.

XX FT Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

XX PS Claim 102; Fig 1; 518pp; English.

XX CC The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemia) and wound healing. The present sequence is human CCR5 HDGNR10 protein

PS Example 40; Page 504-505; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)

CC HDGMR10 polypeptides and polynucleotides. CCR5 HDGMR10 antibodies are

CC useful for treating, preventing or ameliorating a disease or disorder

CC associated with inflammation, defective or aberrant chemotaxis of immune

CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's

CC sarcoma) or defective or aberrant T-cell antigen presenting cell

CC interaction. The disease or disorder may also be an infectious disease

CC (e.g. a viral infection such as an early stage HIV infection, a

CC cytomegalovirus infection, or a poxvirus infection), an autoimmune

CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The

CC disease or disorder may be associated with aberrant CCR5 expression, lack

CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand

CC to increase or decrease storage capabilities. CCR5 HDGMR10 DNA are useful

CC for chromosome identification and in gene therapy. CCR5 HDGMR10 DNA,

CC protein, antibodies, agonists and antagonists are also useful in the

CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal

CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,

CC urogenital); immune disorders (Addison's disease, allergies, autoimmune

CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)

CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The

XX present sequence is human CCR5 HDGMR10 protein

XX Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22

DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 15

AAG80111

ID AAG80111 standard; protein; 352 AA.

AC AAG80111;

DT 17-JAN-2002 (first entry)

XX Human CCR5 protein.

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;

KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;

KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;

KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;

KW antirheumatic; antiarthritic.

OS Homo sapiens.

XX WO200172830-A2.

PN 04-OCT-2001.

XX 02-APR-2001; 2001WO-EP003708.

XX 31-MAR-2000; 2000DB-01016013.

XX (IPFP-) IPF PHARM GMBH.

PA (FORS/) FORSMANN U.

XX Forsemann W, Adermann K, Heitland A, Spodsborg N;

XX WPI; 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands, useful

PT for detecting tumors, inflammation etc., also therapeutic use of ligand

PT inhibitors.

PS Disclosure; Page 10; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least

CC two different ligands (I) for receptors (II) that are implicated in

CC disease. (A) are used for the diagnosis of tumors (especially colorectal

CC or prostatic), organ rejection, inflammation and autoimmune diseases.

CC Also inhibitors of (I) are used therapeutically against tumors (and their

CC metastases), inflammation (particularly bronchial asthma or chronic bowel

CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),

CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,

CC endocrine, motor or urogenital systems or skin are affected, and bone

CC marrow diseases. The products of the invention are chemokine derivatives

CC which have cytostatic, antiinflammatory, antiasthmatic,

CC immunosuppressive, dermatological, antirheumatic, antiarthritic.

CC Chemokines act on specific tumor and inflammatory cells through a

CC constellation of chemokine receptors (CR), which control migration and

CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine

CC fragments used to illustrate the method of the invention

XX Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22

DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 16

AAG804321

ID AAG804321 standard; protein; 352 AA.

AC AAG804321;

DT 04-SEP-2001 (first entry)

XX Human chemokine receptor (CCR), CC-CR-5 related protein #2.

KW Human; transformed mammalian cell; CD4; reporter gene; translocation;

KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;

KW chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;

KW CC-CR-5; envelope glycoprotein; anti-HIV.

OS Homo sapiens.

XX US6258527-B1.

PN 10-JUL-2001.

XX 21-MAY-1997; 97US-00861105.

XX 20-MAY-1996; 96US-0017157P.

PR 19-JUN-1996; 96US-0020043P.

PR 19-MAY-1997; 97US-00858660.

XX (AAFO-) AARON DIAMOND AIDS RES CENT.

PA (UNY) UNIV NEW YORK STATE.

XX Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;

PI WPI; 2001-417127/44.

DR N-PSDB; AAD08577.

XX Transformed mammalian cell (I) that contains a CD4 gene, reporter gene

PT and HIV LTR for identification of drugs and antibodies for treatment of

PT HIV.

XX Disclosure; Col 47-50; 37pp; English.

XX The present invention relates to a transformed mammalian cell that

CC contains a gene encoding CD4, a construct encoding a reporter gene under
 CC the regulation of an human immuno deficiency virus (HIV) long terminal
 CC repeat (LTR) and that has been transduced with a vector encoding a human
 CC chemokine receptor (CCR) where the CD4 and the CCR are present on the
 CC cell surface of transformed mammalian cell. The invention is useful for
 CC identifying drugs or antibodies that interfere with the translocation of
 CC HIV into transformed mammalian cell or for identifying a human chemokine
 CC receptor that facilitates the infection of a particular HIV strain into
 CC the transformed mammalian cell. Compounds identified can be used to treat
 CC cellular dysfunction and to prevent or combat HIV infection. The present
 CC sequence is a human chemokine receptor (CCR), CC-CR-5 related protein.
 CC CC-CR-5 is the principal cofactor for entry mediated by the envelope
 CC glycoproteins of primary macrophage-tropic strains of HIV-1
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIIVLLNTFQEFFGLNCS 22
 |||||
 Db 249 APYNIIVLLNTFQEFFGLNCS 270

RESULT 17
 AAEE07037
 ID AAEE07037 standard; protein; 352 AA.

XX
 AC AAEE07037;

DT 16-OCT-2001 (first entry)

DE Human G-protein chemokine receptor (CCRS) HDGNR10 protein #1.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
 KW cytostatic; immunosuppressive; neutropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Domain 1..36
 FT /label= Extracellular_domain
 FT Domain 37..305
 FT /label= Transmembrane_domain
 FT Domain 37..58
 FT /label= Transmembrane_domain
 FT /note= "Segment 1"
 FT Domain 59..67
 FT /label= Intracellular_loop_1
 FT Domain 68..88
 FT /label= Transmembrane_domain
 FT /note= "Segment 2"
 FT Domain 89..102
 FT /label= Extracellular_loop_1
 FT Domain 103..124
 FT /label= Transmembrane_domain
 FT /note= "Segment 3"
 FT Domain 125..141
 FT /label= Intracellular_loop_2
 FT Domain 142..166
 FT /label= Transmembrane_domain
 FT /note= "Segment 4"
 FT Domain 167..195
 FT /label= Extracellular_loop_2
 FT Domain 196..223

FT /label= Transmembrane_domain
 FT /note= "Segment 5"
 FT Domain 224..235
 FT /label= Intracellular_loop_3
 FT Domain 236..260
 FT /label= Transmembrane_domain
 FT /note= "Segment 6"
 FT Domain 261..274
 FT /label= Extracellular_loop_3
 FT Domain 287..305
 FT /label= Transmembrane_domain
 FT /note= "Segment 7"
 FT Domain 306..352
 FT /label= Intracellular_domain

XX WO200158915-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004152.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUYA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX MPI; 2001-488965/53.

XX N-PSDB; AAD13181.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor

XX (CCRS) HDGNR10 polypeptide useful for preventing or treating autoimmune

XX diseases e.g. rheumatoid arthritis, hyperproliferative disorders and

XX neurodegenerative disorders.

XX Claim 102; Fig 1; 495pp; English.

XX The present sequence is human G-protein chemokine receptor (CCRS) HDGNR10
 CC protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5
 CC HDGNR10 antibodies are useful for treating, preventing or ameliorating a
 CC disease or disorder associated with inflammation, defective or aberrant
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen
 CC presenting cell interaction. The disease or disorder may also be an
 CC infectious disease (e.g. a viral infection such as an early stage HIV
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative
 CC disorder. The disease or disorder may be associated with aberrant CCR5
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or
 CC lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene
 CC therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists
 CC are also useful in the diagnosis, treatment and prevention of cancer
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis); cardiovascular disorders (myocardial ischaemias) and wound
 CC healing

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. NO. 2.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIIVLLNTFQEFFGLNCS 22

Db 249 APYNIIVLLNTFQEFFGLNCS 270

RESULT 18
AAE07039
ID AAE07039 standard; protein; 352 AA.
XX AC AAE07039;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
XX
KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
KW cytosolic; immunosuppressive; neutrotropic; neuroprotective; gene therapy;
KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
KW cardiovascular disorder; myocardial ischaemia.
XX
OS Homo sapiens.
XX
XX WO200158915-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US0004152.
XX
XX 09-FEB-2000; 2000US-0181258P.
PR
PR 09-MAR-2000; 2000US-0187999P.
PR
PR 22-SEP-2000; 2000US-0234336P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Roschke V, Li Y, Ruben SM;
XX
XX WPI; 2001-488965/53.
XX
DR N-PSDB; AAD13198.
XX
XX Isolated nucleic acid encoding a human G-protein chemokine receptor
PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
PT neurodegenerative disorders.
XX
XX Example 40; Page 486-487; 495pp; English.
XX
XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
CC protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
CC ameliorating a disease or disorder associated with inflammation,
CC defective or aberrant chemotaxis of immune cells, HIV infection (such as
CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
CC aberrant T-cell antigen presenting cell interaction. The disease or
CC disorder may also be an infectious disease (e.g. a viral infection such
CC as an early-stage HIV infection, a cytomegalovirus infection, or a
CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
CC a neurodegenerative disorder. The disease or disorder may be associated
CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
CC is used as a food additive or preservative to increase or decrease
CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
CC antibodies, agonists and antagonists are also useful in the diagnosis,
CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
CC disorders (myocardial ischaemia) and wound healing
XX
SQ Sequence 352 AA;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIVLLNTFOBPFGLNCS 22
DB 249 APYNIVLLNTFOBPFGLNCS 270
RESULT 19
AAB46858
ID AAB46858 standard; protein; 352 AA.
XX
XX AAB46858;
XX
DT 16-AUG-2001 (revised)
DT 02-AUG-2001 (revised)
DT 04-MAY-2001 (first entry)
XX
DE Human HDGNR10 protein.
XX
KW HDGNR10; human; G-protein chemokine receptor; antiinflammatory;
KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
KW cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;
KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
KW hyper-ecsinophilic syndrome; vulnerary.
XX
OS Homo sapiens.
XX
XX US2001000241-A1.
XX
PD 12-APR-2001.
XX
XX 29-NOV-2000; 2000US-00725285.
XX
XX 06-JUN-1995; 95US-00466343.
PR
PR 18-NOV-1998; 98US-00195662.
PR
PR 25-JUN-1999; 99US-00399912.
XX
XX (LIYY/) LI Y.
XX (RUBE/) RUBEN S M.
XX
XX Li Y, Ruben SM;
XX
DR WPI; 2001-226317/23.
DR N-PSDB; AAF26390.
XX
XX New human G-protein chemokine receptor polypeptides and polynucleotides,
PT useful for identifying (ant)agonists to the G-protein chemokine receptor.
XX
XX Claim 1a; Page 15; 22pp; English.
XX
XX This invention describes a novel receptor polypeptide (I) selected from
CC (i) a fully defined 329 amino acid sequence (ii) fully disclosed in the
CC specification; and (iii) a polypeptide encoded by the cDNA contained in a
CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
CC products of the invention have antiinflammatory, immunomodulatory
CC anticoagulant, antiallergic, immunosuppressive, vulnerary, cytostatic,
CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic
CC activity and can be used for gene therapy. The G-protein chemokine
CC receptors, HDGNR10, (I) are useful for screening for compounds which
CC activate or inhibit activation of (I). The products of the invention can
CC also be used for stimulating haematopoiesis, wound healing, coagulation,
CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-
CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and
CC stimulating growth factor activity. HDGNR10 is useful for treating
CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
CC reactions, prostaglandin-independent fever, bone marrow failure,

```

CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
CC errors in the keyword formatting)
XX
SQ Sequence 352 AA;
    Query Match          100.0%; Score 118; DB 4; Length 352;
    Best Local Similarity 100.0%; Pred. No. 2.9e-11;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 20
ABB56342
ID ABB56342 standard; protein; 352 AA.
XX
AC ABB56342;
XX
DT 18-FEB-2002 (first entry)
XX
DE Non-endogenous human GPCR protein, SEQ ID NO: 477.
XX
KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW constitutively activated GPCR; agonist; disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200177172-A2.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US011098.
XX
PR 07-APR-2000; 2000US-0195747P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Lehmann-Bruinsma K, Liaw CW, Lin I;
XX
DR WPI; 2001-648759/74.
DR N-PSDB; AB197978.
XX
Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with versions
PT of GPCRs.
XX
PS Claim 1; Page 277-278; 394pp; English.
XX
The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous constitutively
CC activated versions of known GPCRs are used in the invention for the
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists. Such agonists are useful as
CC therapeutic agents for diseases or disorders associated with GPCRs. The
CC present sequence is a non-endogenous version of a known human GPCR
XX
SQ Sequence 352 AA;
    Query Match          100.0%; Score 118; DB 4; Length 352;
    Best Local Similarity 100.0%; Pred. No. 2.9e-11;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 21
AAB83354

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ID AAB83354 standard; protein; 352 AA.
XX
AC AAB83354;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human CCR5 protein sequence.
XX
KW Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
KW human immunodeficiency virus; anti-inflammatory disease; human.
XX
OS Homo sapiens.
XX
PN EP1118858-A2.
XX
PD 25-JUL-2001.
XX
PF 03-JAN-2001; 2001EP-00300020.
XX
PR 12-JAN-2000; 2000GB-00000659.
PR 12-JAN-2000; 2000GB-00000661.
PR 12-JAN-2000; 2000GB-00000663.
XX
PA (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
XX
PI Dobbs S, Perros M, Rickett GA;
XX
DR WPI; 2001-477088/52.
DR N-PSDB; AAF87099.
XX
Determining if an agent can modulate CCR5-gp120 interaction, comprises
PT incubating the agent with CCR5 and gp120 and determining if the agent
PT modulates the interaction.
XX
PS Claim 1; Page 110; 113pp; English.
XX
This sequence represents the human CCR5 protein sequence. The invention
CC relates to a method for determining whether an agent is capable of
CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
CC with gp120, comprising incubating the agent with CCR5 and gp120 and
CC determining whether the agent modulates the interaction, where gp120 is
CC associated with CD4, and where the interaction is a low affinity binding.
CC The method is used to identify an agent capable of modulating the
CC interaction of CCR5 with gp120. An agent identified by the method is used
CC to prepare a pharmaceutical composition for the treatment of a disease or
CC condition associated with CCR5 and gp120 interaction, to treat a subject
CC with a disease or condition associated with CCR5 and gp120 interaction,
CC and for preparing a pharmaceutical for treating human immunodeficiency
CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
CC is commercially useful, amenable to high throughput screening, and
CC detects interaction of gp120 with cells expressing only CCR5
XX
SQ Sequence 352 AA;
    Query Match          100.0%; Score 118; DB 4; Length 352;
    Best Local Similarity 100.0%; Pred. No. 2.9e-11;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 22
AAB82948
ID AAB82948 standard; protein; 352 AA.
XX
AC AAB82948;
XX
DT 21-DEC-2001 (first entry)
XX
DE Human HIV-1 co-receptor CCR5.

```

XX CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
KW infection; therapy; vaccine; anti-HIV-1.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Binding-site 2..18 /note= "binds to HIV-1 gp120"
XX
XX WO200164710-A2.
XX
XX 07-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US006699.
XX
XX 29-FEB-2000; 2000US-0185667P.
XX
XX 19-MAY-2000; 2000US-0205839P.
XX
XX 07-FEB-2001; 2001US-0267231P.
XX
XX (PROG-) PROGENICS PHARM INC.
XX (AARO-) AARON DIAMOND AIDS RES CENT.
XX
XX Dragic T, Olson WC;
XX
XX WPI: 2001-611273/70.
XX
XX N-PSDB; AAH26903.
XX
XX Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-
PT receptor) amino terminal domain including negatively charged and two
PT sulfated tyrosine residues is useful for treating HIV infection in
PT humans.
XX
XX
XX Claim 1; Page 30; 163pp; English.
XX
XX The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids
CC 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding
CC site that determines the specificity of the interaction between CCR5 and
CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the
CC CCR5 N-terminus is required for gp120 binding and may critically modulate
CC the susceptibility of target cells to HIV-1 infection in vivo. The
CC invention provides claimed sulfated peptides (see AAB82947) that are
CC based on the CCR5 N-terminal region and which are effective for
CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed
CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+
CC cells from becoming infected with HIV, of treating a subject whose CD4+
CC cells are infected with HIV, and of identifying an agent which inhibits
CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried
CC out in a subject, especially a human, infected (therapeutic method), not
CC infected with HIV (prophylactic method), or in a subject who is not
XX infected with, but has been exposed to, HIV
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 118; DB 4; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 APYNIVLLNTTQFFFGLNCS 22
XX 249 APYNIVLLNTTQFFFGLNCS 270
XX
XX
XX RESULT 23
XX AAU97150
XX ID AAU97150 standard; protein; 352 AA.
XX
XX AAU97150;
XX
XX 13-AUG-2002 (first entry)
XX
XX Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
XX

KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
XX hyperproliferative disease; neurological disease; receptor.
XX
XX Homo sapiens.
XX
XX US2002048786-A1.
XX
XX 25-APR-2002.
XX
XX 09-FEB-2001; 2001US-00779879.
XX
XX 09-FEB-2000; 2000US-0181258P.
XX
XX 09-MAR-2000; 2000US-0187999P.
XX
XX 22-SEP-2000; 2000US-0234336P.
XX
XX (ROSE/) ROSEN C A.
XX (ROSC/) ROSCHKE V.
XX (LIYY/) LI Y.
XX (RUBE/) RUBEN S M.
XX
XX Rosen CA, Roschke V, Li Y, Ruben SM;
XX
XX WPI: 2002-434754/46.
XX
XX N-PSDB; ABK51853.
XX
XX New nucleic acid encoding an antibody specific for the G-protein
PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
PT inflammation.
XX
XX Claim 61; Fig 1; 180pp; English.
XX
XX The present invention relates to the isolation of a novel human G-protein
CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
CC sequences encoding it. The invention also describes antibodies that bind
CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
CC sequences encoding the antibodies. The antibodies are useful for treating
CC or preventing inflammation, defective or aberrant chemotaxis of immune
CC cells and T-cell/antigen-presenting cell interactions, infections and
CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
CC infections (especially early-stage human immune deficiency virus (HIV),
CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
CC associated with aberrant or deficient expression of the CCR5 receptor or
CC its ligands. The antibodies are also useful to determine CCR5 expression,
CC e.g. for diagnosis, prognosis and monitoring of cancer and other
CC hyperproliferative diseases. The polynucleotide sequences encoding human
CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
CC recombinant receptor, and in the treatment of a wide range of diseases
CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
CC present sequence represents human G-protein chemokine receptor (CCR5)
CC HDGNR10 #1
XX
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 118; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 APYNIVLLNTTQFFFGLNCS 22
XX 249 APYNIVLLNTTQFFFGLNCS 270
XX
XX
XX RESULT 24
XX AAU97152
XX ID AAU97152 standard; protein; 352 AA.
XX
XX AAU97152;
XX
XX 13-AUG-2002 (first entry)
XX

DE Human G-protein chemokine receptor (CCR5) HDGMR10 #2.
 XX Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation;
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.
 XX
 OS Homo sapiens.

XX US2002048786-A1.
 XX 25-APR-2002.

XX 09-FEB-2001; 2001US-00779879.
 XX 09-FEB-2000; 2000US-0181258P.
 XX 09-MAR-2000; 2000US-0187999P.
 XX 22-SEP-2000; 2000US-0234336P.

XX (ROSE/) ROSEN C A.
 XX (ROSC/) ROSCHKE V.
 XX (LIYY/) LI Y.
 XX (RUBE/) RUBEN S M.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2002-434754/46.
 XX N-PSDB; ABK51970.

XX New nucleic acid encoding an antibody specific for the G-protein
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 PT inflammation.

XX Disclosure; Page 165-166; 180pp; English.

XX The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGMR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGMR10 and polynucleotide
 CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune
 CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC infections (especially early-stage human immune deficiency virus (HIV),
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGMR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGMR10 #2

XX Sequence 352 AA;

Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVLLNTTQEPFGLNCS 22
 Db 249 APYIVLLNTTQEPFGLNCS 270

RESULT 25

ID AAM52829 standard; protein; 352 AA.

XX AAM52829;

XX AAM52828

DT 22-FEB-2002 (first entry)
 XX Human CCR5 Gln 55 variant.
 DE CCR5; CC chemokine receptor 5; human; HIV infection;
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
 KW drug screening; identification; variant.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 55 /note= "Glu replaces wild-type Leu; encoded by CTG"
 FT Misc-difference 58 /note= "Encoded by AGC"

XX WO200171346-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009155.

XX 21-MAR-2000; 2000US-0190946P.

XX 21-MAR-2000; 2000US-0190989P.

XX 21-MAR-2000; 2000US-0191299P.

XX 20-MAR-2001; 2001US-00813448.

XX 20-MAR-2001; 2001US-00813651.

XX 20-MAR-2001; 2001US-00813653.

XX (CONS-) CONSENSUS PHARM INC.

XX Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;

XX WPI; 2002-010610/01.

XX N-PSDB; ABA02318.

XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,
 PT comprises binding a molecule from library to a molecule having binding
 PT property corresponding to CCR5 and identifying bound molecule.

XX Example 3; Fig 4B; 50pp; English.

XX The invention relates to a method for identifying a binding compound for
 CC chemokine receptor 5 (CCR5). The method involves screening a library
 CC of test molecules (particularly peptides) with immobilised CCR5, and then
 CC identifying those molecules which bind. The invention also relates to
 CC CCR5-binding molecules identified using the method of the invention, a
 CC methods for identifying consensus motifs for CCR5-binding peptides, a
 CC transfer vector encoding tagged CCR5, a computer-aided methods for
 CC determining the relative binding affinity of a test molecule to CCR5 and
 CC a computer aided drug screening assay that utilises the three-dimensional
 CC structure of CCR5. Compounds identified using the methods of the
 CC invention are useful for treating or preventing HIV (human
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
 CC syndrome) in a patient. The methods of the invention may also be used to
 CC identify agonists or antagonists of the interaction of CCR5 with its
 CC natural ligand, and to determine a binding motif for CCR5. The present
 CC sequence represents a naturally occurring variant of human CCR5 in which
 CC there is a glutamine, rather than a leucine, at position 55

XX Sequence 352 AA;

Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVLLNTTQEPFGLNCS 22

Db 249 APYIVLLNTTQEPFGLNCS 270

RESULT 26

AAM52828

ID XX AAM52828 standard; protein; 352 AA.
 AC XX AAM52828;
 DT XX 22-FEB-2002 (first entry)
 DE XX Human CC chemokine receptor 5 (CCR5).
 XX CCR5; CC chemokine receptor 5; human; HIV infection;
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
 KW drug screening; identification.
 XX Homo sapiens.
 OS WO200171346-A2.
 FN 27-SEP-2001.
 PD 21-MAR-2001; 2001WO-US009155.
 PF 21-MAR-2000; 2000US-0190946P.
 PR 21-MAR-2000; 2000US-0190996P.
 PR 21-MAR-2000; 2000US-0191299P.
 PR 20-MAR-2001; 2001US-00813448.
 PR 20-MAR-2001; 2001US-00813651.
 PR 20-MAR-2001; 2001US-00813653.
 XX (CONS-) CONSENSUS PHARM INC.
 FA Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
 PI WPI: 2002-010610/01.
 XX N-PSDB; ABA2317.
 DR Identifying CC chemokine receptor 5 binding compound for treating AIDS,
 XX comprises binding a molecule from library to a molecule having binding
 PT property corresponding to CCR5 and identifying bound molecule.
 PT Example 3; Fig 4A; 50pp; English.
 PS The invention relates to a method for identifying a binding compound for
 XX CC chemokine receptor 5 (CCR5). The method involves screening a library
 CC of test molecules (particularly peptides) with immobilised CCR5, and then
 CC identifying those molecules which bind. The invention also relates to
 CC CCR5-binding molecules identified using the method of the invention,
 CC methods for identifying consensus motifs for CCR5-binding peptides, a
 CC transfer vector encoding tagged CCR5, a computer-aided method for
 CC determining the relative binding affinity of a test molecule to CCR5 and
 CC a computer aided drug screening assay that utilises the three-dimensional
 CC structure of CCR5. Compounds identified using the methods of the
 CC invention are useful for treating or preventing HIV (human
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
 CC syndrome) in a patient. The methods of the invention may also be used to
 CC identify agonists or antagonists of the interaction of CCR5 with its
 CC natural ligand, and to determine a binding motif for CCR5. The present
 CC sequence represents human CCR5
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFFQFFGLNCS 22
 Db 249 APYNIVLLNTFFQFFGLNCS 270
 RESULT 27
 ABG70597
 ID ABG70597 standard; protein; 352 AA.
 XX AC ABG70597;

XX 03-DEC-2002 (first entry)
 XX Human G-protein chemokine receptor, HDGNR10.
 DE XX Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;
 XX haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;
 KW chronic infection; leukaemia; T-cell mediated autoimmune disease;
 KW parasitic infection; psoriasis; growth factor activity; allergy;
 KW atherogenesis; anaphylaxis; malignancy; inflammation; histamine;
 KW immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;
 KW prostaglandin-independent fever; bone marrow failure; shock;
 KW rheumatoid arthritis; hyper-eosinophilic syndrome; cycostatic;
 KW immunosuppressive; antiparasitic; antipsoriatic; antiallergic;
 KW antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;
 KW antipyretic; receptor.
 XX Homo sapiens.
 OS US2002099176-A1.
 XX 25-JUL-2002.
 PD 25-JUN-1999; 99US-00339912.
 PF 06-JUN-1995; 95US-00466343.
 PR (LIYY/) LI Y.
 PA (RUBE/) RUBEN S M.
 PA Li Y, Ruben SM;
 PI WPI: 2002-690494/74.
 XX N-PSDB; ABS54272.
 DR Novel human G-protein chemokine receptor polypeptide useful for
 XX identifying modulators for stimulating hematopoiesis, wound healing,
 PT leukemia, for treating allergy, rheumatoid arthritis, shock and as
 PT research agents.
 PT Claim 7; Fig 1; 22pp; English.
 XX The present invention relates to the isolation of human G-protein
 CC chemokine receptor, HDGNR10 (CCR5 receptor), and the polynucleotide
 CC sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences
 CC are or useful for diagnosing a disease or a susceptibility to a disease
 CC related to underexpression of HDGNR10. They are useful for identifying
 CC modulators for stimulating haematopoiesis, wound healing, coagulation,
 CC angiogenesis, to treat solid tumours, chronic infections, psoriasis, or
 CC cell mediated autoimmune diseases, parasitic infections, leukaemia, T-
 CC for stimulating growth factor activity. The sequences are also useful for
 CC preventing and/or treating allergy, atherogenesis, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 CC E (IgE)-mediated allergic reactions, prostaglandin-independent fever,
 CC bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. Polynucleotide sequences encoding HDGNR10 can be
 CC used in gene therapy to treat conditions related to underexpression of
 CC HDGNR10. The present sequence represents human G-protein chemokine
 CC receptor, HDGNR10
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFFQFFGLNCS 22
 Db 249 APYNIVLLNTFFQFFGLNCS 270
 RESULT 28
 ABG92883

ID ABG92883 standard; protein; 352 AA.
 XX AC ABG92883;
 XX DT 19-NOV-2002 (first entry)
 XX DE Human immunoglobulin variable heavy domain #1.
 XX
 KW Immunoglobulin; variable heavy chain; variable light chain; human;
 KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
 KW lymphocytopenia.
 XX OS Homo sapiens.
 XX PN WO200264612-A2.
 XX 22-AUG-2002.
 XX
 XX 08-FEB-2002; 2002WO-US003634.
 XX 09-FEB-2001; 2001US-00779880.
 XX 12-JUN-2001; 2001US-0297257P.
 XX 08-AUG-2001; 2001US-0310458P.
 XX 12-OCT-2001; 2001US-0328447P.
 XX 21-DEC-2001; 2001US-0341725P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Roschke V, Rosen CA, Ruben SM;
 XX WPI; 2002-643455/69.
 XX N-PSDB; ABS68606.
 XX
 XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for
 XX treating, preventing, ameliorating or monitoring diseases or disorders
 XX associated with aberrant expression of HDGNR10 e.g. cancer.
 XX
 XX Example 55; Fig 4; 562pp; English.
 XX
 XX The invention describes an isolated polynucleotide encoding a first
 XX antibody at least 95-100% identical to a second antibody consisting of an
 XX amino acid sequence comprising at least one, two or three CDR regions of
 XX a variable heavy (VH) or variable light (VL) domain of the antibody
 XX expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
 XX XF3.6A2, XF3.10B8, XF22.3C9.6, XF27/28.7D5, XF27/28.18B5,
 XX XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
 XX is useful treating, preventing, ameliorating, prognosing or monitoring
 XX cancers or other diseases or disorders e.g. immunologic deficiency
 XX syndromes such as blood protein disorders and ataxia telangiectasia,
 XX inflammation associated disorders such as endotoxin lethality, nephritis
 XX and inflammatory bowel disease, conditions associated with an increase in
 XX chemotaxis of immune cells or T-cell antigen presenting cell interaction,
 XX an infectious disease, an autoimmune disease such as Addison's disease,
 XX dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
 XX disorder, a viral infection e.g. HIV infection, cytomegalovirus or
 XX poxvirus infection, a Pneumocystis carni infection, Kaposi's sarcoma,
 XX cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
 XX disease or disorder associated with aberrant expression of novel human G-
 XX protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
 XX sequence of human immunoglobulin sequence associated with the antibodies
 XX against HDGNR10
 XX Sequence 352 AA;

Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIIVLLINTPQEPFFGLNCS 22
 DB 249 APYNIIVLLINTPQEPFFGLNCS 270
 RESULT 29
 ABG92880
 ID ABG92880 standard; protein; 352 AA.
 XX AC ABG92880;
 XX DT 19-NOV-2002 (first entry)
 XX DE Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
 XX
 KW Immunoglobulin; variable heavy chain; variable light chain; human;
 KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
 KW Pneumocystis carni infection; cardiovascular disorder; atherosclerosis;
 KW lymphocytopenia.
 XX OS Homo sapiens.
 XX PN WO200264612-A2.
 XX 22-AUG-2002.
 XX
 XX 08-FEB-2002; 2002WO-US003634.
 XX 09-FEB-2001; 2001US-00779880.
 XX 12-JUN-2001; 2001US-0297257P.
 XX 08-AUG-2001; 2001US-0310458P.
 XX 12-OCT-2001; 2001US-0328447P.
 XX 21-DEC-2001; 2001US-0341725P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Roschke V, Rosen CA, Ruben SM;
 XX WPI; 2002-643455/69.
 XX N-PSDB; ABS68606.
 XX
 XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for
 XX treating, preventing, ameliorating or monitoring diseases or disorders
 XX associated with aberrant expression of HDGNR10 e.g. cancer.
 XX
 XX Example 55; Fig 4; 562pp; English.
 XX
 XX The invention describes an isolated polynucleotide encoding a first
 XX antibody at least 95-100% identical to a second antibody consisting of an
 XX amino acid sequence comprising at least one, two or three CDR regions of
 XX a variable heavy (VH) or variable light (VL) domain of the antibody
 XX expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
 XX XF3.6A2, XF3.10B8, XF22.3C9.6, XF27/28.7D5, XF27/28.18B5,
 XX XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
 XX is useful treating, preventing, ameliorating, prognosing or monitoring
 XX cancers or other diseases or disorders e.g. immunologic deficiency
 XX syndromes such as blood protein disorders and ataxia telangiectasia,
 XX inflammation associated disorders such as endotoxin lethality, nephritis
 XX and inflammatory bowel disease, conditions associated with an increase in
 XX chemotaxis of immune cells or T-cell antigen presenting cell interaction,
 XX an infectious disease, an autoimmune disease such as Addison's disease,
 XX dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
 XX disorder, a viral infection e.g. HIV infection, cytomegalovirus or
 XX poxvirus infection, a Pneumocystis carni infection, Kaposi's sarcoma,
 XX cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
 XX disease or disorder associated with aberrant expression of novel human G-
 XX protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
 XX sequence of human immunoglobulin sequence associated with the antibodies
 XX against HDGNR10
 XX Sequence 352 AA;

CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
CC disease or disorder associated with aberrant expression of novel human G-
CC protein chemokine receptor (CCR5) HDGNR10. This is an amino acid sequence
CC of Human G-protein chemokine receptor (CCR5) HDGNR10 #1
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
DB 249 APYNIVLLNTFOEFFGLNCS 270
|||||

RESULT 30
AAE25808
ID AAE25808 standard; protein; 352 AA.
XX
AC AAE25808;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human G-protein chemokine receptor (CCR5), HDGNR10 #1.
XX
KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
KW inflammation; viral infection; autoimmune disease; neurodegeneration;
KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
KW hyperproliferative disease; receptor.
XX
OS Homo sapiens.
XX
PN US2002061834-A1.
XX
PD 23-MAY-2002.
XX
PF 09-FEB-2001; 2001US-00779880.
XX
PR 09-FEB-2000; 2000US-0181258P.
PR 09-MAR-2000; 2000US-0187999P.
PR 22-SEP-2000; 2000US-0234336P.
XX
PA (ROSE/) ROSEN C A.
PA (ROSC/) ROSCHKE V.
PA (LIYY/) LI Y.
PA (RUBE/) RUBEN S M.
XX
PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX
DR WPI: 2002-499674/53.
DR N-PSDB; AAD42409.
XX
PT New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
PT useful for treatment, prevention and diagnosis of e.g. cancer, also
PT related antibodies.
XX
PS Claim 61; Page 163-164; 186pp; English.
XX
CC The invention relates to human G-protein chemokine receptor (CCR5), CCR5
CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
CC antibodies are used for the treatment or prevention of inflammation,
CC defective or aberrant chemotaxis of immune cells or T cell antigen-
CC presenting cell interaction, viral infections (specifically human immune
CC deficiency (including its early stages), cytomegalovirus or pox viruses),
CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
CC carinii infection, Kaposi's sarcoma or any condition associated with the
CC aberrant expression of CCR5 or their ligands. They are also used for the
CC detection, diagnosis, prognosis and monitoring of cancers or other
CC hyperproliferative diseases. The present sequence is human G-protein
CC

CC chemokine receptor (CCR5), HDGNR10 DNA
SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
DB 249 APYNIVLLNTFOEFFGLNCS 270
|||||

RESULT 31
AAE25811
ID AAE25811 standard; protein; 352 AA.
XX
AC AAE25811;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human G-protein chemokine receptor (CCR5), HDGNR10 #2.
XX
KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
KW inflammation; viral infection; autoimmune disease; neurodegeneration;
KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
KW hyperproliferative disease; receptor.
XX
OS Homo sapiens.
XX
PN US2002061834-A1.
XX
PD 23-MAY-2002.
XX
PF 09-FEB-2001; 2001US-00779880.
XX
PR 09-FEB-2000; 2000US-0181258P.
PR 09-MAR-2000; 2000US-0187999P.
PR 22-SEP-2000; 2000US-0234336P.
XX
PA (ROSE/) ROSEN C A.
PA (ROSC/) ROSCHKE V.
PA (LIYY/) LI Y.
PA (RUBE/) RUBEN S M.
XX
PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX
DR WPI: 2002-499674/53.
DR N-PSDB; AAD42426.
XX
PT New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
PT useful for treatment, prevention and diagnosis of e.g. cancer, also
PT related antibodies.
XX
PS Disclosure; Page 170; 186pp; English.
XX
CC The invention relates to human G-protein chemokine receptor (CCR5), CCR5
CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
CC antibodies are used for the treatment or prevention of inflammation,
CC defective or aberrant chemotaxis of immune cells or T cell antigen-
CC presenting cell interaction, viral infections (specifically human immune
CC deficiency (including its early stages), cytomegalovirus or pox viruses),
CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
CC carinii infection, Kaposi's sarcoma or any condition associated with the
CC aberrant expression of CCR5 or their ligands. They are also used for the
CC detection, diagnosis, prognosis and monitoring of cancers or other
CC hyperproliferative diseases. The present sequence is human G-protein
CC chemokine receptor (CCR5), HDGNR10 DNA
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
 |||||
 Db 249 APYNIVLLNTFQFFGLNCS 270

RESULT 32
 ABB81054 ID ABB81054 standard; protein; 352 AA.
 XX AC ABB81054;
 XX XX
 XX 05-NOV-2002 (first entry)
 XX XX
 XX G-protein chemokine receptor, HDGNR10.
 XX XX
 XX 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;
 KW G-protein chemokine receptor; haematopoietic; immunosuppressant;
 KW antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic;
 KW antirheumatic; antiarthritic; gene therapy; human; receptor.
 XX XX
 OS Homo sapiens.
 XX XX
 XX US2002076745-A1.
 XX XX
 XX 20-JUN-2002.
 XX XX
 XX 18-NOV-1998; 98US-00195662.
 XX XX
 XX 06-JUN-1995; 95US-00466343.
 XX XX
 XX (LIYY/) LI Y.
 XX (RUBE/) RUBEN S M.
 XX XX
 XX Li Y, Ruben SM;
 XX WPI; 2002-598724/64.
 XX DR N-PSDB; ABB86542.
 XX XX
 XX New polynucleotide encoding a human G protein chemokine receptor HDGNR10,
 PT useful e.g. for treating tumors.
 XX XX
 XX Claim 7; Fig 1; 22pp; English.
 XX XX
 XX The invention relates to a novel human 7-transmembrane receptor, HDGNR10,
 CC which has been identified as a G-protein chemokine receptor. The GPCR
 CC HDGNR10 polypeptide can be expressed by standard recombinant methodology.
 CC Compounds that activate or inhibit the receptor polypeptide, optionally
 CC expressed from DNA in gene therapy vectors, are used to treat diseases
 CC that require: (a) activation of the receptor (e.g. stimulation of
 CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune
 CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the
 CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis
 CC etc). The present sequence represents the human HDGNR10 receptor
 CC polypeptide
 XX XX
 XX Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
 |||||
 Db 249 APYNIVLLNTFQFFGLNCS 270

RESULT 33
 ABB08343 ID ABB08343 standard; protein; 352 AA.
 XX AC ABB08343;
 XX XX

XX 18-JUN-2002 (first entry)
 DT Human chemokine (C-C motif) receptor 5 polypeptide.
 XX DE
 XX Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
 KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
 KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
 KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;
 KW chromosome 3p21.
 XX XX
 OS Homo sapiens.
 XX XX
 XX Key Location/Qualifiers
 FH Misc-difference 55 /label= Leu, Gln
 FT Misc-difference 182 /label= Phe, Leu
 FT Misc-difference 223 /label= Arg, Gln
 FT
 XX WO200177125-A2.
 XX 18-OCT-2001.
 XX 04-APR-2001; 2001WO-US010708.
 XX 05-APR-2000; 2000US-0194361P.
 XX (GENA-) GENAISANCE PHARM INC.
 XX Choi JY, Kliehm SE, Koshy B;
 XX WPI; 2002-041282/05.
 XX N-PSDB; ABA97318, ABA97319.
 XX
 XX New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful
 FT to diagnose and treat diseases associated with its abnormal expression or
 FT function, including human immunodeficiency virus-1 infection.
 XX
 XX Claim 29; Fig 3; 61pp; English.
 XX
 XX The present sequence is that of a polypeptide encoded by the human
 CC chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see
 CC ABA97318, ABA97319). The specification describes haplotyping the CCR5
 CC gene of an individual by determining if the individual has one of the
 CC CCR5 haplotypes or haplotype pairs fully defined in the specification.
 CC The specification also describes an isolated polynucleotide comprising a
 CC nucleotide sequence which is a polymorphic variant of the reference CCR5
 CC gene sequence and comprises an isogene defined by a haplotype described
 CC in the specification and its encoded polypeptide. The methods of the
 CC invention are useful to diagnose and develop treatment for diseases
 CC associated with abnormal expression or function of the gene. The CCR5
 CC isogenes and the screened compounds are useful for treating human
 CC immunodeficiency virus (HIV)-1 infection and the progression to acquired
 CC immunodeficiency syndrome (AIDS). The invention has antiviral
 CC applications. The specification describes genotyping the CCR5 gene of an
 CC individual; predicting a haplotype pair for the CCR5 gene of an
 CC individual; identifying an association between a trait and a haplotype or
 CC haplotype pair of the CCR5 gene. The specification describes a
 CC composition comprising a genotyping oligonucleotide for detecting a CCR5
 CC polymorphism; a recombinant non-human organism transformed with CCR5
 CC polynucleotide expressing a CCR5 protein encoded by the variant sequence;
 CC an isolated antibody specific for the CCR5 polypeptide and a method for
 CC screening drugs targeting the CCR5 polypeptide
 XX XX
 XX Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22

Db	249	APYNIVLLNTFQEFFGLNCS 270	Best Local Similarity 100.0%; Pred. No. 2.9e-11; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 34			
ABG75540			
ID	ABG75540	standard; protein; 352 AA.	
XX	AC	ABG75540;	
XX	DT	16-APR-2003 (first entry)	
XX	DE	Human G-protein chemokine receptor, HDGNR10, protein.	
XX	KW	Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor;	
XX	KW	HDGNR10; signal transduction; gene therapy; haematopoiesis;	
XX	KW	wound healing; coagulation; angiogenesis; tumour; chronic infection;	
XX	KW	leukaemia; T-cell mediated auto-immune disease; parasitic infection;	
XX	KW	psoriasis; growth factor; allergy; atherogenesis; anaphylaxis;	
XX	KW	malignancy; inflammation; histamine; IgE-mediated;	
XX	KW	prostaglandin-independent fever; bone marrow failure; silicosis;	
XX	KW	sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.	
XX	OS	Homo sapiens.	
XX	PN	US2002132269-A1.	
XX	PD	19-SEP-2002.	
XX	PF	11-FEB-2000; 2000US-00502783.	
XX	PR	06-JUN-1995; 95US-00466343.	
XX	PA	(HUMA-) HUMAN GENOME SCI INC.	
XX	PI	Li Y, Ruben SM;	
XX	DR	WPI; 2003-208994/20.	
XX	DR	N-PSDB; ABX10635.	
XX	PT	Novel human G-protein chemokine receptor polypeptide useful for	
XX	PT	diagnostic purposes and for identifying modulators of the polypeptide	
XX	PT	useful for treating leukemia, autoimmune diseases, psoriasis and allergic	
XX	PT	reactions.	
XX	PS	Claim 7; Fig 1; 22pp; English.	
XX	CC	The invention discloses a G-protein chemokine receptor (sometimes	
XX	CC	referred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the	
XX	CC	polynucleotide encoding it. G-protein chemokine receptors are involved in	
XX	CC	signal transduction pathways. The polynucleotide and polypeptide can be	
XX	CC	used to identify compounds which activate or inhibit activation of the	
XX	CC	protein and these compounds are useful for treating a patient having need	
XX	CC	to activate or inhibit a G-protein chemokine receptor. The compound is	
XX	CC	administered by providing to the patient DNA encoding the agonist or	
XX	CC	antagonist and expressing them in vivo (gene therapy). The	
XX	CC	polynucleotides and polypeptide are also useful for diagnosing a	
XX	CC	disease or susceptibility to a disease related to an under-expression of	
XX	CC	the protein, for chromosome identification or as immunogens for producing	
XX	CC	antibodies. Agonists are useful in stimulating haematopoiesis, wound	
XX	CC	healing, coagulation, angiogenesis, to treat solid tumours, chronic	
XX	CC	infections, leukaemia, T-cell mediated auto-immune diseases, parasitic	
XX	CC	infections, psoriasis and to stimulate growth factor activity.	
XX	CC	Antagonists are useful in the prevention and treatment of allergy,	
XX	CC	atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation,	
XX	CC	histamine and IgE-mediated allergic reactions, prostaglandin-independent	
XX	CC	fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis,	
XX	CC	shock and hyper-eosinophilic syndrome. The sequence presented is the	
XX	CC	human HDGNR10 protein	
XX	CC	Sequence 352 AA;	
XX	CC	Query Match 100.0%; Score 118; DB 6; Length 352;	

Sequence 352 AA;

Query Match 100.0%; Score 118; DB 6; Length 352;

Claim 12; Page 745; 767pp; English.

The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in drug screening, particularly for identifying agents for treating these pathologies

New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.

WPI; 2003-354600/33.
N-PSDB; ACC72740.

(EOSB-) EOS BIOTECHNOLOGY INC.

Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
Zlotnik A;

27-MAR-2003.

17-SEP-2002; 2002WO-US029560.

17-SEP-2001; 2001US-0323469P.

20-SEP-2001; 2001US-0323887P.

13-NOV-2001; 2001US-0350666P.

08-FEB-2002; 2002US-0355145P.

08-FEB-2002; 2002US-0355257P.

12-APR-2002; 2002US-0372246P.

09-JUL-2003 (first entry)
Human cancer related protein SEQ ID NO:259.

Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
heart disease; atherosclerosis; endometriosis.

Homo sapiens.

WO2003025138-A2.

27-MAR-2003.

Human cancer related protein SEQ ID NO:259.

1 APYNIVLLNTFQEFFGLNCS 22
249 APYNIVLLNTFQEFFGLNCS 270

```

Query Match      100.0%; Score 118; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNIVLLNTFOEFFGLNCS 22
    |||||
Db 249 APYNIVLLNTFOEFFGLNCS 270
    |||||

RESULT 36
AAO29514
ID AAO29514 standard; protein; 352 AA.
XX
AC AAO29514;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human C-C chemokine receptor type 5 (333) protein.
XX
KW Human; urological disorder; stress urinary incontinence; prostate cancer;
KW benign prostatic hyperplasia; overactive bladder; oversensitive bladder;
KW overflow urinary incontinence; Gene therapy; nephrotropic; prostatitis;
KW kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
XX
OS Homo sapiens.
XX
FN WO2003039475-A2.
XX
PD 15-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US035824.
XX
PR 07-NOV-2001; 2001US-0344552P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Silos-Santiago I;
XX
WPI; 2003-449396/42.
DR N-PSDB; AAL59912.
XX
XX Identifying a compound, capable of treating urological disorder e.g.;
PT benign prostatic hyperplasia, by assaying the ability of the compound to
PT modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or
PT polypeptide activity.
XX
PS Disclosure; Page 81; 87pp; English.
XX
CC The invention relates to a method for treating an urological disorder
CC which comprises assaying the ability of the compound to modulate 313,
CC 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide
CC activity. The method is useful for identifying a compound for treating an
CC urological disorder comprising urinary incontinence e.g., overactive/
CC oversensitive bladder, overflow urinary incontinence, stress urinary
CC incontinence caused by dysfunction of the bladder, urethra or central/
CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
CC prostate cancer or kidney disorders. It is also used in gene therapy. The
CC present sequence is human C-C chemokine receptor type 5 (CCR5; 333)
CC protein. This sequence is used to illustrate the method of the invention
XX
SQ Sequence 352 AA;

Query Match      100.0%; Score 118; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNIVLLNTFOEFFGLNCS 22
    |||||
Db 249 APYNIVLLNTFOEFFGLNCS 270
    |||||

RESULT 37
ABU61654
ID ABU61654 standard; protein; 352 AA.
XX
AC ABU61654;
XX
DT 08-AUG-2003 (first entry)
XX
DE Human G-protein chemokine receptor (HDGNR10) polypeptide.
XX
KW Human; G-protein chemokine receptor; receptor; HDGNR10;
KW 7-transmembrane receptor.
XX
OS Homo sapiens.
XX
FN US2003023044-A1.
XX
PD 30-JAN-2003.
XX
PF 03-SEP-2002; 2002US-00232686.
XX
PR 06-JUN-1995; 95US-00466343.
PR 18-NOV-1998; 98US-00195662.
PR 25-JUN-1999; 99US-00339912.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Li Y, Ruben SM;
XX
WPI; 2003-456307/43.
DR N-PSDB; ACA61721.
XX
XX Producing an antibody, involves immunizing an animal with a polypeptide
PT or with a polypeptide encoded by the human G-protein chemokine receptor
PT clone in ATCC 97183, and recovering the antibody.
XX
PS Claim 1; Fig 1; 23pp; English.
XX
CC The invention relates to a method of producing an antibody, involving
CC immunising an animal with a human G-protein chemokine receptor (HDGNR10)
CC polypeptide (also referred to as a human 7-transmembrane receptor) and
CC recovering an antibody which binds the polypeptide. The method is useful
CC for producing an antibody which binds specifically to the human G-protein
CC chemokine receptor polypeptide. This sequence represents the HDGNR10
CC polypeptide of the invention
XX
SQ Sequence 352 AA;

Query Match      100.0%; Score 118; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNIVLLNTFOEFFGLNCS 22
    |||||
Db 249 APYNIVLLNTFOEFFGLNCS 270
    |||||

RESULT 38
ABP97728
ID ABP97728 standard; protein; 352 AA.
XX
AC ABP97728;
XX
DT 28-MAY-2003 (first entry)
XX
DE Amino acid sequence of human chemokine receptor CCR5.
XX
KW Human; chemokine receptor; CCR5; viral infection; surface protein;
KW respiratory virus infection; respiratory syncytial virus infection;
KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.
XX
OS Homo sapiens.
XX
FN WO2003014153-A2.
XX

```

PD 20-FEB-2003.
 XX
 PF 12-AUG-2002; 2002WO-CA001248.
 XX
 PR 10-AUG-2001; 2001US-0311088P.
 XX
 PA (TOPI-1) TOPIGEN PHARM INC.
 XX
 PI Renzi P, Zemzoumi K;
 XX
 DR WPI; 2003-256541/25.
 DR N-PSDB; ABZ68881.
 XX
 XX Modulating viral infection of a cell, for treating or preventing
 PT respiratory virus infections, bronchitis, pneumonia or asthma, by
 PT modulating a binding interaction between a cell chemokine-receptor and a
 PT surface protein of the virus.
 XX
 PS Disclosure; Page 96-98; 120pp; English.
 XX
 CC The present sequence represents human chemokine receptor CCR5. The
 CC specification describes a method for modulating viral infection of a
 CC cell. The method comprises modulating a binding interaction between a
 CC cell chemokine-receptor and a surface protein of the virus. The proviso
 CC is that the cell chemokine-receptor is not CX3CR1 and that the virus is
 CC not HIV. The method is useful for treating or preventing respiratory
 CC virus infection in vertebrates, more particularly respiratory syncytial
 CC virus (RSV) infections, and related diseases, e.g. bronchiolitis,
 CC bronchitis, pneumonia or asthma
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 6; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFOEFFGLNCS 22
 Db 249 APYNIVLLNTFOEFFGLNCS 270
 XX
 RESULT 39
 ABP81933
 ID ABP81933 standard; protein; 352 AA.
 XX
 AC ABP81933;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Human C-C chemokine receptor 5 protein SEQ ID NO:352.
 XX
 XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 PA
 XX Burmer GC, Roush CL, Brown JP;
 XX
 DR WPI; 2003-045718/04.
 DR N-PSDB; ABZ42781.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX
 PS Disclosure; Fig 1; 523pp; English.
 XX
 CC The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 6; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFOEFFGLNCS 22
 Db 249 APYNIVLLNTFOEFFGLNCS 270
 XX
 RESULT 40
 ADC03341
 ID ADC03341 standard; protein; 352 AA.
 XX
 AC ADC03341;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human chemokine receptor 88-C.
 KW
 KW receptor; human; anti-HIV; virucide; HIV; SIV; 88-C; 88-2B;
 KW chemokine receptor; envelope protein; atherosclerosis;
 KW rheumatoid arthritis; tumour growth suppression; asthma; viral infection;
 KW AIDS; inflammatory condition.
 XX
 OS Homo sapiens.
 XX
 PN US2002150888-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002US-00106623.

XX 20-DEC-1995; 95US-00575967.
 PR 07-JUN-1996; 96US-00661393.
 PR 20-DEC-1996; 96US-00771276.
 XX
 PA (GRAY/) GRAY P W.
 PA (SCHW/) SCHWEICKART V L.
 PA (RAFO/) RAFOU C J.
 XX
 PI Gray PW, Schweickart VL, Raport CJ;
 XX
 XX WPI: 2003-182491/18.
 DR N-PSDB; ADC03340.
 XX
 PT Screening for a modulator of HIV and SIV infection utilizing
 PT polynucleotides that encode the 88C or 88-2B chemokine receptors, useful
 PT for diagnosing and treating disorders such as atherosclerosis, arthritis,
 PT AIDS and asthma.
 XX
 PS Claim 2; Page 17-18; 29pp; English.
 XX
 CC The invention relates to screening for a modulator of human
 CC immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV)
 CC infection, comprising contacting a first composition having an human
 CC (ADC03341) or macaque (ADC03359) 88C chemokine receptor polypeptide with
 CC a second composition having an HIV or SIV envelope protein in the
 CC presence or absence of a compound. Also included are screening for a
 CC modulator of HIV infection, detecting HIV infection of cells (comprising
 CC contacting a cell that has been recombinantly modified to express at
 CC least one of human chemokine receptors 88C and 88-2B with HIV, and
 CC detecting HIV infection in the cell) and inhibiting HIV infection of
 CC cells (comprising contacting cells with an antibody to at least one of
 CC human chemokine receptors 88C and 88-2B with HIV, and detecting HIV
 CC infection of the cell after the contacting step). The methods and
 CC compositions of the present invention are useful for the diagnosis and
 CC treatment of disorders associated with the aberrant expression or
 CC activity of 88C or 88-2B chemokine receptors, such as atherosclerosis,
 CC rheumatoid arthritis, tumour growth suppression, asthma, viral infection,
 CC AIDS and other inflammatory conditions. The genes for human 88-C and 88-
 CC 2B are located on chromosome 3p21. The present sequence represents human
 CC chemokine receptor 88-C.
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 7; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
 Db 249 APYNIVLLNTFOEFFGLNCS 270

Search completed: September 28, 2004, 09:03:38
 Job time : 52.525 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:00:23 ; Search time 19.8 Seconds
(without alignments)
57.362 Million cell updates/sec

Title: US-10-084-813-14
Perfect score: 118
Sequence: 1 APYNIVLLNTQEFGLNCS 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/2/iaa/5B COMB.pcp.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	352	3	US-08-466-343D-2
2	118	100.0	352	3	US-09-087-232A-13
3	118	100.0	352	3	US-08-861-105-14
4	118	100.0	352	3	US-08-575-867A-2
5	118	100.0	352	3	US-09-045-583-52
6	118	100.0	352	4	US-09-517-605-5
7	118	100.0	352	4	US-09-534-185-52
8	118	100.0	352	4	US-08-833-752-5
9	118	100.0	352	4	US-09-502-783A-2
10	118	100.0	352	4	US-08-796-202-1
11	108	91.5	354	4	US-08-724-884A-2
12	103	87.3	329	4	US-09-502-783A-9
13	103	87.3	344	3	US-08-466-343D-9
14	103	87.3	347	1	US-08-461-244-3
15	103	87.3	360	1	US-08-450-393A-4
16	103	87.3	360	3	US-08-446-669-4
17	103	87.3	360	3	US-09-045-583-50
18	103	87.3	360	3	US-09-045-583-51
19	103	87.3	360	4	US-09-534-185-50
20	103	87.3	360	4	US-09-534-185-51
21	103	87.3	360	4	US-08-833-752-7
22	103	87.3	360	4	US-09-131-827A-2
23	103	87.3	360	4	US-09-131-827A-20
24	103	87.3	360	5	PCT-US95-00476-4
25	103	87.3	374	1	US-08-450-393A-2
26	103	87.3	374	3	US-08-446-669-2
27	103	87.3	374	5	PCT-US95-00476-2

28	70	59.3	344	3	US-08-681-192-2	Sequence 2, Appl
29	61	51.7	25	3	US-09-087-232A-22	Sequence 22, Appl
30	56	47.5	355	1	US-08-012-988A-2	Sequence 2, Appl
31	56	47.5	355	1	US-08-450-393A-5	Sequence 5, Appl
32	56	47.5	355	3	US-08-446-669-5	Sequence 5, Appl
33	56	47.5	355	4	US-09-239-938-1	Sequence 1, Appl
34	56	47.5	355	4	US-09-886-319A-14	Sequence 14, Appl
35	56	47.5	355	5	PCT-US95-00476-5	Sequence 5, Appl
36	55	46.6	355	4	US-08-833-752-8	Sequence 8, Appl
37	54	45.8	355	4	US-08-833-752-9	Sequence 9, Appl
38	53	44.9	170	3	US-08-875-573-6	Sequence 6, Appl
39	53	44.9	360	3	US-08-875-573-20	Sequence 20, Appl
40	53	44.9	360	3	US-09-232-878-2	Sequence 2, Appl
41	53	44.9	360	4	US-09-045-583-55	Sequence 55, Appl
42	53	44.9	360	4	US-09-534-185-55	Sequence 55, Appl
43	53	44.9	360	4	US-08-939-107-34	Sequence 34, Appl
44	52	44.1	105	2	US-08-103-170-12	Sequence 12, Appl
45	52	44.1	317	1	US-08-118-270-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-2

Query Match 100.0%; Score 118; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 APYNIVLLNTQEFGLNCS 22
Db 249 APYNIVLLNTQEFGLNCS 270

RESULT 2

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US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087.232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-13

Query Match 100.0%; Score 118; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFFQFFGLNCS 22
Db 249 APYNIVLLNTFFQFFGLNCS 270

RESULT 3
US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 NI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-861-105-14

Query Match 100.0%; Score 118; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFFQFFGLNCS 22
Db 249 APYNIVLLNTFFQFFGLNCS 270

RESULT 4
US-08-575-967A-2
; Sequence 2, Application US/08575967A
; Patent No. 6265184
; GENERAL INFORMATION:
; APPLICANT: Gray et al.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,967A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6265184and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 3291S
; TELECOMMUNICATION INFORMATION:

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;
;
; TELEPHONE: 206-485-1900
;
; TELEFAX: 206-485-1662
;
; INFORMATION FOR SEQ ID NO: 2:
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; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 352 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; FEATURE:
;
; NAME/KEY: misc_feature
;
; OTHER INFORMATION: /= "88C amino acid sequence"
;
US-08-575-967A-2

Query Match      100.0%; Score 118; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
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Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 5
US-09-045-583-52
; Sequence 52, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
;
US-09-045-583-52

Query Match      100.0%; Score 118; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
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Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 6
US-09-517-605-5
; Sequence 5, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-517-605-5

Query Match      100.0%; Score 118; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
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Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 7
US-09-534-185-52
; Sequence 52, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-09-045-583-52

Query Match      100.0%; Score 118; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQEFFGLNCS 270
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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match      100.0%; Score 118; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQFFGLNCS 270

RESULT 8
US-08-833-752-5
; Sequence 5, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CG-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-752-5

Query Match      100.0%; Score 118; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQFFGLNCS 270

RESULT 9
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CRS
; TITLE OF INVENTION: HDGR10
; FILE REFERENCE: 1488.1150006
```

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; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match      100.0%; Score 118; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQFFGLNCS 270

RESULT 10
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match      100.0%; Score 118; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 249 APYNIVLLNTFQFFGLNCS 270

RESULT 11
US-08-724-984A-2
; Sequence 2, Application US/08724984A
; Patent No. 6388055
; GENERAL INFORMATION:
; APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
; TITLE OF INVENTION: NO. 6388055el Mouse Genomic Clone of the CC-
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,984A
; FILING DATE: October 3, 1996
```

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; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-724-984A-2
;
Query Match 91.5%; Score 108; DB 4; Length 354;
Best Local Similarity 95.2%; Pred. No. 2.1e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTFQEPFGLNCS 22
Db 252 PYNIVLLNTFQEPFGLNCS 272

RESULT 12
US-09-502-783A-9
; Sequence 9, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
;
US-09-502-783A-9
Query Match 87.3%; Score 103; DB 4; Length 329;
Best Local Similarity 90.0%; Pred. No. 1.4e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTFQEPFGLNCS 21
Db 226 PYNIVLLNTFQEPFGLSNC 245

RESULT 13
US-08-466-343D-9
; Sequence 9, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA

```

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; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-466-343D-9
Query Match 87.3%; Score 103; DB 3; Length 344;
Best Local Similarity 90.0%; Pred. No. 1.4e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTFQEPFGLNCS 21
Db 241 PYNIVLLNTFQEPFGLSNC 260

RESULT 14
US-08-461-244-3
; Sequence 3, Application US/08461244
; Patent No. 5776729
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESS: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids

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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-244-3

Query Match 87.3%; Score 103; DB 1; Length 347;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFPLGNNC 21
||||:|||||:|||||:|
Db 245 PYNIVLLNTQEFPLGNSC 264

RESULT 15
US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815

; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450.393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserz, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-4

Query Match 87.3%; Score 103; DB 1; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFPLGNNC 21
||||:|||||:|||||:|
Db 258 PYNIVLLNTQEFPLGNSC 277

RESULT 16
US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-4

Query Match 87.3%; Score 103; DB 3; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFPLGNNC 21
||||:|||||:|||||:|
Db 258 PYNIVLLNTQEFPLGNSC 277

RESULT 17
US-09-045-583-50
; Sequence 50, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045.583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.

```

; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-045-583-50

Query Match      87.3%; Score 103; DB 3; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PYNIVLLNTFQFFGLNLC 21
Db      258 PYNIVLLNTFQFFGLSNC 277

RESULT 18
; US-09-045-583-51
; Sequence 51, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-045-583-51

Query Match      87.3%; Score 103; DB 3; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PYNIVLLNTFQFFGLNLC 21
Db      258 PYNIVLLNTFQFFGLSNC 277

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RESULT 19
; US-09-534-185-50
; Sequence 50, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; THEREFOR
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
; US-09-534-185-50

Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PYNIVLLNTFQFFGLNLC 21
Db      258 PYNIVLLNTFQFFGLSNC 277

RESULT 20
; US-09-534-185-51
; Sequence 51, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; THEREFOR
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

```

```
/
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/534,185
/ FILING DATE: 24-Mar-2000
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/045,583
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mandragouras, Amy E.
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: MNI-044
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)742-4214
/
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 360 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FRAGMENT TYPE: internal
/ SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51

Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTQEPFFGLNCC 21
Db      258 PYNIVLLNTQEPFFGLSNC 277

RESULT 21
US-08-833-752-7
/ Sequence 7, Application US/08833752
/ Patent No. 6448375
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ APPLICANT: PARMENTIER, MARC
/ APPLICANT: VASSART, GILBERT
/ APPLICANT: LIBERT, FREDERICK
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/833,752
/ FILING DATE: 9-APR-1997
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER:
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 360 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FRAGMENT TYPE: internal
/ SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-833-752-7

Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTQEPFFGLNCC 21
Db      258 PYNIVLLNTQEPFFGLSNC 277

RESULT 22
US-09-131-827A-2
/ Sequence 2, Application US/09131827A
/ Patent No. 6600030
/ GENERAL INFORMATION:
/ APPLICANT: Dean, Michael
/ APPLICANT: O'Brien, Stephen J.
/ APPLICANT: Smith, Michael
/ APPLICANT: Carrington, Mary
/ TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
/ FILE REFERENCE: 14014.0333
/ CURRENT APPLICATION NUMBER: US/09/131,827A
/ CURRENT FILING DATE: 1998-08-10
/ PRIOR APPLICATION NUMBER: 60/055,659
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 2
/ LENGTH: 360
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-131-827A-2

Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTQEPFFGLNCC 21
Db      258 PYNIVLLNTQEPFFGLSNC 277

RESULT 23
US-09-131-827A-20
/ Sequence 20, Application US/09131827A
/ Patent No. 6600030
/ GENERAL INFORMATION:
/ APPLICANT: Dean, Michael
/ APPLICANT: O'Brien, Stephen J.
/ APPLICANT: Smith, Michael
/ APPLICANT: Carrington, Mary
/ TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
/ FILE REFERENCE: 14014.0333
/ CURRENT APPLICATION NUMBER: US/09/131,827A
/ CURRENT FILING DATE: 1998-08-10
/ PRIOR APPLICATION NUMBER: 60/055,659
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 20
/ LENGTH: 360
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-131-827A-20
```

```
/
/
/ LENGTH: 360 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6448375e
US-08-833-752-7

Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTQEPFFGLNCC 21
Db      258 PYNIVLLNTQEPFFGLSNC 277

RESULT 22
US-09-131-827A-2
/ Sequence 2, Application US/09131827A
/ Patent No. 6600030
/ GENERAL INFORMATION:
/ APPLICANT: Dean, Michael
/ APPLICANT: O'Brien, Stephen J.
/ APPLICANT: Smith, Michael
/ APPLICANT: Carrington, Mary
/ TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
/ FILE REFERENCE: 14014.0333
/ CURRENT APPLICATION NUMBER: US/09/131,827A
/ CURRENT FILING DATE: 1998-08-10
/ PRIOR APPLICATION NUMBER: 60/055,659
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 2
/ LENGTH: 360
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-131-827A-2

Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTQEPFFGLNCC 21
Db      258 PYNIVLLNTQEPFFGLSNC 277

RESULT 23
US-09-131-827A-20
/ Sequence 20, Application US/09131827A
/ Patent No. 6600030
/ GENERAL INFORMATION:
/ APPLICANT: Dean, Michael
/ APPLICANT: O'Brien, Stephen J.
/ APPLICANT: Smith, Michael
/ APPLICANT: Carrington, Mary
/ TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
/ FILE REFERENCE: 14014.0333
/ CURRENT APPLICATION NUMBER: US/09/131,827A
/ CURRENT FILING DATE: 1998-08-10
/ PRIOR APPLICATION NUMBER: 60/055,659
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 20
/ LENGTH: 360
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-131-827A-20
```



```

Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PYNIVLLNTFQEPFGLSNC 21
Db      258 PYNIVLLNTFQEPFGLSNC 277

RESULT 24
PCT-US95-00476-4
; Sequence 4, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-00476-4

Query Match      87.3%; Score 103; DB 5; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PYNIVLLNTFQEPFGLSNC 21
Db      258 PYNIVLLNTFQEPFGLSNC 277

RESULT 25
US-08-450-393A-2
; Sequence 2, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neelley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CcoleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-393A-2

Query Match      87.3%; Score 103; DB 1; Length 374;
Best Local Similarity 90.0%; Pred. No. 1.6e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PYNIVLLNTFQEPFGLSNC 21
Db      258 PYNIVLLNTFQEPFGLSNC 277

RESULT 26
US-08-446-669-2
; Sequence 2, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neelley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CcoleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-393A-2

```

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-2
Query Match 87.3%; Score 103; DB 3; Length 374;
Best Local Similarity 90.0%; Pred. No. 1.6e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 2 PYNIVLLNTQEPFGLNLC 21
Db 258 PYNIVLLNTQEPFGLSNC 277

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RESULT 27

```

PCT-US95-00476-2
; Sequence 2, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berlinet, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-00476-2

```

```

Query Match 87.3%; Score 103; DB 5; Length 374;
Best Local Similarity 90.0%; Pred. No. 1.6e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 2 PYNIVLLNTQEPFGLNLC 21
Db 258 PYNIVLLNTQEPFGLSNC 277

```

RESULT 28

```

US-08-681-192-2
; Sequence 2, Application US/08681192
; Patent No. 6287801
; GENERAL INFORMATION:
; APPLICANT: BERGMA, DEREK
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: SARAU, HENRY
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNFD578

```

```

; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,192
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATG50014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-681-192-2

```

```

Query Match 59.3%; Score 70; DB 3; Length 344;
Best Local Similarity 57.1%; Pred. No. 0.00063;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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QY 1 APYNIIVLLNTQEPFGLNLC 21
Db 252 APYNIIVLLNTQEPFGLSNC 272

```

RESULT 29

```

US-09-087-232A-22
; Sequence 22, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A

```

FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: AP 31115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2628
TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-087-232A-22

Query Match 51.7%; Score 61; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVLLNTF 12
DB 14 APYIVLLNTF 25

RESULT 30
US-08-012-988A-2
Sequence 2, Application US/08012989A
Patent No. 5652133
GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning and Expression of Human
TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
TITLE OF INVENTION: alpha)/RANTES Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,989A
FILING DATE: 19930128
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-012-988A-2

Query Match 47.5%; Score 56; DB 1; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNNC 21
DB 254 PYNILILISVFQDFLFTHEC 273

RESULT 31
US-08-450-393A-5
Sequence 5, Application US/08450393A
Patent No. 5707815
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-450-393A-5

Query Match 47.5%; Score 56; DB 1; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNNC 21
DB 254 PYNILILISVFQDFLFTHEC 273

RESULT 32
US-08-446-669-5
Sequence 5, Application US/08446669
Patent No. 6132987
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto

```

; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-446-669-5

Query Match 47.5%; Score 56; DB 3; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTPOEFFGLNLC 21
Db 254 PYNLTILISVQDFLFTHEC 273

RESULT 33
US-09-239-938-1
; Sequence 1, Application US/09239938
; Patent No. 6329510
; GENERAL INFORMATION:
; APPLICANT: Qln, Shixin
; APPLICANT: Newman, Walter
; APPLICANT: Kassam, Nasim
; APPLICANT: Leukosice, Inc.
; TITLE OF INVENTION: ANTI-CCR1 ANTIBODIES AND METHODS OF USE
; FILE REFERENCE: LKS97-13
; CURRENT APPLICATION NUMBER: US/09/239,938
; CURRENT FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-239-938-1

Query Match 47.5%; Score 56; DB 4; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTPOEFFGLNLC 21
Db 254 PYNLTILISVQDFLFTHEC 273

RESULT 34
US-09-886-319A-14
; Sequence 14, Application US/09886319A

```

```

; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jörn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886,319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-319A-14

Query Match 47.5%; Score 56; DB 4; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTPOEFFGLNLC 21
Db 254 PYNLTILISVQDFLFTHEC 273

RESULT 35
PCT-US95-00476-5
; Sequence 5, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-00476-5

Query Match 47.5%; Score 56; DB 5; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFPFGLNNC 21
|||: :||: :||: :||
Db 254 PYNLTILISVQDFLFTHC 273

RESULT 36
US-08-833-752-8
; Sequence 8, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: FARMETIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
US-08-833-752-9

Query Match 45.8%; Score 54; DB 4; Length 355;
Best Local Similarity 35.0%; Pred. No. 0.35;
Matches 7; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFPFGLNNC 21
|||: :||: :||: :||
Db 254 PYNLTILISVQDFLFTHC 273

RESULT 38
US-08-875-573-6
; Sequence 6, Application US/08875573
; Patent No. 6150132
; GENERAL INFORMATION:
; APPLICANT: Wells, Timothy N.C.
; APPLICANT: Power, Christine A.
; TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO
; TITLE OF INVENTION: MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 No. 6150132th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00143
; FILING DATE: 24-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9501683.8
; FILING DATE: 27-JAN-1995
; ATTORNEY/AGENT INFORMATION:

Query Match 44.9%; Score 53; DB 3; Length 360;
Best Local Similarity 52.4%; Pred. No. 0.53;
Matches 11; Conservative 2; Mismatches 8; Indels

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 28, 2004, 09:06:23 ; Search time 72.875 Seconds
(without alignments)
97.074 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYNIVLLNTFQEFFGLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:*
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	22	14	US-10-084-813-14
2	118	100.0	332	14	US-10-095-876A-2
3	118	100.0	352	9	US-09-725-285-2
4	118	100.0	352	9	US-09-759-841-2
5	118	100.0	352	9	US-09-779-879A-2
6	118	100.0	352	9	US-09-779-879A-22
7	118	100.0	352	9	US-09-779-880A-2
8	118	100.0	352	9	US-09-779-880A-22
9	118	100.0	352	9	US-09-813-653-15
10	118	100.0	352	9	US-09-813-653-17
11	118	100.0	352	9	US-09-796-202-1
12	118	100.0	352	9	US-09-195-662A-2
13	118	100.0	352	9	US-09-339-912A-2
14	118	100.0	352	9	US-09-938-719-5
15	118	100.0	352	9	US-09-939-226-5

15	118	100.0	352	9	US-09-938-703-5	Sequence 5, Appli
17	118	100.0	352	9	US-09-502-783A-2	Sequence 2, Appli
18	118	100.0	352	10	US-09-734-221A-14	Sequence 14, Appl
19	118	100.0	352	11	US-09-826-509-477	Sequence 477, App
20	118	100.0	352	12	US-10-151-274-5	Sequence 5, Appli
21	118	100.0	352	13	US-10-106-623-2	Sequence 2, Appli
22	118	100.0	352	13	US-10-106-623-20	Sequence 20, Appl
23	118	100.0	352	14	US-10-232-886-2	Sequence 2, Appli
24	118	100.0	352	14	US-10-086-814-1	Sequence 1, Appli
25	118	100.0	352	14	US-10-067-800-2	Sequence 2, Appli
26	118	100.0	352	14	US-10-067-800-22	Sequence 22, Appl
27	118	100.0	352	14	US-10-230-058A-6	Sequence 6, Appli
28	118	100.0	352	14	US-10-225-567A-352	Sequence 352, App
29	118	100.0	352	14	US-10-323-314-1	Sequence 1, Appli
30	118	100.0	352	14	US-10-072-301-1	Sequence 1, Appli
31	118	100.0	352	14	US-10-164-849-52	Sequence 52, Appl
32	118	100.0	352	14	US-10-071-866-1	Sequence 1, Appli
33	118	100.0	352	14	US-10-135-839-2	Sequence 2, Appli
34	118	100.0	352	14	US-10-135-839-22	Sequence 22, Appl
35	118	100.0	352	14	US-10-239-423-67	Sequence 67, Appl
36	118	100.0	352	14	US-10-439-845-2	Sequence 2, Appli
37	118	100.0	352	14	US-10-439-845-4	Sequence 4, Appli
38	118	100.0	352	15	US-10-360-828-1	Sequence 1, Appli
39	118	100.0	352	16	US-10-661-798-5	Sequence 5, Appli
40	118	100.0	352	16	US-10-791-905-2	Sequence 2, Appli
41	118	100.0	352	16	US-10-612-791-5	Sequence 5, Appli
42	103	87.3	329	9	US-09-725-285-9	Sequence 9, Appli
43	103	87.3	329	9	US-09-195-662A-9	Sequence 9, Appli
44	103	87.3	329	9	US-09-339-912A-9	Sequence 9, Appli
45	103	87.3	329	9	US-09-502-783A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-10-084-813-14
; Sequence 14, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ IDS NOS: 1242
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 14
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-14

Query Match 100.0%; Score 118; DB 14; Length 22;

Best Local Similarity 100.0%; Pred. No. 1e-11;

Mismatches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22

DB 1 APYNIVLLNTFQEFFGLNCS 22

RESULT 2

US-10-095-876A-2
; Sequence 2, Application US/10095876A
; Publication No. US20030146294A1

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; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice; Bandman, Olga
; APPLICANT: Coleman, Roger; Wilde, Craig G.
; TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
; FILE REFERENCE: PF-0060-1 CON
; CURRENT APPLICATION NUMBER: US/10/095,876A
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 08/638,081
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2

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Query Match      100.0%; Score 118; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
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Db 229 APYNIVLLNTFQEFFGLNCS 250

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RESULT 3
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

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Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
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Db 249 APYNIVLLNTFQEFFGLNCS 270

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RESULT 4
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan

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; APPLICANT: Perros, Manoussos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC10348APME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: US-09-759-841-2

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Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
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Db 249 APYNIVLLNTFQEFFGLNCS 270

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RESULT 5
US-09-779-879A-2
; Sequence 2, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: US-09-779-879A-2

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Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
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Db 249 APYNIVLLNTFQEFFGLNCS 270

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RESULT 6
US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.

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RESULT 8
US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10

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RESULT 10
US-03-813-653-17
; Sequence 17, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehli, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005

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; CURRENT APPLICATION NUMBER: US/09/813.653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-17

Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 11
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 12
US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:

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; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 13
US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2

Query Match      100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 14
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719

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; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5
Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 15
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5
Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 16
US-09-938-703-5
; Sequence 5, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5
Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
Db 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 17
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. US2002013269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
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; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
|||||
DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 18

US-09-734-221A-14
; Sequence 14, Application US/09734221A
; Publication No. US20030096221A1
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.

; DENG, HONGKUI
; ELLMEIER, WILFRIED
; LANDAU, NATHANIEL R.
; LIU, RONG

; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; USES THEREOF

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/734,221A

; FILING DATE: 11-Dec-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/666,020

; FILING DATE: 19-JUN-1996

; APPLICATION NUMBER: US 08/227,319

; FILING DATE: 13-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 1049-1-004 N2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-487-5800

; TELEFAX: 201-343-1684

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 352 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHEetical: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-734-221A-14

Query Match 100.0%; Score 118; DB 10; Length 352;

Best Local Similarity 100.0%; Pred. No. 2e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22

|||||

DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 19

US-09-826-509-477

; Sequence 477, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 477

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-826-509-477

Query Match 100.0%; Score 118; DB 11; Length 352;

Best Local Similarity 100.0%; Pred. No. 2e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22

|||||

DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 20

US-10-151-274-5

; Sequence 5, Application US/10151274

; Publication No. US20030064071A1

; GENERAL INFORMATION:

; APPLICANT: Littman, Dan R.

; APPLICANT: Kwon, Douglas S.

; APPLICANT: van Kooyk, Yvette

; APPLICANT: Geijtenbeek, Theo

; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

; TITLE OF INVENTION: INTO

; FILE REFERENCE: 1049-1-017

; CURRENT APPLICATION NUMBER: US/10/151,274

; CURRENT FILING DATE: 2002-05-20

; PRIOR APPLICATION NUMBER: US/09/517,605

; PRIOR FILING DATE: 2000-03-02

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-151-274-5

Query Match 100.0%; Score 118; DB 12; Length 352;

Best Local Similarity 100.0%; Pred. No. 2e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 APYNIVLLNTQEFFGLNCS 22
      |||||||
Db      249 APYNIVLLNTQEFFGLNCS 270

RESULT 21
US-10-106-623-2
; Sequence 2, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-106-623-20
Query Match      100.0%; Score 118; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APYNIVLLNTQEFFGLNCS 22
      |||||||
Db      249 APYNIVLLNTQEFFGLNCS 270

RESULT 23
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2
Query Match      100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APYNIVLLNTQEFFGLNCS 22
      |||||||
Db      249 APYNIVLLNTQEFFGLNCS 270

RESULT 22
US-10-106-623-20
; Sequence 20, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
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Db 249 APYNI VLLNTFOEFFGLNCS 270

RESULT 24

```

US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US2003092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1

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Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0

QY 1 APYNIVLLNTTQEFFGLNCS 22
 249 APYNIVLLNTTQEFFGLNCS 270
 D'b

RESULT 25

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US-10-067-800-2
; Sequence 2, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-2

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Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0

QY 1 APYNIVLLNTFOEFFGLNCS 22
|||
db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 26

US-10-067-800-22
; Sequence 22, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:

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/ APPLICANT: Roschke, Viktor
/ APPLICANT: Rosen, Craig A.
/ APPLICANT: Ruben, Steven, M.
/ TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
/ FILE REFERENCE: 1498.1150001
/ CURRENT APPLICATION NUMBER: US/10/067,800
/ CURRENT FILING DATE: 2002-02-08
/ PRIOR APPLICATION NUMBER: PCT/US01/04153
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 09/779,880
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/297,257
/ PRIOR FILING DATE: 2001-06-12
/ PRIOR APPLICATION NUMBER: 60/310,458
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: 60/328,447
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 60/341,725
/ PRIOR FILING DATE: 2001-12-21
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 22
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-067-800-22

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Query Match      100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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QY 1 APYNIVLLNTFOEFFGLNCS 22
|||
Db 249 APYNIVLLNTFOEFFGLNCS 270
|||

RESULT 27

```

RESUL 27
US-10-290-058A-6
; sequence 6, Application US/10290058A
; Publication No. US20030104455A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
; FILE REFERENCE: MP101-289PIRM
; CURRENT APPLICATION NUMBER: US/10/290,058A
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/344,552
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-290-058A-6

```

```
Query Match      100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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```

QY      1 APYNIVLLNTFQEFFGLNCS 22
      |||||
db     249 APYNIVLLNTFQEFFGLNCS 270

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RESULT 28
US-10-225-567A-352

<pre>; SEQ ID NO 1 ; LENGTH: 352 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-072-301-1 Query Match 100.0%; Score 118; DB 14; Length 352; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 APYNIVLLNTFQEFFGLNCS 22 Db 249 APYNIVLLNTFQEFFGLNCS 270 RESULT 31 US-10-164-649-52 ; Sequence 52, Application US/10164649 ; Publication No. US20030162943A1 ; GENERAL INFORMATION: ; APPLICANT: Graham, Gerard J. et al. ; TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled ; NUMBER OF SEQUENCES: 56 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: LAHIVE & COCKFIELD, LLP ; STREET: 28 State Street ; CITY: Boston ; STATE: Massachusetts ; COUNTRY: USA ; ZIP: 02109 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: PatentIn Release #1.0, Version #1.25 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/10/164,649 ; FILING DATE: 07-Jun-2002 ; CLASSIFICATION: <Unknown> ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US/09/045,583 ; FILING DATE: 20-MAR-1998 ; ATTORNEY/AGENT INFORMATION: ; NAME: Mandragouras, Amy E. ; REGISTRATION NUMBER: 36,207 ; REFERENCE/DOCKET NUMBER: MNI-044 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (617)227-7400 ; TELEFAX: (617)742-4214 ; INFORMATION FOR SEQ ID NO: 52: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 352 amino acids ; TYPE: amino acid ; TOPOLOGY: linear ; MOLECULE TYPE: peptide ; FRAGMENT TYPE: internal ; SEQUENCE DESCRIPTION: SEQ ID NO: 52: ; US-10-164-649-52 Query Match 100.0%; Score 118; DB 14; Length 352; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 APYNIVLLNTFQEFFGLNCS 22 Db 249 APYNIVLLNTFQEFFGLNCS 270 RESULT 32 US-10-071-866-1 ; Sequence 1, Application US/10071866 ; Publication No. US20030165988A1 ; GENERAL INFORMATION:</pre>	<pre>; Sequence 352, Application US/10225567A ; Publication No. US20030113798A1 ; GENERAL INFORMATION: ; APPLICANT: LifeSpan Biosciences ; APPLICANT: Brown, Joseph P. ; APPLICANT: Burner, Glenna C. ; APPLICANT: Roush, Christine L. ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS ; FILE REFERENCE: 1920-4-4 ; CURRENT APPLICATION NUMBER: US/10/225,567A ; CURRENT FILING DATE: 2001-12-19 ; PRIOR APPLICATION NUMBER: 60/257,144 ; PRIOR FILING DATE: 2000-12-19 ; NUMBER OF SEQ ID NOS: 2292 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 352 ; LENGTH: 352 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-225-567A-352 Query Match 100.0%; Score 118; DB 14; Length 352; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 APYNIVLLNTFQEFFGLNCS 22 Db 249 APYNIVLLNTFQEFFGLNCS 270 RESULT 29 US-10-323-314-1 ; Sequence 1, Application US/10323314 ; Publication No. US20030139571A1 ; GENERAL INFORMATION: ; APPLICANT: Dragic, Tatjana ; APPLICANT: Olson, William ; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION ; FILE REFERENCE: 2048/61010-1/JPM/MAF/DJK ; CURRENT APPLICATION NUMBER: US/10/323,314 ; CURRENT FILING DATE: 2002-12-19 ; NUMBER OF SEQ ID NOS: 17 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 1 ; LENGTH: 352 ; TYPE: PRT ; ORGANISM: human US-10-323-314-1 Query Match 100.0%; Score 118; DB 14; Length 352; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 APYNIVLLNTFQEFFGLNCS 22 Db 249 APYNIVLLNTFQEFFGLNCS 270 RESULT 30 US-10-072-301-1 ; Sequence 1, Application US/10072301 ; Publication No. US20030152913A1 ; GENERAL INFORMATION: ; APPLICANT: Hua, Shao-bing ; APPLICANT: Pauling, Michelle H. ; APPLICANT: Zhu, Li ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF ; TITLE OF INVENTION: VIRUS ; FILE REFERENCE: 25636-718 ; CURRENT APPLICATION NUMBER: US/10/072,301 ; CURRENT FILING DATE: 2002-02-08 ; NUMBER OF SEQ ID NOS: 54 ; SOFTWARE: PatentIn version 3.1</pre>
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; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-10-439-845-2

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 37
US-10-439-845-4
; Sequence 4, Application US/10439845
; Publication No. US20030195348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-10-439-845-2

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 38
US-10-360-828-1
; Sequence 1, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-360-828-1

Query Match 100.0%; Score 118; DB 15; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 39
US-10-661-798-5
; Sequence 5, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Fressard, Albert
; TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV Ent
; FILE REFERENCE: 9409/2023F
; CURRENT APPLICATION NUMBER: US/10/661,798
```

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/ CURRENT FILING DATE: 2003-09-12
/ PRIOR APPLICATION NUMBER: 09/938,703
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: 09/625,939
/ PRIOR FILING DATE: 2000-07-27
/ PRIOR APPLICATION NUMBER: 08/833,752
/ PRIOR FILING DATE: 1997-04-09
/ PRIOR APPLICATION NUMBER: 08/810,028
/ PRIOR FILING DATE: 1997-03-03
/ PRIOR APPLICATION NUMBER: EP 96870021.1
/ PRIOR FILING DATE: 1996-03-01
/ PRIOR APPLICATION NUMBER: EP 96870102.9
/ PRIOR FILING DATE: 1996-08-06
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-661-738-5

Query Match      100.0%; Score 118; DB 16; Length 352;
Best Local Similarity 100.0%; Pred.No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
DB 249 APYNIVLLNTFQFFGLNCS 270

RESULT 40
US-10-791-905-2
/ Sequence 2, Application US/10791905
/ Publication No. US20040151719A1
/ GENERAL INFORMATION:
/ APPLICANT: Li, Yi
/ APPLICANT: Ruben, Steven, M.
/ TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGMR10
/ FILE REFERENCE: 1488.115000P
/ CURRENT APPLICATION NUMBER: US/10791,905
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 10/127,764
/ PRIOR FILING DATE: 2002-04-23
/ PRIOR APPLICATION NUMBER: 09/502,783
/ PRIOR FILING DATE: 2000-02-11
/ PRIOR APPLICATION NUMBER: 09/339,912
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 09/195,662
/ PRIOR FILING DATE: 1998-11-18
/ PRIOR APPLICATION NUMBER: 08/465,343
/ PRIOR FILING DATE: 1995-06-06
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-791-905-2

Query Match      100.0%; Score 118; DB 16; Length 352;
Best Local Similarity 100.0%; Pred.No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
DB 249 APYNIVLLNTFQFFGLNCS 270
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Search completed: September 28, 2004, 09:44:42
Job time : 73.875 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:57:36 ; Search time 11.925 Seconds
(without alignments)
178.961 Million cell updates/sec

Title: US-10-084-813-14
Perfect score: 118
Sequence: 1 APYNIVLLNTFFQEFGLNCS 22
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.c*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	118	100.0	352 2 A43113	chemokine (C-C) re
2	103	87.3	360 2 JC2443	chemokine (C-C) re
3	103	87.3	374 2 I38450	chemokine (C-C) re
4	70	59.3	344 2 JC5942	chemokine receptor
5	56	47.5	355 2 A45177	chemokine (C-C) re
6	54.5	46.2	1075 2 T07448	probable DNA-direc
7	53	44.9	360 2 A57160	chemokine (C-C) re
8	52	44.1	355 2 G02436	chemokine (C-C) re
9	52	44.1	360 2 JC4587	chemokine (C-C) re
10	52	44.1	383 2 S55394	G protein-coupled
11	52	44.1	466 2 JH0197	muscarinic acetyl
12	52	44.1	466 2 S10126	muscarinic acetyl
13	52	44.1	466 2 S10856	muscarinic acetyl
14	52	44.1	466 2 A27386	muscarinic acetyl
15	51	43.2	589 2 A29476	muscarinic acetyl
16	50	42.4	490 2 A35546	muscarinic acetyl
17	48	40.7	294 2 AG2937	hypothetical prote
18	48	40.7	300 2 F98344	histidinol-phospha
19	48	40.7	342 2 G69502	MIP-1 alpha recept
20	48	40.7	359 2 I49341	muscarinic acetyl
21	48	40.7	589 2 S48557	muscarinic acetyl
22	48	40.7	589 2 B29514	muscarinic acetyl
23	48	40.7	590 2 S10128	muscarinic acetyl
24	48	40.7	590 2 S01114	muscarinic acetyl
25	48	40.7	590 2 S47572	muscarinic acetyl
26	48	40.7	639 2 A55019	muscarinic acetyl
27	47	39.8	352 2 B69901	fatty-acid desatur
28	47	39.8	478 2 C29514	muscarinic acetyl
29	47	39.8	479 2 S10127	muscarinic acetyl

RESULT 1

A43113
chemokine (C-C) receptor 5 - human
N:Alternate names: C-C CKR-5; CCR5
C:Species: Homo sapiens (man)
C>Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text_change 20-Jun-2000
C:Accession: A43113; S71808; A58834; A58832; G02653; A58833
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A:Title: Molecular cloning and functional expression of a new human CC-chemokine receptor:
A:Reference number: A43113; MUID:96241590; PMID:8639485
A:Accession: A43113
A:Molecule type: mRNA
A:Residues: 1-352 <SAM1>
A:Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811
R:Samson, M.; Libert, P.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pau
Nature 382, 722-725, 1996
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of
A:Reference number: S71808; MUID:96345670; PMID:8751444
A:Accession: S71808
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206;207-230 <SAM2>
A:Accession: A58834
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184, 'IKDSHLGAGPAAACHGHLILGNPKNSASVSK' <SAM3>
A:Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A:Note: this frameshift mutation results in a non-functional receptor but confers a degra
nd may have had a selective advantage by conferring resistance to Yersinia plague infecti
R:Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rece
A:Reference number: A58832; MUID:96295970; PMID:8699119
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A:Experimental source: Clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadiere, C.
Submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89, 'L', 91-352 <COM2>
A:Cross-references: EMBL:U057840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine
A:Reference number: A58833; MUID:96291862; PMID:8663314

ALIGNMENTS

muscarinic acetyl
probable sugar tra
hypothetical prote
glutamine ABC tran
macrophage inflam
G protein-coupled
G protein-coupled
hypothetical prote
DNA-directed RNA p
hypothetical prote
probable G protein
G protein-coupled
pentamidine resist
guanylate cyclase
guanylate cyclase-

30 47 39.8 479 2 S33776
31 47 39.8 507 2 T01844
32 46.5 39.4 87 2 T31013
33 46 39.0 216 2 E69633
34 46 39.0 355 2 I49339
35 46 39.0 374 2 S42628
36 46 39.0 374 2 S32785
37 46 39.0 613 2 T28952
38 45.5 38.6 1070 2 C29959
39 45 38.1 312 2 T25510
40 45 38.1 354 2 I58186
41 45 38.1 355 2 JC5067
42 44.5 37.7 423 2 S67163
43 44 37.3 199 2 S68838
44 44 37.3 201 2 C55331
45 44 37.3 202 2 B55331

A;Accession: A58833
 A;Molecule type: mRNA
 A;Residues: 1-352 <RAP>
 A;Cross-references: GB:U54984; NID:gl1457945; PIDN:AAC50598.1; PID:gl1457946
 C;Comment: This is a receptor for chemokines MIP-lalpha (see PIR:A30574), MIP-lbeta (see PIR:A30575) and dual-tropic strains of HIV-1 bind to a complex of chemokine (C-C) receptor 2 and dual-tropic strains of HIV-1 bind to a complex of chemokine (C-C) receptor 2.
 C;Genetics:
 A;Gene: GDB:CMKBR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
 A;Cross-references: GDB:1230510; OMIM:601373
 A;Map position: 3p21-3p21
 C;Function:
 A;Description: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta and RANTES.
 A;Note: probably acts to control granulocyte proliferation and differentiation
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;132-56/Domain: transmembrane #status predicted <TM1>
 F;167-87/Domain: transmembrane #status predicted <TM2>
 F;103-124/Domain: transmembrane #status predicted <TM3>
 F;142-166/Domain: transmembrane #status predicted <TM4>
 F;193-218/Domain: transmembrane #status predicted <TM5>
 F;236-257/Domain: transmembrane #status predicted <TM6>
 F;285-300/Domain: transmembrane #status predicted <TM7>
 F;20-269,101-178/disulfide bonds: #status predicted
 F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
 F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 118; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.5e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVILLNTFOEFGFLNCS 22
 DB 249 APYIVILLNTFOEFGFLNCS 270

RESULT 2
 Jc2443
 chemokine (C-C) receptor 2, splice form B - human
 N;Alternate names: C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine receptor
 C;Species: Homo sapiens (man)
 C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
 C;Accession: Jc2443; I38463
 R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
 A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor
 A;Reference number: Jc2443; MUID:94324942; PMID:8048929
 A;Accession: Jc2443
 A;Molecule type: mRNA
 A;Residues: 1-360 <YAM>
 A;Cross-references: DBJ:J29884; NID:G531246; PIDN:BA06253.1; PID:G531247
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A;Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2
 A;Reference number: A53477; MUID:94195821; PMID:8146186
 A;Accession: I38463
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-360 <RES>
 A;Cross-references: EMBL:U03905; NID:G472557; PIDN:AAA19120.1; PID:G472558
 C;Genetics:
 A;Gene: GDB:CMKBR2
 A;Cross-references: GDB:337364; OMIM:601267
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
 F;43-70/Domain: transmembrane #status predicted <TM1>
 F;81-100/Domain: transmembrane #status predicted <TM2>
 F;115-136/Domain: transmembrane #status predicted <TM3>
 F;154-178/Domain: transmembrane #status predicted <TM4>
 F;207-226/Domain: transmembrane #status predicted <TM5>
 F;244-268/Domain: transmembrane #status predicted <TM6>
 F;287-309/Domain: transmembrane #status predicted <TM7>

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;113-190/disulfide bonds: #status predicted

Query Match 87.3%; Score 103; DB 2; Length 360;
 Best Local Similarity 90.0%; Pred. No. 9.3e-09;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVILLNTFOEFGFLNCS 21
 DB 258 PYNIVILLNTFOEFGFLNCS 277

RESULT 3
 I38450
 chemokine (C-C) receptor 2, splice form A - human
 N;Alternate names: C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine receptor
 C;Species: Homo sapiens (man)
 C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
 C;Accession: I38450
 R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A;Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2
 A;Reference number: A53477; MUID:94195821; PMID:8146186
 A;Accession: I38450
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-374 <RES>
 A;Cross-references: EMBL:U03882; NID:G472555; PIDN:AAA19119.1; PID:G472556
 C;Genetics:
 A;Gene: GDB:CMKBR2
 A;Cross-references: GDB:337364; OMIM:601267
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
 F;44-68/Domain: transmembrane #status predicted <TM1>
 F;79-99/Domain: transmembrane #status predicted <TM2>
 F;115-136/Domain: transmembrane #status predicted <TM3>
 F;154-178/Domain: transmembrane #status predicted <TM4>
 F;208-226/Domain: transmembrane #status predicted <TM5>
 F;244-265/Domain: transmembrane #status predicted <TM6>
 F;292-309/Domain: transmembrane #status predicted <TM7>
 F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;113-190/disulfide bonds: #status predicted

Query Match 87.3%; Score 103; DB 2; Length 374;
 Best Local Similarity 90.0%; Pred. No. 9.6e-09;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVILLNTFOEFGFLNCS 21
 DB 258 PYNIVILLNTFOEFGFLNCS 277

RESULT 4
 Jc5942
 chemokine receptor - human
 C;Species: Homo sapiens (man)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C;Accession: Jc5942
 R;Pan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
 Biochem. Biophys. Res. Commun. 243, 264-268, 1998
 A;Title: Cloning and characterization of a novel human chemokine receptor.
 A;Reference number: Jc5942; MUID:98139902; PMID:9473515
 A;Accession: Jc5942
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-344 <PAN>
 A;Cross-references: GB:U97123; NID:G2897070; PIDN:AAC39595.1; PID:G2897071
 C;Superfamily: vertebrate rhodopsin

Query Match 59.3%; Score 70; DB 2; Length 344;
 Best Local Similarity 57.1%; Pred. No. 0.0018;
 Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOFFGLNNC 21
 ||||| |::| |::|
 Db 252 APYNIAFFLSTFKHFSLSDC 272

RESULT 5
 A45177
 chemokine (C-C) receptor 1 - human
 N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C;Accession: A45177; I55671
 R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
 Cell 72, 415-425, 1993
 A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C
 A;Reference number: A45177; MUID:93161416; PMID:7679328
 A;Accession: A45177
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-355 <NEO>
 A;Cross-references: GB:110918; NID:G292416; PIDN:AAA36543.1; PID:G292417
 A;Experimental source: HL60 cells
 A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
 R;Gao, J.
 J. Exp. Med. 177, 1421-1427, 1993
 A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
 A;Reference number: I55671; MUID:93240122; PMID:7683036
 A;Accession: I55671
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-355 <RES>
 A;Cross-references: GB:110918; NID:G292416; PIDN:AAA36543.1; PID:G292417
 C;Genetics:
 A;Gene: GDB:CMKBR1; CMKR-1
 A;Cross-references: GDB:138446; OMIM:601159
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tr
 F;36-60/Domain: transmembrane #status predicted <TM1>
 F;71-91/Domain: transmembrane #status predicted <TM2>
 F;108-129/Domain: transmembrane #status predicted <TM3>
 F;147-171/Domain: transmembrane #status predicted <TM4>
 F;205-223/Domain: transmembrane #status predicted <TM5>
 F;240-264/Domain: transmembrane #status predicted <TM6>
 F;288-305/Domain: transmembrane #status predicted <TM7>
 F;5/Binding site: carbohydrate (asn) (covalent) #status predicted
 F;24-273,106-183/Disulfide bonds: #status predicted
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 47.5%; Score 56; DB 2; Length 355;
 Best Local Similarity 40.0%; Pred. No. 0.33;
 Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOFFGLNNC 21
 ||||| |::| |::|
 Db 254 PYNLTILISVFQDFLFTHC 273

RESULT 6
 T07448
 Probable DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Japanese black pine chlor
 C;Species: Chloroplast Pinus thunbergiana (Japanese black pine)
 C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 18-Aug-2000
 C;Accession: T07448
 R;Makasugi, T.; Tsudzuki, J.; Ito, S.; Nakaashima, K.; Tsudzuki, T.; Sugiura, M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
 A;Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
 A;Reference number: Z16030; MUID:95024047; PMID:7937893
 A;Accession: T07448
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1075 <WAX>

A:Molecule type: DNA
A:Residues: 1-355 <PON>
A:Cross-references: ENBL:U49727; NID:gl477560; PIDN:AAB09726.1; PID:gl477561
R:Combadhere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A:Reference number: A57237; MUID:95348056; PMID:7622448
A:Accession: A57237
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
A:Cross-references: GB:U28694; NID:gl199579; PIDN:AAC50469.1; PID:gl199580
A>Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.
C:Genetics:
A:Gene: GDB:CMKBR3
A:Cross-references: GDB:579624; OMIM:601268
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-261/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:24-273, 106-183/disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 355;
Best Local Similarity 40.0%; Pred. No. 1.4;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFGLNLC 21
|||:||||:|
Db 254 PYNVAILSSVQSILFGNDC 273

RESULT 9
JC4587
chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: JC4587
R:Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A:Reference number: JC4587; MUID:96136324; PMID:8573157
A:Accession: JC4587
A:Molecule type: mRNA
A:Residues: 1-360 <HOO>
A:Cross-references: ENBL:X90862; NID:gl167851; PIDN:CRA62372.1; PID:gl167852
A:Experimental source: thymus
C:Genetics:
A:Gene: cc ckr-4
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
F:2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:2,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 360;
Best Local Similarity 47.6%; Pred. No. 1.5;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFGLNLC 22
|||:||||:|
Db 257 PYNVVLFTLVEVLQDCT 277

RESULT 10
S55594

G protein-coupled receptor E1 - equine herpesvirus 2
C:Species: equine herpesvirus 2
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: S55594
R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:Title: The DNA sequence of equine herpesvirus 2.
A:Reference number: S55594; MUID:95302501; PMID:7783207
A:Accession: S55594
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-383 <TEL>
A:Cross-references: GB:U20824; NID:ig695172; PIDN:AAC13788.1; PID:ig695173
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 44.1%; Score 52; DB 2; Length 383;
Best Local Similarity 90.9%; Pred. No. 1.6;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
|||||:|
Db 293 PYNIVLLSTF 303

RESULT 11
JH0197
muscarinic acetylcholine receptor M2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 24-Nov-1999
C:Accession: JH0197; D37121
R:Lai, J.; Bloom, J.W.; Yamamura, H.I.; Roeske, W.R.
Life Sci. 47, 1001-1013, 1990
A:Title: Amplification of the rat m2 muscarinic receptor gene by the polymerase chain re
A:Reference number: JH0197; MUID:91041524; PMID:2172674
A:Accession: JH0197
A:Molecule type: DNA
A:Residues: 1-466 <LAI>
R:Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invol
A:Reference number: A37121; MUID:90337982; PMID:2380182
A:Accession: D37121
A>Status: preliminary
A:Molecule type: protein
A:Residues: 60-122 <KUR>
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmem
F:23-48/Domain: transmembrane #status predicted <TM1>
F:61-85/Domain: transmembrane #status predicted <TM2>
F:98-119/Domain: transmembrane #status predicted <TM3>
F:139-162/Domain: transmembrane #status predicted <TM4>
F:184-207/Domain: transmembrane #status predicted <TM5>
F:389-409/Domain: transmembrane #status predicted <TM6>
F:421-442/Domain: transmembrane #status predicted <TM7>

Query Match 44.1%; Score 52; DB 2; Length 466;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTF 12
|||||:|
Db 401 APYNIVLLNTF 412

RESULT 12
S10126
muscarinic acetylcholine receptor M2 - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Nov-1999
C:Accession: S10126
R:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987

A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of muscarinic acetylcholine receptors in the rat brain
A;Reference number: S04326; MUID:88166632; PMID:3443095
A;Accession: S10126
A;Molecule type: DNA
A;Residues: 1-466 <P>
A;Cross-references: EMBL:X15264; NID:g32319; PIDN:CAA33335.1; PID:g32320
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase C
F;23-48/Domain: transmembrane #status predicted <TM1>
F;60-89/Domain: transmembrane #status predicted <TM2>
F;98-119/Domain: transmembrane #status predicted <TM3>
F;139-162/Domain: transmembrane #status predicted <TM4>
F;184-207/Domain: transmembrane #status predicted <TM5>
F;389-409/Domain: transmembrane #status predicted <TM6>
F;421-442/Domain: transmembrane #status predicted <TM7>
F;2,6,9/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 466;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTF 12
|||||:|:|:|
Db 401 APYINVLLNTF 412

RESULT 13
S10856
muscarinic acetylcholine receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999
C;Accession: S10856
F;60-89/Domain: transmembrane #status predicted <TM1>
F;98-119/Domain: transmembrane #status predicted <TM2>
F;139-162/Domain: transmembrane #status predicted <TM3>
F;184-207/Domain: transmembrane #status predicted <TM4>
F;389-409/Domain: transmembrane #status predicted <TM5>
F;421-442/Domain: transmembrane #status predicted <TM6>
F;2,6,9/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 466;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTF 12
|||||:|:|:|
Db 401 APYINVLLNTF 412

RESULT 14
A27386
muscarinic acetylcholine receptor, cardiac - pig
N;Alternate names: muscarinic acetylcholine receptor M2
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2000
C;Accession: A27386; A25656
R;Peralta, B.G.; Winslow, J.W.; Peterson, G.L.; Smith, D.H.; Askenazi, A.; Ramachandran
Science 236, 600-605, 1987
A;Title: Primary structure and biochemical properties of an M-2 muscarinic receptor.
A;Reference number: A27386; MUID:87206169; PMID:3107123
A;Accession: A27386
A;Molecule type: DNA; mRNA
A;Residues: 1-466 <P>

A;Cross-references: GB:M16331; NID:g164311; PIDN:AAA30986.1; PID:g164313
A;Experimental source: atrial muscle
A;Note: the protein sequence derived from the mRNA clones differs from that of the genomic
R;Castro, J.
FEBS Lett. 209, 367-372, 1986
A;Title: Primary structure of porcine cardiac muscarinic acetylcholine receptor deduced from
A;Reference number: A25656; MUID:87080790; PMID:3792555
A;Accession: A25656
A;Molecule type: mRNA
A;Residues: 1-329, 'K', 331-466 <K>
A;Cross-references: GB:X04708; NID:g1859; PIDN:CAA28413.1; PID:g1860
C;Superfamily: vertebrate rhodopsin
C;Keywords: cardiac muscle; G protein-coupled receptor; glycoprotein; heart; neurotransmitter
F;23-48/Domain: transmembrane #status predicted <TM1>
F;61-85/Domain: transmembrane #status predicted <TM2>
F;98-119/Domain: transmembrane #status predicted <TM3>
F;139-162/Domain: transmembrane #status predicted <TM4>
F;184-207/Domain: transmembrane #status predicted <TM5>
F;389-409/Domain: transmembrane #status predicted <TM6>
F;421-442/Domain: transmembrane #status predicted <TM7>

Query Match 44.1%; Score 52; DB 2; Length 466;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTF 12
|||||:|:|:|
Db 401 APYINVLLNTF 412

RESULT 15
A29476
muscarinic acetylcholine receptor M4 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Feb-2000
C;Accession: A29476
R;Braun, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 149, 125-132, 1987
A;Title: A novel subtype of muscarinic receptor identified by homology screening.
A;Reference number: A29476; MUID:88077068; PMID:3120722
A;Accession: A29476
A;Molecule type: mRNA
A;Residues: 1-589
A;Cross-references: GB:M18086; NID:g202657; PIDN:AAA40659.1; PID:g202658
C;Experimental source: brain
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane
F;67-90/Domain: transmembrane #status predicted <TM1>
F;104-124/Domain: transmembrane #status predicted <TM2>
F;142-163/Domain: transmembrane #status predicted <TM3>
F;184-206/Domain: transmembrane #status predicted <TM4>
F;230-251/Domain: transmembrane #status predicted <TM5>
F;492-512/Domain: transmembrane #status predicted <TM6>
F;527-545/Domain: transmembrane #status predicted <TM7>

Query Match 43.2%; Score 51; DB 2; Length 589;
Best Local Similarity 61.5%; Pred. No. 3.5;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFQ 14
|||||:|:|:|
Db 505 PYNIVLLNTFQ 517

RESULT 16
A35546
muscarinic acetylcholine receptor M4 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 21-Jul-2000
C;Accession: A35546
R;Tietje, K.M.; Goldman, P.S.; Nathanson, N.M.
J. Biol. Chem. 265, 2828-2834, 1990

```

A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-359 <RES>
A:Cross-references: EMBL:U28406; NID:g881551; PID:g881552
C:Superfamily: vertebrate rhodopsin

Query Match      40.7%; Score 48; DB 2; Length 359;
Best Local Similarity 45.0%; Pred. No. 6.4;
Matches          9; Conservative      8; Indels      0; Gaps      0;

QY      2 PYNIVLLNTTQEFFGLNNC 21
|||:||| : | : |
DB      258 PYNIVLLFSAFHSTFLETSC 277

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S48657
 muscarinic acetylcholine receptor MR - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: S48657; S24948
 R:Hertera, L.; Carvallo, P.; Antonelli, M.; Olate, J.
 FEBS Lett. 352, 175-179, 1994
 A:Title: Cloning of a Xenopus laevis muscarinic receptor encoded by an intronless gene.
 A:Reference number: S48657; MUID:95010703; PMID:7925970
 A:Accession: S48657
 A:Molecule type: mRNA
 A:Residues: 1-484 <HER>
 A:Cross-references: GB:X65865; NID:G64900; PIDN:CAA4694.1; PID:G64901
 R:Olate, J.
 submitted to the EMBL Data Library, April 1992
 A:Reference number: S24948
 A:Accession: S24948
 A:Molecule type: mRNA
 A:Residues: 1-131, 'X', 133-484 <OLA>
 A:Cross-references: EMBL:X65865; NID:G64900; PID:G64901
 C:Superfamily: vertebrate rhodopsin
 F:73-58/Domain: transmembrane #status predicted <TM1>
 F:71-95/Domain: transmembrane #status predicted <TM2>
 F:108-129/Domain: transmembrane #status predicted <TM3>
 F:149-172/Domain: transmembrane #status predicted <TM4>
 F:194-217/Domain: transmembrane #status predicted <TM5>
 F:407-427/Domain: transmembrane #status predicted <TM6>
 F:439-460/Domain: transmembrane #status predicted <TM7>
 Query Match 40.7%; Score 48; DB 2; Length 484;
 Best Local Similarity 63.6%; Pred. No. 8.7;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PYNIVLLNTF 12
 Db 420 PYNVWLNTF 430
 RESULT 22
 B29514
 muscarinic acetylcholine receptor M3 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Feb-2000
 C:Accession: B94518; B94293; B37121; B29514
 R:Bonner, T.I.
 submitted to GenBank, July 1987
 A:Reference number: A94518
 A:Accession: B94518
 A:Molecule type: mRNA
 A:Residues: 1-589 <BO1>
 R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
 Science 237, 527-532, 1987
 A:Title: Identification of a family of muscarinic acetylcholine receptor genes.
 A:Reference number: A94293; MUID:87263421; PMID:3037705
 A:Accession: B94293
 A:Molecule type: mRNA
 A:Residues: 1-269,463-589 <BO2>
 A:Experimental source: cerebral cortex
 A:Note: only a part of the protein translation is given; none of the nucleotide sequence
 R:Kurenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
 J. Biol. Chem. 265, 13702-13708, 1990
 A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies inv
 A:Reference number: A37121; MUID:90337982; PMID:2380182
 A:Accession: B37121
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 104-166 <KUR>
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
 F:67-90/Domain: transmembrane #status predicted <TM1>
 F:104-124/Domain: transmembrane #status predicted <TM2>
 F:142-163/Domain: transmembrane #status predicted <TM3>

F:184-206/Domain: transmembrane #status predicted <TM4>
 F:230-251/Domain: transmembrane #status predicted <TM5>
 F:492-512/Domain: transmembrane #status predicted <TM6>
 F:527-545/Domain: transmembrane #status predicted <TM7>
 F:6,15,41,48,52/Binding site: carboxylate (Asn) (covalent) #status predicted
 Query Match 40.7%; Score 48; DB 2; Length 589;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PYNIVLLNTF 12
 Db 505 PYNIMVLNTF 515
 RESULT 23
 S10128
 muscarinic acetylcholine receptor M4 - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Feb-2000
 C:Accession: S10128
 R:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
 EMBO J. 6, 3923-3929, 1987
 A:Title: Distinct primary structures, ligand-binding properties and tissue-specific expre
 A:Reference number: S04336; MUID:89166632; PMID:3443095
 A:Accession: S10128
 A:Molecule type: DNA
 A:Residues: 1-590 <PER>
 A:Cross-references: EMBL:X15266; NID:G32323; PIDN:CAA33337.1; PID:G32324
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmen
 F:68-95/Domain: transmembrane #status predicted <TM1>
 F:105-131/Domain: transmembrane #status predicted <TM2>
 F:143-164/Domain: transmembrane #status predicted <TM3>
 F:185-207/Domain: transmembrane #status predicted <TM4>
 F:231-252/Domain: transmembrane #status predicted <TM5>
 F:493-513/Domain: transmembrane #status predicted <TM6>
 F:525-546/Domain: transmembrane #status predicted <TM7>
 F:5,6,15,41/Binding site: carboxylate (Asn) (covalent) #status predicted
 Query Match 40.7%; Score 48; DB 2; Length 590;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PYNIVLLNTF 12
 Db 506 PYNIMVLNTF 516
 RESULT 24
 S01114
 muscarinic acetylcholine receptor M2, glandular - pig
 N:Alternate names: muscarinic acetylcholine receptor III
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Feb-2000
 C:Accession: S01114
 R:Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.
 FEBS Lett. 235, 257-261, 1988
 A:Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonis
 A:Reference number: S01114; MUID:88296835; PMID:3402600
 A:Accession: S01114
 A:Molecule type: DNA
 A:Residues: 1-590 <AKT>
 A:Cross-references: EMBL:X12712; NID:G1861; PIDN:CAA31215.1; PID:G1862
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmen
 F:68-91/Domain: transmembrane #status predicted <TM1>
 F:105-125/Domain: transmembrane #status predicted <TM2>
 F:143-164/Domain: transmembrane #status predicted <TM3>
 F:185-207/Domain: transmembrane #status predicted <TM4>
 F:231-253/Domain: transmembrane #status predicted <TM5>
 F:493-513/Domain: transmembrane #status predicted <TM6>
 F:528-546/Domain: transmembrane #status predicted <TM7>

Query Match 40.7%; Score 48; DB 2; Length 590;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
 |||:::|
 Db 506 PYNIMVLVNTF 516

RESULT 25
 S47572
 muscarinic acetylcholine receptor m3 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Feb-2000
 C:Accession: S47572
 R:Lee, P.H.K.; Hodges, P.K.; Glickman, P.; Chang, K.J.
 Biochim. Biophys. Acta 1223, 151-154, 1994
 A:Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 re
 A:Reference number: S47572; MUID:94339178; PMID:8061048
 A:Accession: S47572
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-590 <LEB>
 A:Cross-references: EMBL:U08286; NID:9520465; PIDN:AAA51866.1; PID:9520466
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 40.7%; Score 48; DB 2; Length 590;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
 |||:::|
 Db 506 PYNIMVLVNTF 516

RESULT 26
 A55019
 muscarinic acetylcholine receptor, M3 isoform - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 21-Jul-2000
 C:Accession: A55019
 R:Gadbut, A.P.; Galper, J.B.
 J. Biol. Chem. 269, 25823-25829, 1994
 A:Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and
 A:Reference number: A55019; MUID:95014393; PMID:7929287
 A:Accession: A55019
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-639 <GAD>
 A:Cross-references: GB:L10617; NID:9530097; PIDN:AAA65961.1; PID:9530098
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 40.7%; Score 48; DB 2; Length 639;
 Best Local Similarity 72.7%; Pred. No. 12;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
 |||:::|
 Db 556 PYNIMVLVNTF 566

RESULT 27
 B69901
 fatty-acid desaturase homolog yocE - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C:Accession: B69901
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert
 Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.;
 Koether, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauviel,
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A:Authors: Schleith, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: B69901
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-352 <KUN>
 A:Cross-references: GB:Z99114; GB:AL009126; NID:92634230; PIDN:CAB13810.1; PID:92634311
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yocE
 C:Superfamily: omega-3 fatty acid desaturase

Query Match 39.8%; Score 47; DB 2; Length 352;
 Best Local Similarity 60.0%; Pred. No. 9.1;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 NIVLLNTQEFFGL 18
 ::::|
 Db 28 SLIQLLNTPIPFGL 42

RESULT 28
 C29514
 muscarinic acetylcholine receptor M4 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999
 C:Accession: C94518; C94293; E37121; C29514
 R:Bonner, T.I.
 submitted to GenBank, July 1987
 A:Reference number: A94518
 A:Accession: C94518
 A:Molecule type: mRNA
 A:Residues: 1-478 <BOI>
 R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
 Science 237, 527-532, 1987
 A:Title: Identification of a family of muscarinic acetylcholine receptor genes.
 A:Reference number: A94293; MUID:87263421; PMID:3037705
 A:Accession: C94293
 A:Molecule type: mRNA
 A:Residues: 1-233;373-478 <BO2>
 A:Experimental source: cerebral cortex
 A>Note: only a part of the protein translation is given; none of the nucleotide sequence
 R:Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
 J. Biol. Chem. 265, 13702-13708, 1990
 A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invol
 A:Reference number: A37121; MUID:90337982; PMID:2380182
 A:Accession: E37121
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 68-130 <KUR>
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho

Query Match 39.8%; Score 47; DB 2; Length 478;

Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
||||:|:|:|
Db 414 PYNVMVLVNTF 424

RESULT 29
S10127
muscarinic acetylcholine receptor M3 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Nov-1999
C;Accession: S10127
R;Paralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of three human muscarinic acetylcholine receptor subtypes
A;Reference number: S04326; MUID:8816632; PMID:3443095
A;Accession: S10127
A;Molecule type: DNA
A;Residues: 1-479 <PER>
A;Cross-references: EMBL:X15265; NID:g32321; PIDN:CAA33336.1; PID:g32322
C;Superfamily: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatidylinositol 3-OH kinase activator
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatidylinositol 3-OH kinase activator
F;32-57/Domain: transmembrane #status predicted <TM1>
F;70-94/Domain: transmembrane #status predicted <TM2>
F;106-128/Domain: transmembrane #status predicted <TM3>
F;148-171/Domain: transmembrane #status predicted <TM4>
F;192-216/Domain: transmembrane #status predicted <TM5>
F;401-422/Domain: transmembrane #status predicted <TM6>
F;433-456/Domain: transmembrane #status predicted <TM7>
F;3,8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.8%; Score 47; DB 2; Length 479;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
||||:|:|:|
Db 415 PYNVMVLVNTF 425

RESULT 30
S33776
muscarinic acetylcholine receptor m4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 24-Nov-1999
C;Accession: S33776; S33135
R;van Koppen, C.J.; Lenz, W.; Nathanson, N.M.
Biochim. Biophys. Acta 1173, 342-344, 1993
A;Title: Isolation, sequence and functional expression of the mouse m4 muscarinic acetylcholine receptor cDNA
A;Reference number: S33776; MUID:93305731; PMID:7916637
A;Accession: S33776
A;Molecule type: DNA
A;Residues: 1-479 <KOP>
A;Cross-references: EMBL:X63473; NID:g296913; PIDN:CAA45071.1; PID:g296914
C;Superfamily: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatidylinositol 3-OH kinase activator
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatidylinositol 3-OH kinase activator
F;31-56/Domain: transmembrane #status predicted <TM1>
F;69-93/Domain: transmembrane #status predicted <TM2>
F;106-127/Domain: transmembrane #status predicted <TM3>
F;147-170/Domain: transmembrane #status predicted <TM4>
F;192-215/Domain: transmembrane #status predicted <TM5>
F;402-422/Domain: transmembrane #status predicted <TM6>
F;434-455/Domain: transmembrane #status predicted <TM7>

Query Match 39.8%; Score 47; DB 2; Length 479;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
||||:|:|:|
Db 415 PYNVMVLVNTF 425

RESULT 31
T01844
Probable sugar transport protein PSD12.9 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Sep-1999
C;Accession: T01844
R;Murray, J.; Langston, Y.; Ahrens, C.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of Arabidopsis thaliana F9D12.
A;Reference number: Z14444
A;Accession: T01844
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-507 <MUR>
A;Cross-references: EMBL:AF077407; NID:g3319339; PIDN:AAC26232.1; PID:g3319343
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
A;Introns: 44/1; 150/3; 359/3
A;Note: F9D12.9
C;Superfamily: glucose transport protein
C;Keywords: sugar transport; transmembrane protein
Query Match 39.8%; Score 47; DB 2; Length 507;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFQBFGLN 19
|:|:|:|:|:|:|
Db 280 PFVIGMLQFFQFTGIN 297

RESULT 32
T31013
hypothetical protein 87 - Sulfolobus sp. plasmid pNOB8
C;Species: Sulfolobus sp.
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T31013
R;She, Q.; Phan, H.; Garrett, R.A.; Albers, S.V.; Stedman, K.M.; Zillig, W.
Extremophiles 2, 417-425, 1998
A;Title: Genetic profile of pNOB8 from Sulfolobus: the first conjugative plasmid from an extremophile
A;Reference number: Z20959; MUID:9044580; PMID:9827331
A;Accession: T31013
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-87 <SHE>
A;Cross-references: EMBL:AJ010405; NID:el351926; PID:el351935; PIDN:CAA09119.1
A;Experimental source: strain NOB8H2
C;Genetics:
A;Genome: plasmid pNOB8

Query Match 39.4%; Score 46.5; DB 2; Length 87;
Best Local Similarity 47.4%; Pred. No. 2.6;
Matches 9; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 3 YNIVLL-LNTFOFFGLNN 20
|||:|:|:|:|:|
Db 18 YNIIHISNFIQLGLNN 36

RESULT 33
E69633
glutamine ABC transporter (membrane protein) glmM - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: E69633
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Ewing, J.; Fabre, C.; Ferrari, E.; Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier

Db 459 ILNTFNKIFGLN 470

RESULT 38

C29959

DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - spinach chloroplast

C;Species: chloroplast Spinacia oleracea (spinach)

C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 18-Jun-1999

C;Accession: C29959

R;Hudson, G.S.; Holton, T.A.; Whitfield, P.R.; Bottomley, W.

J. Mol. Biol. 200, 639-654, 1988

A;Title: Spinach chloroplast rpoBC genes encode three subunits of the chloroplast RNA po

A;Reference number: A29959; MUID:88316931; PMID:3045324

A;Accession: C29959

A;Molecule type: DNA

A;Residues: 1-1070 <HUD>

A;Cross-references: GB:M55297; NID:G295119; PIDN:AAA84637.1; PID:G295121

C;Genetics:

A;Gene: rpoB

A;Genome: chloroplast

C;Superfamily: DNA-directed RNA polymerase beta chain

C;Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 38.6%; Score 45.5; DB 2; Length 1070;

Best Local Similarity 45.8%; Pred. No. 50;

Matches 11; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

Qy 2 PYNIVL---LLNTFQEFFGLNCS 22

Db 352 PQNLVTSTPLTTTFESFFGLHPLS 375

RESULT 39

T25510

hypothetical protein C04E6.10 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Jun-2000

C;Accession: T25510

R;Bentley, D.; Gattung, S.

submitted to the EMBL Data Library, April 1997

A;Description: The sequence of C. elegans cosmid C04E6.

A;Reference number: 220043

A;Accession: T25510

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-312 <BEN>

A;Cross-references: EMBL:U97012; PIDN:AAB52330.1; GSPDB:GN00023; CESP:C04E6.10

A;Experimental source: strain Bristol N2; clone C04E6

C;Genetics:

A;Gene: CESP:C04E6.10

A;Map position: 5

A;Introns: 68/2; 97/2; 148/3; 241/3; 263/1

C;Superfamily: Caenorhabditis hypothetical protein C49G7.2

Query Match 38.1%; Score 45; DB 2; Length 312;

Best Local Similarity 44.4%; Pred. No. 17;

Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 5 IVLLNTFQEFFGLNCS 22

Db 78 ITYILNGFTVFLSTCA 95

RESULT 40

I58186

probable G protein-coupled receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C;Accession: I58186

R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.

Neurosci. Lett. 169, 85-89, 1994

A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and h

A;Reference number: I58186; MUID:94323113; PMID:8047298

A;Accession: I58186

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-354 <RES>

A;Cross-references: EMBL:U04808; NID:G2538635; PIDN:AAB87093.1; PID:G439861

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 38.1%; Score 45; DB 2; Length 354;

Best Local Similarity 58.8%; Pred. No. 19;

Matches 10; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Qy 2 PYNIVLLNT--FOEFF 16

Db 247 PYNIVIFLETLKFNFF 263

Search completed: September 28, 2004, 09:07:10

Job time : 13.075 secs

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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:55:11 ; Search time 6.875 Seconds
(without alignments)
166.624 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYNIVLLNTQEFPLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118	100.0	352	1	CKR5_CERAE
2	118	100.0	352	1	CKR5_CERP
3	118	100.0	352	1	CKR5_CERTO
4	118	100.0	352	1	CKR5_GORGO
5	118	100.0	352	1	CKR5_HUMAN
6	118	100.0	352	1	CKR5_HYLLE
7	118	100.0	352	1	CKR5_HYLLM
8	118	100.0	352	1	CKR5_HYLSY
9	118	100.0	352	1	CKR5_MACMU
10	118	100.0	352	1	CKR5_PANTR
11	118	100.0	352	1	CKR5_PAPHA
12	118	100.0	352	1	CKR5_PONPY
13	118	100.0	352	1	CKR5_PYGBI
14	118	100.0	352	1	CKR5_PYGNE
15	118	100.0	352	1	CKR5_TRAPR
16	118	100.0	352	1	CKR5_TRAPH
17	108	91.5	354	1	CKR5_MOUSE
18	105	89.0	354	1	CKR5_RAT
19	103	87.3	360	1	CKR2_MACMU
20	103	87.3	374	1	CKR2_HUMAN
21	87	73.7	373	1	CKR2_RAT
22	79	66.9	373	1	CKR2_MOUSE
23	56	47.5	355	1	CKR1_HUMAN
24	54.5	46.2	1075	1	RPOB_FINTH
25	53	44.9	360	1	CKR4_HUMAN
26	52	44.1	355	1	CKR3_HUMAN
27	52	44.1	359	1	CKR3_RAT
28	52	44.1	360	1	CKR4_MOUSE
29	52	44.1	440	1	ACM2_PANTR
30	52	44.1	466	1	ACM2_HUMAN
31	52	44.1	466	1	ACM2_MOUSE
32	52	44.1	466	1	ACM2_PIG
33	52	44.1	466	1	ACM2_RAT

34 51.5 43.6 355 1 CKR3_CERAE P56492 cercopithec
35 51.5 43.6 355 1 CKR3_MACMU P56483 macaca mula
36 51 43.2 355 1 CKR1_MACMU P56482 macaca mula
37 50 42.4 490 1 ACM4_CHICK P17200 gallus gall
38 48 40.7 342 1 H182_ARCFU O28255 archaeoglob
39 48 40.7 359 1 CKR3_MOUSE P51678 mus musculus
40 48 40.7 484 1 ACM4_XENLA P30544 xenopus lae
41 48 40.7 589 1 ACM3_MOUSE Q9erz3 mus musculus
42 48 40.7 589 1 ACM3_RAT P08483 rattus norv
43 48 40.7 590 1 ACM3_BOVIN P41984 bos taurus
44 48 40.7 590 1 ACM3_GORGO Q9n2a3 gorilla gor
45 48 40.7 590 1 ACM3_HUMAN P20309 homo sapien

ALIGNMENTS

RESULT 1

CKR5_CERAE
ID CKR5_CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=980011387; PubMed=9343222;
RA Kuhnmann S.B., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U03324; AAC51795.1; -;
CC EMBL; U03325; AAC51796.1; -;
CC EMBL; AB015944; BAA31328.1; -;
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00362; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
Polymorphism.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

```

FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT VARIANT 352 352 F -> L.
SQ SEQUENCE 352 AA; 40561 MW; 7528690C72EC29A CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTQFFFGLNCS 22
DB 249 APYNIIVLLNTQFFFGLNCS 270

RESULT 2
CKR5_CERY
ID CKR5_CERY STANDARD; PRT; 352 AA.
AC Q9TV42.
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKBR5.
OS Cercopithecus pygerythrus (Vervet monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=100;
RX MEDLINE=99335215; PubMed=10408730;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
RA Diop O., Rigoulet J., Haire-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with HIV
RT carrier status in African nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC -----
CC EMBL; AF035222; AAD44015.1;
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00337; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00362; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT VARIANT 14 14 N -> Y.
SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTQFFFGLNCS 22
DB 249 APYNIIVLLNTQFFFGLNCS 270

RESULT 3
CKR5_CERTO
ID CKR5_CERTO STANDARD; PRT; 352 AA.
AC Q62743; Q62744; Q62745; Q62746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKBR5.
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate 079; 085, 087, and 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettler A., Ho D.D., Marx P.A.;
RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of primary SIVsm, HIV-2, and SIVmac.";
RL Virology 246:113-124(1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC -----
CC EMBL; AF035222; AAD44015.1;
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.

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DR EMBL; AF051902; AAC39830.1; -
DR EMBL; AF051903; AAC39831.1; -
DR EMBL; AF051904; AAC39832.1; -
DR EMBL; AF051905; AAC39833.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT VARIANT 2 2
FT VARIANT 3 3
FT VARIANT 25 25
FT VARIANT 100 100
FT VARIANT 107 107
FT VARIANT 134 134
FT VARIANT 146 146
FT VARIANT 340 340
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNVLLNTFOEFFGLNCS 22
Db 249 APYNVLLNTFOEFFGLNCS 270

RESULT 4
CKR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
GN CKR5 OR CKR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268697; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by

```

```

CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF005659; AAB62553.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT SEQUENCE 352 AA; 40515 MW; D0B6FCB9FE5EAC84 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNVLLNTFOEFFGLNCS 22
Db 249 APYNVLLNTFOEFFGLNCS 270

RESULT 5
CKR5_HUMAN STANDARD; PRT; 352 AA.
ID CKR5_HUMAN STANDARD; PRT; 352 AA.
AC P51581; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708; O15538; Q9UFA4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS)
DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
GN CKR5 OR CKR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241590; PubMed=8639485;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RT "Molecular cloning and functional expression of a new human

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CC-chemokine receptor gene.";
 RA Biochemistry 35:3362-3367(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96291862; PubMed=8663314;
 RA Report C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
 RT "Molecular cloning and functional characterization of a novel human
 CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";
 RL J. Biol. Chem. 271:17161-17166(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96295970; PubMed=8699119;
 RA Conbadriere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
 RT "Cloning and functional expression of CC CR5, a human monocyte CC
 chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
 RANTES.";
 RL J. Leukoc. Biol. 60:147-152(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98001387; PubMed=9343222;
 RA Kuhnann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 CC implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses.";
 RL J. Virol. 71:8642-8656(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98049523; PubMed=9388201;
 RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
 CC with 5'-end heterogeneity, dual promoter usage, and evidence for
 RT polymorphisms within the regulatory regions and noncoding exons.";
 RL J. Biol. Chem. 272:30662-30671(1997).
 RN [6]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-178.
 RA Magierowska M., Barre-Sinoussi F., Issatras H., Theodorou I.,
 RA Debre P.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98260017; PubMed=8649511;
 RA Deng H., Liu R., Elmeier W., Choe S., Umriz M., Burkhardt M.,
 RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
 RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
 RT "Identification of a major co-receptor for primary isolates of
 HIV-1.";
 RL Nature 381:661-666(1996).
 RN [11]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE=96260018; PubMed=8649512;
 RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
 RA Paxton W.A.;
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
 CC CC-CKR-5.";
 RL Nature 381:667-673(1996).
 RN [12]
 RP SULFATION
 RX MEDLINE=99189752; PubMed=10089882;
 RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
 entry.";
 RL Cell 96:667-676(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and rantes and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation. Acts as co-receptor with CD4 for primary non-
 CC syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1
 CC virus. It promotes Env-mediated fusion of the virus.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Found in promyelocytic cells.
 CC -!- PTM: Sulfation contributes to the efficiency of HIV-1 entry.
 CC -!- PTM: Modified by O-linked glycosylation, but not by N-linked
 CC glycosylation.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X51492; CAA62796.1; -
 CC EMBL; U54994; AAC50598.1; -
 CC EMBL; U57840; AAB17071.1; -
 CC EMBL; U95626; AAB57793.1; -
 CC EMBL; U83326; AAC51797.1; -
 CC EMBL; AF011500; AAB65700.1; -
 CC EMBL; AF011501; AAB65701.1; -
 CC EMBL; AF011502; AAB65702.1; -
 CC EMBL; AF011503; AAB65703.1; -
 CC EMBL; AF011505; AAB65705.1; -
 CC EMBL; AF011506; AAB65706.1; -
 CC EMBL; AF011507; AAB65707.1; -
 CC EMBL; AF011508; AAB65708.1; -
 CC EMBL; AF011509; AAB65709.1; -
 CC EMBL; AF011510; AAB65710.1; -
 CC EMBL; AF011511; AAB65711.1; -
 CC EMBL; AF011512; AAB65712.1; -
 CC EMBL; AF011513; AAB65713.1; -
 CC EMBL; AF011514; AAB65714.1; -
 CC EMBL; AF011515; AAB65715.1; -
 CC EMBL; AF011516; AAB65716.1; -
 CC EMBL; AF011517; AAB65717.1; -
 CC EMBL; AF011518; AAB65718.1; -
 CC EMBL; AF011519; AAB65719.1; -
 CC EMBL; AF011520; AAB65720.1; -
 CC EMBL; AF011521; AAB65721.1; -
 CC EMBL; AF011522; AAB65722.1; -
 CC EMBL; AF011523; AAB65723.1; -
 CC EMBL; AF011524; AAB65724.1; -
 CC EMBL; AF011525; AAB65725.1; -
 CC EMBL; AF011526; AAB65726.1; -
 CC EMBL; AF011527; AAB65727.1; -
 CC EMBL; AF011528; AAB65728.1; -
 CC EMBL; AF011529; AAB65729.1; -
 CC EMBL; AF011530; AAB65730.1; -
 CC EMBL; AF011531; AAB65731.1; -
 CC EMBL; AF011532; AAB65732.1; -

RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry.";
RL J. Virol. 71:2705-2714(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors";
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch.
CC -----
DR EMBL; U77672; AAC51108.1; -;
DR EMBL; U73739; AAC51158.1; -;
DR EMBL; U96762; AAC34132.1; -;
DR EMBL; AF005660; AAB62554.1; -;
DR EMBL; AF005661; AAB62555.1; -;
DR EMBL; AF005662; AAB62556.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 241 241 M -> I (IN REF. 3).
FT CONFLICT 292 292 I -> M (IN REF. 3).
SEQUENCE 352 AA; 40507 MW; 58896C890909FACB2 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. NO. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYINIVLLNTFQFFGLNCS 22
DB 249 APYINIVLLNTFQFFGLNCS 270
RESULT 10
ID_CKRS_PANTR STANDARD; PRT; 352 AA.
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKRS.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX Zimmerman P.A., Buckler-White A., Alkhatib G.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.;
RT "HIV type 1 subtype, coreceptor usage, and CCR5 polymorphism";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97426118; PubMed=9282822;
RA Zacharova V., Zachar V., Goustin A.S.;
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
RT HIV type 1 host";
RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1";
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RN [6]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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EMBL; AF005663; AAB62557.1; -
DR EMBL; U94329; AAB58446.1; -
DR EMBL; AF011542; AAB65742.1; -
DR EMBL; U97666; AAC51670.1; -
DR EMBL; AF011540; AAB65740.1; -
DR EMBL; U89797; AAC03717.1; -
DR EMBL; AF177894; AAK43377.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT TRANSMEM 352 352
FT DISULFID 101 178
FT MOD RES 3 3
FT MOD RES 10 10
FT MOD RES 14 14
FT MOD RES 15 15
FT CARBOHYD 268 268
FT CONFLICT 123 123
SQ SEQUENCE 352 AA; 40539 MW; 4A33B69B80FE34C CRC64;
T -> S (IN REF. 1).
Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVILLNTFFQFFGLNCS 22
DB 249 APYIVILLNTFFQFFGLNCS 270
|||||

RESULT 11
ID_CKRS_PAPHA STANDARD; PRT; 352 AA.
AC P56441;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CC-CR-5) (CCR-5) (CCR5).
GN CCR5 OR CXCR5
OS Papio hamadryas (Hamadryas baboon), and
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557, 9555;
[1]
RN SEQUENCE FROM N.A.
RP SPECIES=P.hamadryas;
RX MEDLINE=97269687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;

RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RP SPECIES=P.hamadryas;
RX MEDLINE=99210133; PubMed=10195758;
RA Sakseena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
RT nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
RN [3]
RP SEQUENCE FROM N.A.
RP SPECIES=P.anubis;
RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokines. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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EMBL; AF005658; AAB62552.1; -
DR EMBL; AF105287; AAD20556.1; -
DR EMBL; AF105288; AAD20557.1; -
DR EMBL; AF105289; AAD20558.1; -
DR EMBL; AF105290; AAD20559.1; -
DR EMBL; AF023452; AAC63830.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD RES 3 3
FT MOD RES 10 10
FT MOD RES 14 14
FT MOD RES 15 15
FT CARBOHYD 268 268
SQ SEQUENCE 352 AA; 40489 MW; 5E150A9BA1FE8B2 CRC64;
Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVILLNTFFQFFGLNCS 22
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Db 249 APYNVILLNTQEFGLNCS 270
RESULT 12
CKR5_PONPY STANDARD; PRT; 352 AA.
AC O9780;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKRS.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OC NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC
CC EMBL; AF075446; AAD19858.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT TRANSMEM 219 235
FT TRANSMEM 236 260
FT TRANSMEM 261 277
FT DOMAIN 278 301
FT TRANSMEM 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;
Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNVILLNTQEFGLNCS 22
|||||

Db 249 APYNVILLNTQEFGLNCS 270
RESULT 13
CKR5_PYGBI STANDARD; PRT; 352 AA.
AC O9780;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKRS.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OC NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075445; AAD19857.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT TRANSMEM 219 235
FT TRANSMEM 236 260
FT TRANSMEM 261 277
FT DOMAIN 278 301
FT TRANSMEM 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;
Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNVILLNTQEFGLNCS 22
|||||
```

Db 249 APYNIIVLLNTQEFFGLNCS 270
|||||

RESULT 14

ID CKR5 PYGNE STANDARD; PRT; 352 AA.
AC 097882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCRS).
GN Pygathrix nemaeus (Dove langur).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; AF075448; AAD19860.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 BY SIMILARITY.
FT DISULFID 101 178 SULFATION (BY SIMILARITY).
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3E961 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNIIVLLNTQEFFGLNCS 22
|||||
Db 249 APYNIIVLLNTQEFFGLNCS 270
|||||

RESULT 15

ID CKR5 TRAFR STANDARD; PRT; 352 AA.
AC 097878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCRS).
GN TRAF5 OR CMKBR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; AF075442; AAD19854.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 BY SIMILARITY.
FT DISULFID 101 178 SULFATION (BY SIMILARITY).
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22 PRT; 352 AA.
DB 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 16
CKR5 TRAPH
ID CKR5 TRAPH STANDARD; PRT; 352 AA.
AC O97879;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: AF075443; AAD19855.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1;
DR PROSITE: PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
DB 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 17
CKR5 MOUSE
ID CKR5 MOUSE STANDARD; PRT; 354 AA.
AC P51682; O35313; O35891; P97308; P97405; Q61867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (MIP-1
DE alpha receptor).
GN CKR5 OR CMKBR5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SvJ; TISSUE=Spleen;
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Monteciarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT 1 alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9";
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96278910; PubMed=8662890;
RA Meyer A., Coyly A.J., Proudfoot A.E.L., Wells T.N.C., Power C.A.;
RT "Cloning and characterization of a novel murine macrophage
RT inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 271:14445-14451(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=129/Ola;
RA Kuziel W.A., Beck W.A., Dawson T.C., Maeda N.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=129;
RX MEDLINE=97404635; PubMed=9261347;
RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
RT "Two distinct CCR5 domains can mediate coreceptor usage by human
RT immunodeficiency virus type 1.";
RL J. Virol. 71:6305-6314(1997).
RN [6]
RP SEQUENCE FROM N.A.
RA Guo B., Kuno K., Harada A., Matsushima K.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.


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Qy 2 PYNIVLLNTFQEFFGLNCS 22
Db 252 PYNIVLLNTFQEFFGLNCS 272

RESULT 19
ID CRK2 MACMU STANDARD; PRT; 360 AA.
AC O18793;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-CR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
GN CCR2 OR CMKBR2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).
CC -1- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=B;
CC IsoId=O18793-1; Sequence=Displayed;
CC Name=A;
CC IsoId=O18793-2; Sequence=Not described;
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; AF013958; AAD11572.1; -
DR InterPro; IPR000276; GPCR_Rhodopn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Alternative splicing.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 70 1 (POTENTIAL).
FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 100 2 (POTENTIAL).
FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 136 3 (POTENTIAL).
FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 178 4 (POTENTIAL).
FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC...) (POTENTIAL).
FT MOD_RES 26 26 SULFATION (BY SIMILARITY).

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FT DISULFID 113 190 BY SIMILARITY.
SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;

Query Match 87.3%; Score 103; DB 1; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTFQEFFGLNCS 21
Db 258 PYNIVLLNTFQEFFGLSNC 277

RESULT 20
ID CRK2 HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 2 (C-CR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
GN CCR2 OR CMKBR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=94195821; PubMed=8146186;
RA Charo I.F., Myers S.J., Herman A., Francis C., Connolly A.J.,
RA Coughlin S.R.;
RT "Molecular cloning and functional expression of two monocyte
RT chemoattractant protein 1 receptors reveals alternative splicing of
RT the carboxyl-terminal tails."
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756 (1994).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=94324942; PubMed=8048929;
RA Yanagani S., Tokuda Y., Ishii K., Tanaka H., Endo N.;
RT "cDNA cloning and functional expression of a human monocyte
RT chemoattractant protein 1 receptor."
RL Biochem. Biophys. Res. Commun. 202:1156-1162 (1994).
RN [3]
SEQUENCE FROM N.A.
RX MEDLINE=97150864; PubMed=9995400;
RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
RT chemoattractant protein 1 receptor gene. Evidence for the role of the
RT carboxyl-terminal tail in receptor trafficking."
RL J. Biol. Chem. 272:1038-1045 (1997).
RN [4]
SEQUENCE FROM N.A.
RP McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Farrell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Baside M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RN Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.
RA Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldansk S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
SULFATION OF TYR-26, AND N-GLYCOSYLATION.
RX MEDLINE=20501139; PubMed=11046064;
RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
RA Chakravarty L., Kolattukudy P.E.;
RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
RT has tyrosine sulfation in a conserved extracellular N-terminal
RT region."

```

```

J. Immunol. 165:5295-5303(2000).
-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
Transduces a signal by increasing the intracellular calcium ions
level. Alternative coreceptor with CD4 for HIV-1 infection.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=A;
IsoId=P41597-1; Sequence=Displayed;
Name=B;
IsoId=P41597-2; Sequence=VSP_001893;
-!- PTM: N-glycosylated.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
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or send an email to license@isb-sib.ch).
-----
EMBL; U03882; AAA19119.1; -
EMBL; U03905; AAA19120.1; -
EMBL; D29984; BAA06253.1; -
EMBL; U80924; AAC51637.1; -
EMBL; U80924; AAC51636.1; -
EMBL; U95626; AAB57791.1; -
EMBL; U95626; AAB57792.1; -
EMBL; AF545480; AAN16400.1; -
PIR; I38450; I38450.
PIR; JC2443; JC2443.
PDB; 1KAD; 14-AUG-02.
PDB; 1KPI; 23-JAN-02.
GeneW; HGNC:1603; CCR2.
MIM; 601267; -
GO; GO:0005887; C: integral to plasma membrane; TAS.
GO; GO:0005625; C: soluble fraction; TAS.
GO; GO:0005625; P: chemokine receptor activity; TAS.
GO; GO:0004950; P: antimicrobial humoral response (sensu Inver. . .); TAS.
GO; GO:0006960; P: cellular defense response; TAS.
GO; GO:0006968; P: chemotaxis; TAS.
GO; GO:0006935; P: cytosolic calcium ion concentration elevation; TAS.
GO; GO:0007204; P: inflammatory response; TAS.
GO; GO:0006954; P: inflammatory growth; TAS.
GO; GO:0007125; P: invasive growth; TAS.
GO; GO:0007259; P: JAK-STAT cascade; TAS.
GO; GO:0007194; P: negative regulation of adenylate cyclase ac. . .; TAS.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm1.1;
PRINTS; PR00237; GPCRHHODOPSN.
PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
PROSITE; PS0262; G-PROTEIN RECEPT_F2_1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
Polymorphism; Alternative splicing; 3D-structure.
EXTRACELLULAR (POTENTIAL).
DOMAIN 1 42
TRANSMEM 43 70
DOMAIN 71 80
TRANSMEM 81 100
TRANSMEM 101 114
EXTRACELLULAR (POTENTIAL).
DOMAIN 115 136
TRANSMEM 137 153
CYTOPLASMIC (POTENTIAL).
DOMAIN 154 178
TRANSMEM 179 206
EXTRACELLULAR (POTENTIAL).
DOMAIN 207 226
TRANSMEM 227 243
CYTOPLASMIC (POTENTIAL).
DOMAIN 244 268
TRANSMEM 269 285
EXTRACELLULAR (POTENTIAL).
DOMAIN 286 309
TRANSMEM 310 374
CYTOPLASMIC (POTENTIAL).
DOMAIN 314 374
N-LINKED (GLCNAC. . .) (POTENTIAL).
MOD RES 14 14
MOD RES 26 26
SULFATION.
FT DISULFID 113 190
FT VARSPPLIC 314 374
SLFHIALGSCRIAPLQKPGVCGPGVPRPGNVKVVTTQGLDGR

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KGKSGIAPASIQDKEGA -> RYLSVFRKHITKRFCK
 QCPVYRETVGVSTINTPSTGEQVSAGL (in
 isoform B)
 /FTid=VSP_001893.
 V -> I (in dbSNP:1799864).
 /FTid=VAR_014339.
 G -> E.
 /FTid=VAR_014340.
 F865E0D39E74CF0F CRC64;
 Query Match 87.3%; Score 103; DB 1; Length 374;
 Best Local Similarity 90.0%; Pred. No. 1, 1e-08;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEPFGLNLC 21
 |||||:|||||:|||||:
 Db 258 PYNIVLLNTQEPFGLSNC 277

RESULT 21
 CKR2 RAT STANDARD; PRT; 373 AA.
 ID CKR2 RAT
 AC O55193;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2).
 GN CCR2 OR CMKBR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA MEDLINE=98318173; PubMed=9655467;
 RX Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 RA deFiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis".
 RL J. Neuroimmunol. 86:1-12(1998).
 CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
 CC chemokines. Transduces a signal by increasing the intracellular
 CC calcium ions level (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
 CC macrophages.
 CC -!- INDUCTION: In animals in which experimental allergic
 CC encephalomyelitis (EAE) has been induced.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U77349; AAC03242.1; -
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm1.1;
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECEPT_F2_1.
 CC G-protein coupled receptor; Transmembrane.
 CC Polymorphism; Alternative splicing; 3D-structure.
 CC EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 1 42
 CC TRANSMEM 43 70
 CC DOMAIN 71 80
 CC TRANSMEM 81 100
 CC TRANSMEM 101 114
 CC EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 115 136
 CC TRANSMEM 137 153
 CC CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 154 178
 CC TRANSMEM 179 206
 CC EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 207 226
 CC TRANSMEM 227 243
 CC CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 244 268
 CC TRANSMEM 269 285
 CC EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 286 309
 CC TRANSMEM 310 374
 CC CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 314 374
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC MOD RES 14 14
 CC MOD RES 26 26
 CC SULFATION.
 CC FT DISULFID 113 190
 CC FT VARSPPLIC 314 374

Matches 12; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 2 PYNV---LLNTFQBFPG 17

Db 355 PQLVTSLLKNTFQDFPG 373

RESULT 25

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CKR4 HUMAN
ID CKR4 HUMAN STANDARD; PRT; 360 AA.
AC P51679; Q9ULY6; Q9ULY7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 4 (C-CR-4) (CCR-4) (CCR4)
DE (K5-5).
GN GN CCR4 OR CMKR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=95370289; PubMed=7642634;
RA Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,
RA Proudfoot A.E.I., Wells T.N.C.;
RA "Molecular cloning and functional expression of a novel CC chemokine
RT receptor cDNA from a human basophilic cell line.";
RL J. Biol. Chem. 270:19495-19500(1995).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=21040311; PubMed=11196669;
RA Kato H., Tsuchiya N., Izumi S., Miyamae M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RA "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
[3]
RN SEQUENCE FROM N.A.
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
[4]
RN FUNCTION.
RX MEDLINE=97313486; PubMed=9169480;
RA Inai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
RT "The T cell-directed CC chemokine TARC is a highly specific
RT biological ligand for CC chemokine receptor 4.";
RL J. Biol. Chem. 272:15036-15042(1997).
[5]
RN FUNCTION.
RX MEDLINE=98104168; PubMed=9430724;
RA Inai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,
RA Yoshie O., Gray P.W.;
RT "Macrophage-derived chemokine is a functional ligand for the CC
RT chemokine receptor 4.";
RL J. Biol. Chem. 273:1764-1768(1998).
[6]
RN FUNCTION.
RX MEDLINE=99394604; PubMed=10466728;
RA Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P.,
RA Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher E.C.;
RT "The chemokine receptor CCR4 in vascular recognition by cutaneous but
RT not intestinal memory T cells.";
RL Nature 400:776-780(1999).
[7]
RN FUNCTION. TISSUE SPECIFICITY AND PHOSPHORYLATION.
RX MEDLINE=20219238; PubMed=10754297;
RA Inngjerdengen M., Dama J.B., Magnazachi A.A.;
RT "Human NK cells express CC chemokine receptors 4 and 8 and respond to
RT thymus and activation-regulated chemokine, macrophage-derived
RT chemokine, and I-309.";

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J. Immunol. 164:4048-4054(2000).
-!- FUNCTION: High affinity receptor for the C-C type chemokines
TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is
mediated by G(i) proteins which activate a phosphatidylinositol-
calcium second messenger system. Can function as a chemottractant
homing receptor on circulating memory lymphocytes and as a
coreceptor for some primary HIV-2 isolates. In the CNS, could
mediate hippocampal-neuron survival.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Predominantly expressed in the thymus, in
peripheral blood leukocytes, including T cells, mostly cd4+ cells,
and basophils, and in platelets; at lower levels, in the spleen
and in monocytes. Detected also in macrophages, IL-2-activated
natural killer cells and skin-homing memory T cells. Mostly the
ones expressing the cutaneous lymphocyte antigen (CLA). Expressed
in brain microvascular and coronary artery endothelial cells.
-!- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
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EMBL; X85740; CAA59743.1; -
EMBL; AB023888; BAA86965.1; -
EMBL; AB023889; BAA86966.1; -
EMBL; AB023890; BAA86967.1; -
EMBL; AB023891; BAA86968.1; -
EMBL; AB023892; BAA86969.1; -
EMBL; AY322539; AAP84352.1; -
PIR; A57160; A57160.
Genew; HGNC:1605; CCR4.
MIM; 604836; -
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:0006955; P:chemotaxis; TAS.
GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO:0006954; P:immune response; TAS.
GO; GO:0006954; P:inflammatory response; TAS.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm1.1.
PRINTS; PR00237; GPCRHOPOSPN
PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Phosphorylation; Polymorphism.
DOMAIN 1 39
TRANSMEM 40 67
DOMAIN 68 77
TRANSMEM 78 98
DOMAIN 99 111
TRANSMEM 112 133
DOMAIN 134 150
TRANSMEM 151 175
DOMAIN 176 206
TRANSMEM 207 226
DOMAIN 227 242
TRANSMEM 243 267
DOMAIN 268 284
TRANSMEM 285 308
DOMAIN 309 360
TRANSMEM 183 194
CARBOHYD 194 194
DISULFID 110 187
VARIANT 130 130
VARIANT 178 178
C -> S.

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DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Polymorphism.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 62 1 (POTENTIAL).
FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 93 2 (POTENTIAL).
FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT VARIANT 218 218 the population; may show reduced activity.
FT CONFLICT 276 276 /FTID-VAR_010668.
FT SEQUENCE 355 AA; 41043 MW; E95DCD7A6C643874 CRC64;
Query Match 44.1%; Score 52; DB 1; Length 355;
Best Local Similarity 40.0%; Pred. No. 1;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 2 PYNIVLLNTFOEPPGLNLC 21
|||:||||:|:|
Db 254 PYNVAILLSSYSILFGNDC 273
RESULT 27
CKR3_RAT STANDARD; PRT; 359 AA.
AC O54814; O55169;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
DE (CKR3).
GN CCR3 OR CMKBR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Spleen;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafianca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
allergic encephalomyelitis";
RL J. Neuroimmunol. 86:1-12(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RX Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in spleen but not in astrocytes or
microglia.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF003954; AAC03337.1; -.
DR EMBL; Y13400; CAA73830.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 64 1 (POTENTIAL).
FT DOMAIN 65 74 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 75 95 2 (POTENTIAL).
FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 113 133 3 (POTENTIAL).
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 4 (POTENTIAL).
FT DOMAIN 176 206 5 (POTENTIAL).
FT TRANSMEM 207 227 6 (POTENTIAL).
FT DOMAIN 228 243 7 (POTENTIAL).
FT TRANSMEM 244 264 8 (POTENTIAL).
FT DOMAIN 265 288 9 (POTENTIAL).
FT TRANSMEM 289 309 10 (POTENTIAL).
FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 164 164 F -> L (IN REF. 2).
SQ SEQUENCE 359 AA; 41643 MW; 880F682984F501DA CRC64;
Query Match 44.1%; Score 52; DB 1; Length 359;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 2 PYNIVLLNTFOEPPGLNLC 21
|||:||||:|:|
Db 258 PYNVILLSSAFHSTFLETSC 277
RESULT 28
CKR4_MOUSE STANDARD; PRT; 360 AA.
AC P51880;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 4 (C-C CKR-4) (CC-CKR-4) (CCR-4) (CCR4).
DE CCR4 OR CMKBR4.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96136324; PubMed=8573157;
RA Hoogwerf A.J., Black D., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Molecular cloning of murine CC CKR-4 and high affinity binding of
chemokines to murine and human CC CKR-4";
RL Biochem. Biophys. Res. Commun. 218:337-343(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Cytotoxic T-cell;
RX MEDLINE=97335974; PubMed=9192769;
RA Yoon B.-S., Kim S.-H., Lyu M.-S., Kozak C.A., Taub D.D., Kwon B.S.;
RT "Molecular cloning and characterization of a cDNA, CHEMRL1, encoding a
chemokine receptor with a homology to the human C-C chemokine
receptor, CCR-4";
RL Blood 89:4448-4460(1997).
RN [3]
RP FUNCTION.

RX MEDLINE=20273981; PubMed=10811868;
 RA Buser R., Conquet F., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
 RT "A key role for CC chemokine receptor 4 in lipopolysaccharide-induced
 RL endotoxic shock";
 RL J. Exp. Med. 191:1755-1764 (2000).
 CC -!- FUNCTION: High affinity receptor for the C-C type chemokines
 CC TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is
 CC mediated by G(i) proteins which activate a phosphatidylinositol-
 CC calcium second messenger system. Could play a role in
 CC lipopolysaccharide (LPS)-induced endotoxic shock. In the CNS,
 CC could mediate hippocampal-neuron survival.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in the thymus, macrophages and T-
 CC and B-cells.
 CC -!- DEVELOPMENTAL STAGE: Low expression at 7.5 dpc and 12.5 dpc in the
 CC yolk sac.
 CC -!- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
 CC PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
 CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2 (BY SIMILARITY).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC
 DR EMBL; X90862; CAA62372.1; -;
 DR EMBL; U15208; AAA92582.1; -;
 DR PIR; JC4587; JC4587.
 DR MGD; MGI:107824; Ccr4.
 DR GO; GO:0016493; P:C-C chemokine receptor activity; IMP.
 DR GO; GO:0066935; P:chemotaxis; IMP.
 DR GO; GO:0066954; P:inflammatory response; IMP.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
 DR G-protein coupled receptor; transmembrane; Glycoprotein;
 KW Phosphorylation.
 FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 40 67 1 (POTENTIAL).
 FT DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 78 98 2 (POTENTIAL).
 FT DOMAIN 99 111 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 112 133 3 (POTENTIAL).
 FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 151 175 4 (POTENTIAL).
 FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 207 226 5 (POTENTIAL).
 FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 243 267 6 (POTENTIAL).
 FT DOMAIN 268 284 7 (POTENTIAL).
 FT TRANSSEM 285 308 8 (POTENTIAL).
 FT DOMAIN 309 360 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 343 346 POLY-SER.
 FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 110 187 BY SIMILARITY.
 FT CONFLICT 4 4 T -> I (IN REF. 2).
 FT CONFLICT 145 145 S -> T (IN REF. 2).
 FT CONFLICT 181 181 E -> Q (IN REF. 2).
 FT CONFLICT 205 205 E -> D (IN REF. 2).
 FT CONFLICT 221 221 W -> C (IN REF. 2).
 FT CONFLICT 241 241 V -> L (IN REF. 2).
 FT CONFLICT 246 246 G -> A (IN REF. 2).
 FT CONFLICT 293 293 G -> A (IN REF. 2).
 FT CONFLICT 311 311 F -> S (IN REF. 2).
 SQ SEQUENCE 360 AA; 41462 MW; 97BD8C96D259AE3 CRC64;
 Query Match 44.1%; Score 52; DB 1; Length 360;
 Best Local Similarity 47.6%; Pred. No. 1;
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 2 PYNIVLLNTQEFFGLNCS 22
 DB 257 PYNVVFLETLVELEVLQDCT 277
 RESULT 29
 ACM2_PANTR
 ID ACM2_PANTR STANDARD; PRT; 440 AA.
 AC Q9NZAF; 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Muscarinic acetylcholine receptor M2 (Fragment).
 GN CHRM2.
 OS Pan troglodytes (Chimpanzee).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 ON NCBI_TaxID=9598;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate 220;
 RA Kitano T., Kobayakawa H., Saitou N.;
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
 CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
 CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
 CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
 CC ADENYLATE CYCLASE INHIBITION.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC or send an email to license@isb-sib.ch).
 CC
 EMBL; AB041392; BAA94477.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
 DR Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
 KW Phosphorylation; Multigene family; G-protein coupled receptor.
 FT NON_TER 1 1
 FT TRANSSEM <1 19 1 (POTENTIAL).
 FT DOMAIN 20 33 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 34 54 2 (POTENTIAL).
 FT DOMAIN 55 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 72 93 3 (POTENTIAL).
 FT DOMAIN 94 113 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 114 136 4 (POTENTIAL).
 FT DOMAIN 137 158 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 159 181 5 (POTENTIAL).
 FT DOMAIN 182 362 6 (POTENTIAL).
 FT TRANSSEM 363 383 7 (POTENTIAL).
 FT DOMAIN 384 397 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 398 417 7 (POTENTIAL).
 FT DOMAIN 418 440 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 70 150 BY SIMILARITY.
 FT MOD_RES 420 420 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 424 424 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 439 439 PHOSPHORYLATION (POTENTIAL).
 SQ SEQUENCE 440 AA; 48854 MW; 12B0324E13D37DDF CRC64;


```
FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 5 (POTENTIAL).
FT TRANSMEM 198 223 6 (POTENTIAL).
FT DOMAIN 224 239 7 (POTENTIAL).
FT TRANSMEM 240 264 8 (POTENTIAL).
FT DOMAIN 265 281 9 (POTENTIAL).
FT TRANSMEM 282 305 10 (POTENTIAL).
FT DOMAIN 306 355 11 (POTENTIAL).
FT CARBOHYD 5 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
SQ SEQUENCE 355 AA; 41198 MW; 41CBA7CC19D23D4 CRC64;

Query Match 43.2%; Score 51; DB 1; Length 355;
Best Local Similarity 45.0%; Pred. No. 1.4;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQFFGLNCC 21
    |||: ||: |||: |
Db 254 PYNLTSLISVQEFLEFLTHLC 273

RESULT 37
ACM4 CHICK STANDARD; PRT; 490 AA.
AC P17200;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Muscarinic acetylcholine receptor M4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90153912; PubMed=2154460;
RA Tietje K.M., Goldman P.S., Nathanson N.M.;
RT "Cloning and functional analysis of a gene encoding a novel
  muscarinic acetylcholine receptor expressed in chick heart and
  brain."
RL J. Biol. Chem. 265:2828-2834 (1990).
CC -!- FUNCTION: The muscarinic acetylcholine receptor mediates various
  cellular responses, including inhibition of adenylyl cyclase,
  breakdown of phosphoinositides and modulation of potassium
  channels through the action of G proteins. Primary transducing
  effect is inhibition of adenylyl cyclase. May couple to multiple
  functional responses in cell lines.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in heart and brain.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; J05218; AAA48563.1; -
CC FIR; A35546; A35546.
CC HSP; P02699; 1BOU.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC

KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW Phosphorylation; Multigene family; G-protein coupled receptor.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 64 1 (POTENTIAL).
FT DOMAIN 65 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 99 2 (POTENTIAL).
FT DOMAIN 100 116 3 (POTENTIAL).
FT TRANSMEM 117 138 4 (POTENTIAL).
FT DOMAIN 139 158 5 (POTENTIAL).
FT TRANSMEM 159 181 6 (POTENTIAL).
FT DOMAIN 182 203 7 (POTENTIAL).
FT TRANSMEM 204 226 8 (POTENTIAL).
FT DOMAIN 227 412 9 (POTENTIAL).
FT TRANSMEM 413 433 10 (POTENTIAL).
FT DOMAIN 434 447 11 (POTENTIAL).
FT TRANSMEM 448 467 12 (POTENTIAL).
FT DOMAIN 468 490 13 (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 115 195 BY SIMILARITY.
SQ SEQUENCE 490 AA; 54937 MW; 2CDFB5FA7D2298E CRC64;

Query Match 42.4%; Score 50; DB 1; Length 490;
Best Local Similarity 61.5%; Pred. No. 2.8;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQF 14
    |||: ||: |||: |
Db 426 PYNVNLINTFCE 438

RESULT 38
HI82_ARCFU STANDARD; PRT; 342 AA.
ID HI82_ARCFU STANDARD; PRT; 342 AA.
AC O28255;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histidinol-phosphate aminotransferase 2 (EC 2.6.1.9) (Imidazole
  acetol-phosphate transaminase 2).
OS Archaeoglobus fulgidus.
GN HISC2 OR AF2024.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
  Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
  Richardson D.L., Kerlavage A.R., Graham D.E., Kyripides N.C.,
  Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
  Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
  Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
  Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
  Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
  Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
  Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
  Venter J.C.;
RA "The complete genome sequence of the hyperthermophilic, sulphate-
  reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370 (1997).
CC -!- CATALYTIC ACTIVITY: L-histidinol-phosphate + 2-oxoglutarate = 3-
  (imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: Histidine biosynthesis; seventh step.
CC -!- SIMILARITY: Belongs to class-II of pyridoxal-phosphate-dependent
  aminotransferases. Histidinol-phosphate aminotransferases
  subfamily.
CC
```

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CC -----
 DR EMBL; AF000963; AAB89229.1; --
 DR PIR; G69502; G69502.
 DR HSP; P06986; 1FG7.
 DR TIGR; AF2024; --
 DR HAMAP; MF_01023; --; 1.
 DR InterPro; IPR004839; AminoTrans_I/II.
 DR InterPro; IPR001317; AminoTrans_II.
 DR InterPro; IPR005861; HisP_AminoTrans.
 DR Pfam; PF00155; aminotran_1.2; 1.
 DR TIGRFAMs; TIGR01141; hisC_1.
 DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; FALSE NEG.
 KW Histidine biosynthesis; Transferase; AminoTransferase;
 FT Pyridoxal phosphate; Complete proteome.
 FT BINDING 206 206 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 342 AA; 38941 MW; F71DA0FD66191D80 CRC64;

Query Match 40.7%; Score 48; DB 1; Length 342;
 Best Local Similarity 50.0%; Pred. No. 4.1; Mismatches 3; Indels 0; Gaps 0;
 Matches 8; Conservative 5;

QY 3 YNIVLLNTFOEFFGL 18
 |||::|::|::|::|
 Db 195 YNVLIVRSFKFFGL 210

RESULT 39

CC CRK3_MOUSE
 ID CRK3_MOUSE STANDARD; PRT; 359 AA.
 AC P51678;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable C-C chemokine receptor type 3 (C-CR3) (CC-CR3) (CCR-3)
 DE (CCR3) (CCR3) (Macrophage inflammatory protein-1 alpha receptor-like
 DE 2) (MIP-1 alpha RL2).
 OS MURUS MUSCULUS (Mouse).
 GN CRK3 OR CMKBR3 OR CMKBR1L2.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RX MEDLINE=96072806; PubMed=7594543;
 RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
 RA Gerard C.;
 RT "Molecular characterization of two murine eosinophil beta chemokine
 RT receptors.";
 RL J. Immunol. 155:5299-5305 (1995).
 RN [2]

CC SEQUENCE FROM N.A.
 CC STRAIN=129/SvJ;
 CC MEDLINE=95340546; PubMed=7542241;
 RA Gao J.-L., Murphy P.M.;
 RT "Cloning and differential tissue-specific expression of three mouse
 RT beta chemokine receptor-like genes, including the gene for a
 RT functional macrophage inflammatory protein-1 alpha receptor.";
 RL J. Biol. Chem. 270:17494-17501 (1995).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
 CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
 CC amounts in leukocytes.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC -----
 DR EMBL; U29677; AAA86118.1; --
 DR EMBL; U28406; AAA89155.1; --
 DR MGD; MGI:104616; Ccr3.
 DR GO; GO:0016493; F1C-C chemokine receptor activity; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0006935; P:chemotaxis; IDA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 38
 FT TRANSMEM 39 64
 FT DOMAIN 65 68
 FT TRANSMEM 69 95
 FT DOMAIN 96 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 150
 FT TRANSMEM 151 175
 FT DOMAIN 176 201
 FT TRANSMEM 202 227
 FT DOMAIN 228 243
 FT TRANSMEM 244 268
 FT DOMAIN 269 285
 FT TRANSMEM 286 309
 FT DOMAIN 310 359
 FT DISULFID 110 187
 FT CONFLICT 270 270 R -> S (IN REF. 2).
 SQ SEQUENCE 359 AA; 41825 MW; AC11ED6E283CEAF CRC64;

Query Match 40.7%; Score 48; DB 1; Length 359;
 Best Local Similarity 45.0%; Pred. No. 4.3;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNCC 21
 |||::|::|::|::|
 Db 258 PYNVLVLSAFHRTLETSC 277

RESULT 40

CC ACN4_XENLA
 ID ACN4_XENLA STANDARD; PRT; 484 AA.
 AC P30544;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Muscarinic acetylcholine receptor M4.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=95010703; PubMed=7925970;
 RA Herrera L., Carvallo P., Antonelli M., Olate J.;
 RT "Cloning of a Xenopus laevis muscarinic receptor encoded by an
 RT intronless gene.";
 RL FEBS Lett. 352:175-179 (1994).
 CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
 CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
 CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS

CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
CC INHIBITION OF ADENYLATE CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
CC EMBL; X65865; CAA46694.1; --
CC PIR; S48657; S48657.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOSPN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
CC Phosphorylation; Multigene family; G-protein coupled receptor.
CC DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 33 55 1 (POTENTIAL).
CC DOMAIN 56 69 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 70 90 2 (POTENTIAL).
CC DOMAIN 91 107 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 108 129 3 (POTENTIAL).
CC DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 150 172 4 (POTENTIAL).
CC DOMAIN 173 194 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 195 217 5 (POTENTIAL).
CC DOMAIN 218 406 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 407 427 6 (POTENTIAL).
CC DOMAIN 428 441 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 442 461 7 (POTENTIAL).
CC DOMAIN 462 484 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC DISULFID 106 186 BY SIMILARITY.
CC SEQUENCE 484 AA; 54135 MW; D83BD856DE302BE8 CRC64;

Query Match 40.7%; Score 48; DB 1; Length 484;
Best Local Similarity 63.6%; Pred.No. 5.8;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PYNIVLLINTF 12
| | | | | | | | | |
Db 420 PYNVVLINTF 430

Search completed: September 28, 2004, 09:04:07
Job time : 7.875 secs

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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:56:16 ; Search time 35.2 Seconds
(without alignments)
197.199 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYNIVLLNTFQEFFGLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	333	4	014694
2	118	100.0	334	6	Q9TUQ7
3	118	100.0	339	4	Q9UN24
4	118	100.0	339	4	Q9UN26
5	118	100.0	339	4	Q9UN23
6	118	100.0	339	4	Q9UN37
7	118	100.0	339	4	Q9UN25
8	118	100.0	339	4	Q9UN27
9	118	100.0	339	4	Q9UN29
10	118	100.0	339	6	Q9TQW0
11	118	100.0	339	6	Q9TUX1
12	118	100.0	339	6	Q9TUU9
13	118	100.0	339	6	Q9TUW8
14	118	100.0	339	6	Q9TUT4
15	118	100.0	339	6	Q9TUW9
16	118	100.0	339	6	Q9TSQ1

17	118	100.0	339	6	Q9TUU8	Q9tuu8 cercopithec
18	118	100.0	339	6	Q9TQW4	Q9tqw4 pan troglod
19	118	100.0	339	6	Q9TUW4	Q9tuw4 pan troglod
20	118	100.0	339	6	Q9TQW7	Q9tqw7 cercopithec
21	118	100.0	339	6	Q9TUQ5	Q9tuq5 erythrocebu
22	118	100.0	339	6	Q9TUR9	Q9tur9 saquinus sp
23	118	100.0	339	6	Q9TQT0	Q9tqt0 macaca fasc
24	118	100.0	339	6	Q9TUT9	Q9tut9 macaca mula
25	118	100.0	339	6	Q9TSN2	Q9tsn2 macaca fasc
26	118	100.0	339	6	Q9TUR6	Q9tur6 cercopithec
27	118	100.0	339	6	Q9TQV6	Q9tqv6 colobus gue
28	118	100.0	339	6	Q9TUQ9	Q9tuq9 cercopithec
29	118	100.0	339	6	Q9TSN3	Q9tsn3 macaca fasc
30	118	100.0	339	6	Q9TUU7	Q9tuu7 macaca fusc
31	118	100.0	339	6	Q9TQV0	Q9tqv0 papio papio
32	118	100.0	339	6	Q9TQV5	Q9tqv5 cercopithec
33	118	100.0	339	6	Q9TUS7	Q9tus7 papio papio
34	118	100.0	339	6	Q9TUW7	Q9tuw7 pan troglod
35	118	100.0	339	6	Q9TUW3	Q9tuw3 pongo pygma
36	118	100.0	339	6	Q9TUS5	Q9tus5 papio papio
37	118	100.0	339	6	Q9TUU0	Q9tuu0 macaca mula
38	118	100.0	339	6	Q9TQV2	Q9tqv2 papio papio
39	118	100.0	339	6	Q9TQV3	Q9tqv3 cercopithec
40	118	100.0	339	6	Q9TUQ8	Q9tuq8 cercopithec
41	118	100.0	339	6	Q9TUR3	Q9tur3 erythrocebu
42	118	100.0	339	6	Q9TQW2	Q9tqw2 pongo pygma
43	118	100.0	339	6	Q9TUU1	Q9tuu1 macaca mula
44	118	100.0	339	6	Q9TUT6	Q9tut6 macaca neme
45	118	100.0	339	6	Q9TQX2	Q9tqx2 erythrocebu

ALIGNMENTS

RESULT 1

014694	PRELIMINARY;	PRT;	333 AA.
ID	014694		
AC	014694;		
DT	01-JAN-1998 (TREMREL. 05, Created)		
DT	01-JAN-1998 (TREMREL. 05, Last sequence update)		
DT	01-JUN-2003 (TREMREL. 24, Last annotation update)		
DE	CCR5 receptor (Fragment).		
GN	CCR5.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,		
RA	Ho D.D.;		
RT	"HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism."		
RL	AIDS Res. Hum. Retroviruses 0:0-0(1997).		
DR	EMBL; AF011504; AAB65704.1; "		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm.1; 1.		
DR	PRINTS; PR00237; GPCRHHODOPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.		
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.		
KW	Receptor.		
FT	NON_TER	333	
SQ	SEQUENCE	333 AA;	AEFBA07A67893AEB CRC64;
Query Match		100.0%;	Score 118; DB 4; Length 333;
Best Local Similarity		100.0%;	Pred. No. 2.1e-10;
Matches	22;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	APYNIVLLNTFQEFFGLNCS 22	

Db 230 APYINVLLNTFQEFFGLNCS 251

RESULT 2

Q9TUQ7 PRELIMINARY; PRT; 334 AA.

AC Q9TUQ7; 1 339

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Erythrocybus patas (Red guenon) (Husar).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Erythrocebus.

OX NCBI_TaxID=9538;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

RT species."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF162049; AAD47804.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_Rhodopsin.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

DR Receptor.

FT NON_TER 1 334

FT NON_TER 334

SQ SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 334;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEFFGLNCS 22

Db 237 APYINVLLNTFQEFFGLNCS 258

RESULT 3

Q9UN24 PRELIMINARY; PRT; 339 AA.

AC Q9UN24; 1 339

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

RT species."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161919; AAD47676.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_Rhodopsin.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

DR Receptor.

FT NON_TER 1 339

FT NON_TER 339

SQ SEQUENCE 339 AA; 39162 MW; A56369FB0529F4B CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEFFGLNCS 22

Db 242 APYINVLLNTFQEFFGLNCS 263

RESULT 5

Q9UN23 PRELIMINARY; PRT; 339 AA.

AC Q9UN23; 1 339

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Homo sapiens (Human).

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_Rhodopsin.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

DR Receptor.

FT NON_TER 1 339

FT NON_TER 339

SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEFFGLNCS 22

Db 242 APYINVLLNTFQEFFGLNCS 263

RESULT 4

Q9UN26 PRELIMINARY; PRT; 339 AA.

AC Q9UN26; 1 339

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;

RT "Sequences of the CCR5 genes from diverse simian and prosimian

RT species."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161916; AAD47673.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_Rhodopsin.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

DR Receptor.

FT NON_TER 1 339

FT NON_TER 339

SQ SEQUENCE 339 AA; 39162 MW; A56369FB0529F4B CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEFFGLNCS 22

Db 242 APYINVLLNTFQEFFGLNCS 263

RESULT 5

Q9UN23 PRELIMINARY; PRT; 339 AA.

AC Q9UN23; 1 339

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE C-C chemokine receptor 5 (Fragment).

GN CCR5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
|||||
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 6
Q9UBJ7
ID Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FFF1F2F27A CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
|||||
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 7
Q9UN25
ID Q9UN25 PRELIMINARY; PRT; 339 AA.
AC Q9UN25
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161918; AAD47675.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFQEFFGLNCS 22
|||||
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 8
Q9UN27
ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

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DR GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39086 MW; 89AD8B44E2CB4EC2 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVILLNTFOEFFGLNCS 22
DB 242 APYINVILLNTFOEFFGLNCS 263

RESULT 9
Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47687.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO:00016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVILLNTFOEFFGLNCS 22
DB 242 APYINVILLNTFOEFFGLNCS 263

RESULT 10
Q9TQW0 PRELIMINARY; PRT; 339 AA.
AC Q9TQW0;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.
DR GO:00016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVILLNTFOEFFGLNCS 22
DB 242 APYINVILLNTFOEFFGLNCS 263

RESULT 11
Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO:00016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1

```

```

FT NON TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257BF8B34C4AE CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
DB 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 12
Q9TUW8 PRELIMINARY; PRT; 339 AA.
AC Q9TUW8
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161948; AAD47704.1; -.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0004872; F:receptor activity; IEA.
GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 339
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
DB 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 13
Q9TUW8 PRELIMINARY; PRT; 339 AA.
AC Q9TUW8
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,

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RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161948; AAD47851.1; -.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0004872; F:receptor activity; IEA.
GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 339
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39079 MW; 4A479753DA2F7AAF CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
DB 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 14
Q9TUT4 PRELIMINARY; PRT; 339 AA.
AC Q9TUT4
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161979; AAD47734.1; -.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0004872; F:receptor activity; IEA.
GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 339 339
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39092 MW; 84B51B9548E0703C CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
DB 242 APYNIVLLNTFQEFFGLNCS 263

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RESULT 15
Q9TUW9 PRELIMINARY; PRT; 339 AA.
AC Q9TUW9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39024 MW; EC4CB48DEEFP107E CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
    |||||
DB 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 16
Q9TSQ1 PRELIMINARY; PRT; 339 AA.
AC Q9TSQ1;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162023; AAD47778.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.

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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39216 MW; 847E935FA403E52D CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
    |||||
DB 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 17
Q9TUU8 PRELIMINARY; PRT; 339 AA.
AC Q9TUU8;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161949; AAD47705.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39049 MW; 6D1A933F66270F3ED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
    |||||
DB 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 18
Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

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OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161905; AAD47662.1; -;
DR EMBL; AF161898; AAD47655.1; -;
DR EMBL; AF161901; AAD47658.1; -;
DR EMBL; AF161904; AAD47661.1; -;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39129 MW; 4A88F8BB601D46A4 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFOEFFGLNCS 22
Db 242 APYNVLLNTFOEFFGLNCS 263

RESULT 19
Q9TUW4 PRELIMINARY; PRT; 339 AA.
AC Q9TUW4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39159 MW; 8B699B882BAC0E84 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFOEFFGLNCS 22
Db 242 APYNVLLNTFOEFFGLNCS 263

RESULT 20
Q9TUW7 PRELIMINARY; PRT; 339 AA.
AC Q9TUW7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -;
DR EMBL; AF162042; AAD47797.1; -;
DR EMBL; AF162044; AAD47799.1; -;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39150 MW; 847D5F92BB03E6E2 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFOEFFGLNCS 22
Db 242 APYNVLLNTFOEFFGLNCS 263

RESULT 21
Q9TUQ5 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";

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RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162054; AAD47809.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39048 MW; 1A2E19E3A6A5A52A CRC64;

Query Match
Best Local Similarity 100.0%; Score 118; DB 6; Length 339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
Db 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 22
Q9TUT9
ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162015; AAD4770.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39063 MW; 78BCB7A84B877085 CRC64;

Query Match
Best Local Similarity 100.0%; Score 118; DB 6; Length 339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
Db 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 23
Q9TQTO
ID Q9TQTO PRELIMINARY; PRT; 339 AA.
AC Q9TQTO

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161954; AAD47710.1; -.
DR EMBL; AF161950; AAD47706.1; -.
DR EMBL; AF161952; AAD47708.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match
Best Local Similarity 100.0%; Score 118; DB 6; Length 339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
Db 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 24
Q9TUT9
ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161972; AAD47727.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

```

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39067 MW; 5BFCBCSBA96C2F9E CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNIIVLLNTFOEFFGLNCS 22
Db 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 25
ID Q9TSN2 PRELIMINARY; PRT; 339 AA.
AC Q9TSN2;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161953; AAD47709.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39137 MW; 9B626ED3288607C1 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNIIVLLNTFOEFFGLNCS 22
Db 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 26
ID Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecus.

OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162026; AAD47781.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39178 MW; 9DF2A6F446C55AED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNIIVLLNTFOEFFGLNCS 22
Db 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 27
ID Q9TOV6 PRELIMINARY; PRT; 339 AA.
AC Q9TOV6;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Colobus guereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162005; AAD47760.1; -
DR EMBL; AF162000; AAD47755.1; -
DR EMBL; AF162001; AAD47756.1; -
DR EMBL; AF162002; AAD47757.1; -
DR EMBL; AF162003; AAD47758.1; -
DR EMBL; AF162004; AAD47759.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39168 MW; 6A4BF72FEBFF566F CRC64;

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Query Match      100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
  |||||
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 28
Q9TUQ9 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ9;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCRS.
OS Cercopithecus mona.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36226;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF162041; AAD47796.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39019 MW; 7176940AF11F3ED CRC64;

Query Match      100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
  |||||
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 29
Q9TSN3 PRELIMINARY; PRT; 339 AA.
AC Q9TSN3;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCRS.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF162041; AAD47796.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39019 MW; 7176940AF11F3ED CRC64;

Query Match      100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
  |||||
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 30
Q9TUU7 PRELIMINARY; PRT; 339 AA.
AC Q9TUU7;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCRS.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF161955; AAD47711.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match      100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
  |||||
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 31
Q9TQV0

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ID Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162046; AAD47744.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39113 MW; 7F9803EA0E0AF9ED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.le-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 242 APYNIVLLNTFQEFFGLNCS 263
|||||
|

RESULT 32
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162046; AAD47801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39178 MW; 847F8F936B00E6E2 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.le-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 242 APYNIVLLNTFQEFFGLNCS 263
|||||
|

RESULT 33
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161995; AAD47750.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39068 MW; 84EB018085DC0A62 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.le-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 242 APYNIVLLNTFQEFFGLNCS 263
|||||
|

RESULT 34
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

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OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161899; AAD47656.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39157 MW; 49AEBAD183E8E72D CRC64;

 Query Match 100.0%; Score 118; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2.le-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 APYINVLLNTFQEFFGLNCS 22
 [|||||]|||||
 Db 242 APYINVLLNTFQEFFGLNCS 263

 RESULT 35
 Q9TUW3
 ID Q9TUW3 PRELIMINARY; PRT; 339 AA.
 AC Q9TUW3
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (fragment).
 GN CCR5.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161908; AAD47665.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39103 MW; 4350CA4625FB0657C CRC64;

 Query Match 100.0%; Score 118; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2.le-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 APYINVLLNTFQEFFGLNCS 22
 [|||||]|||||
 Db 242 APYINVLLNTFQEFFGLNCS 263

Db 242 APYINVLLNTFQEFFGLNCS 263

 RESULT 36
 Q9TUS5
 ID Q9TUS5 PRELIMINARY; PRT; 339 AA.
 AC Q9TUS5
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (fragment).
 GN CCR5.
 OS Papio papio (Guinea baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Papio.
 OX NCBI_TaxID=100937;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161997; AAD47752.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39028 MW; 8C9C978FDB80B936 CRC64;

 Query Match 100.0%; Score 118; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2.le-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 APYINVLLNTFQEFFGLNCS 22
 [|||||]|||||
 Db 242 APYINVLLNTFQEFFGLNCS 263

 RESULT 37
 Q9TUU0
 ID Q9TUU0 PRELIMINARY; PRT; 339 AA.
 AC Q9TUU0
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (fragment).
 GN CCR5.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161970; AAD47725.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.

DT	01-MAY-2000	(TEMBLrel. 13, Last sequence update)
DT	01-JUN-2003	(TEMBLrel. 24, Last annotation update)
DE	C-C chemokine receptor 5 (Fragment).	
GN	CCR5.	
OS	Cercopithecus mona.	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;	
OC	Cercopitheciinae; Cercopithecus.	
OX	NCBI_TaxID=36226;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Kunstanman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,	
RA	Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;	
RT	"Sequences of the CCR5 genes from diverse simian and prosimian	
RT	species.";	
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBDJ databases.	
DR	EMBL; AF162040; AAD47795.1; -.	
DR	EMBL; AF162038; AAD47793.1; -.	
DR	GO; GO:0016021; C:integral to membrane; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	GO; GO:0001584; F:rhopodopsin-like receptor activity; IEA.	
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin.. ; IEA.	
DR	InterPro; IPR000276; GPCR_Rhodpsn.	
DR	Pfam; PF00001; 7tm 1; 1.	
DR	PRINTS; PR00237; GFCRRHODPSN.	
DR	PROSITE; PS00237; G PROTEIN RECEPT_F1_1; 1.	
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.	
KW	Receptor.	
FT	NON_TER	1
FT	NON_TER	339
SQ	SEQUENCE	339 AA; 33079 MW; 717653EA0E00F3ED CRC64;
Query Match 100.0%; Score 118; DB 6; Length 339;		
Best Local Similarity 100.0%; Pred. No. 2,1e-10;		
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps		
Qy	1 APYNVILLNTFOEFFGLNCS 22	
Dd	242 APYNVILLNTFOEFFGLNCS 263	
RESULT 40		
Q9TU08		
ID	Q9TU08 PRELIMINARY; PRT; 339 AA.	
AC	Q9TU08	
DT	01-MAY-2000 (TEMBLrel. 13, Created)	
DT	01-MAY-2000 (TEMBLrel. 13, Last sequence update)	
DE	C-C chemokine receptor 5 (Fragment).	
GN	CCR5.	
OS	Cercopithecus nictians (white-nosed guenon).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;	
OC	Cercopitheciinae; Cercopithecus.	
OX	NCBI_TaxID=36228;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Kunstanman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,	
RA	Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;	
RT	"Sequences of the CCR5 genes from diverse simian and prosimian	
RT	species.";	
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBDJ databases.	
DR	EMBL; AF162045; AAD47800.1; -.	
DR	GO; GO:0016021; C:integral to membrane; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	GO; GO:0001584; F:rhopodopsin-like receptor activity; IEA.	
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin.. ; IEA.	
DR	InterPro; IPR000276; GPCR_Rhodpsn.	
DR	Pfam; PF00001; 7tm 1; 1.	
DR	PRINTS; PR00237; GFCRRHODPSN.	
DR	PROSITE; PS00237; G PROTEIN RECEPT_F1_1; 1.	
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.	
KW	Receptor.	

FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39148 MW; 0CA289CDDDEDE831 CRC64;
 Query Match 100.0%; Score 118; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
 |||||
 Db 242 APYNIVLLNTFQEFFGLNCS 263
 |||||

Search completed: September 28, 2004, 09:06:20
 Job time : 36.2 secs

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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:51:21 ; Search time 42.975 Seconds
(without alignments)
118.345 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGEKFRNLLVFFQK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	95	100.0	18	4 AAB88982	Aab88982 HIV gp120
2	95	100.0	18	4 AAB88997	Aab88997 HIV gp120
3	95	100.0	27	5 AAE14757	Aae14757 Human CCR
4	95	100.0	43	5 AAE14756	Aae14756 Human CCR
5	95	100.0	58	5 AAE14759	Aae14759 Human CCR
6	95	100.0	58	5 AAE14755	Aae14755 Human CCR
7	95	100.0	268	7 ADC10142	Adc10142 Human NOV
8	95	100.0	268	7 ADC10144	Adc10144 Human NOV
9	95	100.0	332	2 AAW26766	Aaw26766 Human che
10	95	100.0	352	2 AAW27407	Aaw27407 Human CCR
11	95	100.0	352	2 AAW27123	Aaw27123 Human che
12	95	100.0	352	2 AAW27125	Aaw27125 Macaque c
13	95	100.0	352	2 AAW07602	Aaw07602 Human G-p
14	95	100.0	352	2 AAW23835	Aaw23835 Human CC
15	95	100.0	352	2 AAW82332	Aaw82332 HIV-1 co-
16	95	100.0	352	3 AAY80128	Aay80128 Human G-p
17	95	100.0	352	4 AAG79089	Aag79089 Amino aci
18	95	100.0	352	4 AAE07046	Aae07046 Human G-p
19	95	100.0	352	4 AAE07048	Aae07048 Human G-p
20	95	100.0	352	4 AAG80111	Aag80111 Human CCR
21	95	100.0	352	4 AAE04321	Aae04321 Human che
22	95	100.0	352	4 AAE07037	Aae07037 Human G-p
23	95	100.0	352	4 AAE07039	Aae07039 Human G-p
24	95	100.0	352	4 AAB46858	Aab46858 Human HDG
25	95	100.0	352	4 ABB56342	Abb56342 Non-endog

26	95	100.0	352	4 AAB83354	Aab83354 Human CCR
27	95	100.0	352	4 AAB82948	Aab82948 Human HIV
28	95	100.0	352	5 AAU97150	Aau97150 Human G-p
29	95	100.0	352	5 AAU97152	Aau97152 Human G-p
30	95	100.0	352	5 AAM52829	Aam52829 Human CCR
31	95	100.0	352	5 AAM52828	Aam52828 Human CC
32	95	100.0	352	5 ABG70597	Abg70597 Human G-p
33	95	100.0	352	5 ABG92883	Abg92883 Human imm
34	95	100.0	352	5 ABG92880	Abg92880 Human G-p
35	95	100.0	352	5 AAE25808	Aae25808 Human G-p
36	95	100.0	352	5 AAE25811	Aae25811 Human G-p
37	95	100.0	352	5 ABB81054	Abb81054 G-protein
38	95	100.0	352	5 ABB08343	Abb08343 Human che
39	95	100.0	352	6 ABG75540	Abg75540 Human G-p
40	95	100.0	352	6 ABR58602	Abr58602 Human can
41	95	100.0	352	6 AAO29514	Aao29514 Human C-C
42	95	100.0	352	6 ABU61654	Abu61654 Human G-p
43	95	100.0	352	6 ABP97728	Abp97728 Amino aci
44	95	100.0	352	6 ABP81933	Abp81933 Human C-C
45	95	100.0	352	7 ADC03341	Adc03341 Human che

ALIGNMENTS

RESULT 1
AAB88982
ID AAB88982 standard; peptide; 18 AA.
XX AAB88982;
AC
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #75.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US0233505.
XX
PR 27-AUG-1999; 99US-0151270P.
XX
PS (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions.
XX
PS Example 1; Page 37; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus.
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

```

Db      1 YAFVGEKFRNLLVFFQK 18
|||||
RESULT 2
AAB88997
ID AAB88997 standard; peptide; 18 AA.
XX AC AAB88997;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #90.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Homo sapiens.
XX FN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US023505.
XX PR 27-AUG-1999; 99US-0151270P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions.
XX PS Claim 21; Page 38; 114pp; English.
XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the virus.
XX CC The present sequence is an example of a peptide of the invention
XX SQ Sequence 18 AA;
Query Match 100.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
Db 1 YAFVGEKFRNLLVFFQK 18
|||||
RESULT 3
AAE14757
ID AAE14757 standard; peptide; 27 AA.
XX AC AAE14757;
XX DT 04-OCT-2002 (first entry)
XX DE Human CCR5 chemokine receptor deletion mutant fragment (aa 295-321).
XX KW Chemokine receptor CCR5; P2 protein; HIV infection; AIDS;
XX KW human immunodeficiency virus; gene therapy; human; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers

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FT Misc-difference 27 /note= "Wild-type Cys replaced by Glx"
FT XX
PN EP1207202-A1.
XX PD 22-MAY-2002.
XX PF 12-NOV-2001; 2001EP-00126500.
XX PR 16-NOV-2000; 2000EP-00125052.
XX PA (MOEL/) MOELLING K.
XX PI Moelling K, Schweneker M;
XX DR WPI; 2002-437464/47.
XX PT Nucleic acid encoding a protein which interacts with the carboxy terminus
XX PT of the chemokine receptor CCR5 isolated from a human B cell cDNA library
XX PT is useful to detect, treat and prevent HIV infection.
XX PS Example 2; Fig 2A; 28pp; English.
XX CC The invention relates to nucleic acid encoding a protein which interacts
XX CC with the carboxy terminus of the chemokine receptor CCR5 or of other
XX CC chemokine receptor family members. Molecules of the invention are used to
XX CC detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
XX CC -derived peptides, or compounds derived from the protein of the invention
XX CC (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
XX CC of the invention would block HIV infection. The present sequence is human
XX CC chemokine receptor CCR5 C-terminal fragment deletion mutant which is
XX CC incapable of interacting with the protein of the invention
XX SQ Sequence 27 AA;
Query Match 100.0%; Score 95; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
Db 3 YAFVGEKFRNLLVFFQK 20
|||||
RESULT 4
AAE14756
ID AAE14756 standard; peptide; 43 AA.
XX AC AAE14756;
XX DT 04-OCT-2002 (first entry)
XX DE Human CCR5 chemokine receptor deletion mutant fragment (aa 295-337).
XX KW Chemokine receptor CCR5; P2 protein; HIV infection; AIDS;
XX KW human immunodeficiency virus; gene therapy; human; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 43 /note= "Wild-type Ser replaced by Glx"
FT XX
PN EP1207202-A1.
XX PD 22-MAY-2002.
XX PF 12-NOV-2001; 2001EP-00126500.
XX PR 16-NOV-2000; 2000EP-00125052.
XX PA (MOEL/) MOELLING K.
XX PI Moelling K, Schweneker M;
XX DR WPI; 2002-437464/47.
XX PT Nucleic acid encoding a protein which interacts with the carboxy terminus
XX PT of the chemokine receptor CCR5 isolated from a human B cell cDNA library
XX PT is useful to detect, treat and prevent HIV infection.
XX PS Example 2; Fig 2A; 28pp; English.
XX CC The invention relates to nucleic acid encoding a protein which interacts
XX CC with the carboxy terminus of the chemokine receptor CCR5 or of other
XX CC chemokine receptor family members. Molecules of the invention are used to
XX CC detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
XX CC -derived peptides, or compounds derived from the protein of the invention
XX CC (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
XX CC of the invention would block HIV infection. The present sequence is human
XX CC chemokine receptor CCR5 C-terminal fragment deletion mutant which is
XX CC incapable of interacting with the protein of the invention
XX SQ Sequence 27 AA;
Query Match 100.0%; Score 95; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
Db 3 YAFVGEKFRNLLVFFQK 20
|||||
RESULT 4
AAE14756
ID AAE14756 standard; peptide; 43 AA.
XX AC AAE14756;
XX DT 04-OCT-2002 (first entry)
XX DE Human CCR5 chemokine receptor deletion mutant fragment (aa 295-337).
XX KW Chemokine receptor CCR5; P2 protein; HIV infection; AIDS;
XX KW human immunodeficiency virus; gene therapy; human; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 43 /note= "Wild-type Ser replaced by Glx"
FT XX
PN EP1207202-A1.
XX PD 22-MAY-2002.
XX PF 12-NOV-2001; 2001EP-00126500.
XX PR 16-NOV-2000; 2000EP-00125052.
XX PA (MOEL/) MOELLING K.

```

XX Moelling K, Schwenecker M;
XX WPI; 2002-437464/47.
XX Nucleic acid encoding a protein which interacts with the carboxy terminus
XX of the chemokine receptor CCR5 isolated from a human B cell cDNA library
XX is useful to detect, treat and prevent HIV infection.
XX Example 2; Fig 2A; 28pp; English.
XX The invention relates to nucleic acid encoding a protein which interacts
XX with the carboxy terminus of the chemokine receptor CCR5 or of other
XX chemokine receptor family members. Molecules of the invention are used to
XX detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
XX -derived peptides, or compounds derived from the protein of the invention
XX (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
XX of the invention would block HIV infection. The present sequence is human
XX chemokine receptor CCR5 C-terminal fragment deletion mutant which is
XX incapable of interacting with the protein of the invention
XX Sequence 43 AA;
XX Query Match 100.0%; Score 95; DB 5; Length 43;
XX Best Local Similarity 100.0%; Pred. No. 2e-08;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNYLLVFFQK 18
DB 3 YAFVGEKFRNYLLVFFQK 20
|||||
RESULT 5
AAE14759
ID AAE14759 standard; peptide; 58 AA.
XX AC AAE14759;
XX DT 04-OCT-2002 (first entry)
XX Human CCR5 chemokine receptor C-terminal mutant fragment (aa 295-352).
XX Chemokine receptor CCR5; P2 protein; HIV infection; AIDS;
XX human immunodeficiency virus; gene therapy; human; mutant; muten.
XX Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 58
XX /note= "Wild-type Leu replaced by Pro"
XX EPI207202-A1.
XX 22-MAY-2002.
XX 12-NOV-2001; 2001EP-00126500.
XX 16-NOV-2000; 2000EP-00125052.
XX (MOEL/) MOELLING K.
XX Moelling K, Schwenecker M;
XX WPI; 2002-437464/47.
XX Nucleic acid encoding a protein which interacts with the carboxy terminus
XX of the chemokine receptor CCR5 isolated from a human B cell cDNA library
XX is useful to detect, treat and prevent HIV infection.
XX Example 2; Fig 2A; 28pp; English.
XX The invention relates to nucleic acid encoding a protein which interacts

XX with the carboxy terminus of the chemokine receptor CCR5 or of other
XX chemokine receptor family members. Molecules of the invention are used to
XX detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
XX -derived peptides, or compounds derived from the protein of the invention
XX (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
XX of the invention would block HIV infection. The present sequence is human
XX chemokine receptor CCR5 C-terminal mutant fragment which is incapable of
XX interacting with the protein of the invention
XX Sequence 58 AA;
XX Query Match 100.0%; Score 95; DB 5; Length 58;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-08;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNYLLVFFQK 18
DB 3 YAFVGEKFRNYLLVFFQK 20
|||||
RESULT 6
AAE14755
ID AAE14755 standard; peptide; 58 AA.
XX AC AAE14755;
XX DT 04-OCT-2002 (first entry)
XX Human CCR5 chemokine receptor C-terminal fragment (residues 295-352).
XX Chemokine receptor CCR5; P2 protein; HIV infection;
XX human immunodeficiency virus; AIDS; gene therapy; human.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Binding-site 58
XX /note= "Essential for binding to human protein P2
XX (AAE14754)"
XX EPI207202-A1.
XX 22-MAY-2002.
XX 12-NOV-2001; 2001EP-00126500.
XX 16-NOV-2000; 2000EP-00125052.
XX (MOEL/) MOELLING K.
XX Moelling K, Schwenecker M;
XX WPI; 2002-437464/47.
XX Nucleic acid encoding a protein which interacts with the carboxy terminus
XX of the chemokine receptor CCR5 isolated from a human B cell cDNA library
XX is useful to detect, treat and prevent HIV infection.
XX Example 2; Fig 2A; 28pp; English.
XX The invention relates to nucleic acid encoding a protein which interacts
XX with the carboxy terminus of the chemokine receptor CCR5 or of other
XX chemokine receptor family members. Molecules of the invention are used to
XX detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
XX -derived peptides, or compounds derived from the protein of the invention
XX (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
XX of the invention would block HIV infection. The present sequence is human
XX chemokine receptor CCR5 C-terminal fragment
XX Sequence 58 AA;
XX Query Match 100.0%; Score 95; DB 5; Length 58;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-08;

AAW26766;
21-MAY-1998 (first entry)
Human chemokine receptor MMLR-CCR.
Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human; inflammation; macrophage; chemotaxis; haematopoiesis; infection; monocytosis; proliferative disease; cardiovascular disease; tumour; rheumatoid arthritis; alveolitis; atherosclerosis; chronic granulomatous disease; asthma; myasthenia gravis; diabetes; inflammatory bowel disease; toxic shock syndrome; septic shock; Chediak-Higashi syndrome; therapy; diagnosis.
Homo sapiens.
Key Location/Qualifiers
Peptide 107..128
FTH /note= "Conserved peptide"
FT Misc-difference 121
FT /note= "a claimed polypeptide has isoleucine at residue
FT 121"
WO9741225-A2.
NPN
NN
PPD 06-NOV-1997.
PPF 25-APR-1997; 97WO-US0005993.
PPR 26-APR-1996; 96US-00638081.
XX (INCY-) INCYTE PHARM INC.
XU Au-Young J, Bandman O, Coleman R, Wilde CG;
XX WPI; 1997-549729/50.
XX N-FSDB; AAT99542.
XX Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful
XX to study, diagnose and treat, e.g. infection, inflammation, solid tumour
XX and proliferative and cardiovascular disease.
XX Claim 8; Page 37-38; 59pp; English.
XX This protein comprises human MMLR-CCR, a novel C-C chemokine receptor
XX associated with monocyte/macrophage infiltration and chemotaxis and
XX haematopoiesis. The amino acid sequence was deduced from a cDNA clone
XX (see AAT99542) obtained from a cDNA library made from mononuclear cells
XX collected on day 2 of a mixed lymphocyte culture, i.e. cells associated
XX with inflammation and immunomodulation. Another novel chemokine receptor,
XX MPHG-CCR (see AAW36767), is also claimed. MMLR-CCR contains 7
XX transmembrane spanning segments connected by a series of intracellular
XX and extracellular loops. MMLR-CCR and MPHG-CCR can be used to study,
XX diagnose and treat disease states in which normal leukocyte function is
XX perturbed by normal leukopenias or inappropriate activation via
XX chemokine agonists or antagonists, such as infection, inflammation,
XX proliferative disease, tumorigenesis, autoimmune disease, rheumatoid
XX proliferation, solid tumours, cardiovascular disease, rheumatoid
XX arthritis, alveolitis, atherosclerosis, chronic granulomatous disease,
XX asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic
XX shock syndrome, septic shock and Chediak-Higashi syndrome
XX Sequence 332 AA;
Query Match 100.0%; Score 95; DB 2; Length 332;
Best Local Similarity 100.0%; Pred.No. 1.7e-07; Indels 0; Gaps 0
Matches 18; Conservative 0; Mismatches 0;
1 YAFVGKFRNYLLVFQK 18
277 YAFVGKFRNYLLVFQK 294

RESULT 10
AAW27407
ID AAW27407 standard; protein; 352 AA.
XX AC
XX DT 14-APR-1998 (first entry)
XX DE Human CCR5.
XX KW Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
KW atherosclerosis; autoimmune disorder.
XX OS Homo sapiens.
XX PN WO9732019-A2.
XX PD 04-SEP-1997.
XX PF 28-FEB-1997; 97WO-BE000023.
XX PR 01-MAR-1996; 96EP-00870021.
XX PR 06-AUG-1996; 96EP-00870102.
XX PA (EURO-) EUROSCREEN SA.
XX PI Samson M, Parmentier M, Vaseart G, Libert F;
XX WPI; 1997-479829/44.
XX DR N-PSDB; AAT90117.
XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
PT disease and viral infection.
XX PS Claim 4; Fig 1b-c; 94pp; English.
XX CC The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but
CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,
CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency
CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to
CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
CC atherosclerosis and autoimmune disorders
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 95; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314
RESULT 11
AAW27123
ID AAW27123 standard; protein; 352 AA.
XX AC AAW27123;
XX DT 14-DEC-1997 (first entry)
XX DE Human chemokine receptor 88C.
XX KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;

KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
KW modulator; antibody; human.
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX Domain 1..32
XX FT /label= Extracellular_domain
XX FT 56..67
XX FT /label= Intracellular_domain
XX FT 89..112
XX FT /label= Extracellular_domain
XX FT 125..145
XX FT /label= Intracellular_domain
XX FT 166..191
XX FT /label= Extracellular_domain
XX FT 213..235
XX FT /label= Intracellular_domain
XX FT 259..280
XX FT /label= Extracellular_domain
XX FT 301..352
XX FT /label= Intracellular_domain
XX PN WO9722698-A2.
XX XX
XX PD 26-JUN-1997.
XX PF 20-DEC-1996; 96WO-US020759.
XX PR 20-DEC-1995; 95US-00575967.
XX PR 07-JUN-1996; 96US-00661393.
XX PA (ICOS-) ICOS CORP.
XX PI Gray PW, Schweickart VL, Raport CJ;
XX WPI; 1997-341689/31.
XX DR N-PSDB; AAT85161.
XX PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
PT tumours, viral infections, auto-immune diseases, etc.
XX PS Claim 16; Page 47-48; 65pp; English.
XX CC This polypeptide sequence comprises novel human chemokine receptor 88C, a
CC G protein coupled receptor that is involved in leukocyte trafficking. Its
CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
CC macrophage library. It shows 62% identity to CCKR1. Chemokine receptor
CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
CC and their polypeptide fragments can be produced in transformed host
CC cells. The receptors, peptides comprising one or more of the
CC extracellular or intracellular domains, and anti-receptor antibodies can
CC be used to modulate receptor activities, particularly ligand and G
CC protein binding, and are potentially potentially useful in the treatment
CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
CC infection, AIDS, inflammatory conditions, pathological immune response,
CC abnormal haematopoietic processes etc
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 95; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314
RESULT 12
AAW27125

```

ID AAW27125 standard; protein; 352 AA.
XX
AC AAW27125;
XX
DT 14-DEC-1997, (first entry)
XX
DE Macaque chemokine receptor 88C.
XX
XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
XX KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
XX KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX KW modulator; antibody.
XX
OS Macaca sp.
XX
XX WO9722698-A2.
XX
XX 26-JUN-1997.
XX
XX 20-DEC-1996; 96WO-US020759.
XX
XX 20-DEC-1995; 95US-00575967.
XX
XX 07-JUN-1996; 96US-00661393.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX
XX WPI; 1997-341689/31.
XX
XX N-PSDB; AAT85163.
XX
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX PT tumours, viral infections, auto-immune diseases, etc.
XX
XX Claim 36; Page 57-58; 65pp; English.
XX
XX This polypeptide sequence comprises macaque chemokine receptor 88C, a G
XX CC protein coupled receptor that is involved in leukocyte trafficking. Its
XX CC amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
XX CC amplification. It shows 97% identity to human 88C (AAW27123). 88C
XX CC receptors and their polypeptide fragments can be produced in transformed
XX CC host cells. The receptors, peptides comprising one or more of the
XX CC extracellular or intracellular domains, and anti-receptor antibodies can
XX CC be used to modulate receptor activities, particularly ligand and G
XX CC protein binding, and are potentially useful in the treatment
XX CC of atherosclerosis, and are potentially useful in the treatment
XX CC of infection, AIDS, inflammatory conditions, pathological immune response,
XX CC abnormal haematopoietic processes etc. A hybridoma that produces an
XX CC antibody that specifically binds to macaque 88C is claimed
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YAFVGEKFRNYLLVFFQK 18
XX Db 297 YAFVGEKFRNYLLVFFQK 314
XX
XX RESULT 13
XX AAW07602
XX ID AAW07602 standard; protein; 352 AA.
XX
XX AC AAW07602;
XX
XX 26-FEB-1997 (first entry)
XX
XX Human G-protein chemokine receptor HDGNR10.
XX
XX G-protein chemokine receptor; HDGNR10; signal transduction;
XX
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YAFVGEKFRNYLLVFFQK 18
XX Db 297 YAFVGEKFRNYLLVFFQK 314
XX
XX RESULT 14
XX AAW23835
XX ID AAW23835 standard; protein; 352 AA.
XX
XX AC AAW23835;
XX
XX 08-JUN-1998 (first entry)
XX
XX Human CC chemokine receptor 5 (CCR5).
XX
XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;
XX KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Domain 29..55
XX FT /label= I
XX FT /note= "transmembrane domain"
XX FT Domain 104..126
XX FT /label= III
XX FT /note= "transmembrane domain"
XX FT Region 109..120
XX FT /note= "extracellular loop-1 (Claim 19)"
XX FT Domain 143..171
XX FT /label= IV
XX FT /note= "transmembrane domain"

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KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
KW therapy.
XX
XX Homo sapiens.
XX
XX WO9639437-A1.
XX
XX 12-DEC-1996.
XX
XX 06-JUN-1995; 95WO-US007173.
XX
XX 06-JUN-1995; 95WO-US007173.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Li Y, Ruben SM;
XX
XX WPI; 1997-043072/04.
XX
XX N-PSDB; AAT44042.
XX
XX Human G-protein chemokine receptor, HDGNR10 - useful to identify
XX PT (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and
XX PT acute inflammation, rheumatoid arthritis, etc.
XX
XX Claim 1; Page 44-46; 61pp; English.
XX
XX Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7
XX CC -transmembrane protein involved in signal transduction. Its amino acid
XX CC sequence was deduced from a cDNA clone (AAT44042) isolated from a human
XX CC monocyte library. Isolation of the cDNA allows prodn. of recombinant
XX CC HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant
XX CC receptor can be used to identify agonists or antagonists of the receptor;
XX CC such cpds. can be used to treat conditions related to the under- and over
XX CC -expression of G-protein chemokine receptors
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YAFVGEKFRNYLLVFFQK 18
XX Db 297 YAFVGEKFRNYLLVFFQK 314
XX
XX RESULT 14
XX AAW23835
XX ID AAW23835 standard; protein; 352 AA.
XX
XX AC AAW23835;
XX
XX 08-JUN-1998 (first entry)
XX
XX Human CC chemokine receptor 5 (CCR5).
XX
XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;
XX KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Domain 29..55
XX FT /label= I
XX FT /note= "transmembrane domain"
XX FT Domain 104..126
XX FT /label= III
XX FT /note= "transmembrane domain"
XX FT Region 109..120
XX FT /note= "extracellular loop-1 (Claim 19)"
XX FT Domain 143..171
XX FT /label= IV
XX FT /note= "transmembrane domain"

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FT Region 187..210
FT /note= "extracellular loop-2 (Claim 19)"
FT Domain 194..219
FT /label= V
FT /note= "transmembrane domain"
FT Domain 238..258
FT /label= VI
FT /note= "transmembrane domain"
FT Region 261..276
FT /note= "extracellular loop-3 (Claim 19)"
FT Domain 277..300
FT /label= VII
FT /note= "transmembrane domain"
FT XX
XX WO9745543-A2.
XX
XX 04-DEC-1997.
XX
XX 28-MAY-1997; 97WO-US009586.
XX
XX 28-MAY-1996; 96US-0018508P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
XX Broder CC, Kennedy PE;
XX WPI; 1998-032650/03.
XX N-PSDB; AAT76920.
XX
XX CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
XX between HIV and a target cell.
XX Claim 68; Fig 1C; 70pp; English.
XX
XX This protein sequence comprises of a novel human macrophage-selective CC
XX chemokine receptor that has been designated CCR5. The sequence was
XX deduced from an isolated cDNA clone (see AAT76920). An Ala127Leu variant
XX (see W238340 of CCR5 was also identified. The susceptibility of human
XX macrophages to HIV infection depends on cell surface expression of CD4
XX and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
XX protein coupled cell surface molecules. It plays an essential role in the
XX membrane fusion step of infection by some HIV isolates. The establishment
XX of stable, non-human cell lines and transgenic mammals having cells that
XX coexpress human CD4 and CCR5 provides valuable tools for research of HIV
XX infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
XX agents capable of blocking membrane fusion between HIV and target cells
XX represent potential anti-HIV therapeutics for macrophage tropic strains
XX of HIV
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 YAFVGEKFRNLLVFFQK 18
XX |||||
XX 297 YAFVGEKFRNLLVFFQK 314
XX
XX Db
XX
XX RESULT 15
XX AAW88232
XX ID AAW88232 standard; protein; 352 AA.
XX
XX AAW88232;
XX
XX 15-MAR-1999 (first entry)
XX
XX HIV-1 co-receptor CCR5.
XX
XX HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
XX gene therapy; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 32..56
XX /note= "transmembrane domain 1"
XX Domain 67..87
XX /note= "transmembrane domain 2"
XX Misc-difference 101
XX /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA
XX (stop) in Ccr5m303"
XX Domain 103..124
XX /note= "transmembrane domain 3"
XX Domain 142..167
XX /note= "transmembrane domain 4"
XX Domain 200..223
XX /note= "transmembrane domain 5"
XX Domain 236..260
XX /note= "transmembrane domain 6"
XX Domain 275..301
XX /note= "transmembrane domain 7"
XX
XX WO9854317-A1.
XX
XX 03-DEC-1998.
XX
XX 29-MAY-1998; 98WO-BP003437.
XX
XX 30-MAY-1997; 97US-0048057P.
XX
XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX
XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
XX WPI; 1999-059835/05.
XX N-PSDB; AAV84126.
XX
XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
XX resistance of CCR5-expressing cells to HIV-1 infection.
XX
XX Disclosure; Page 34-35; 55pp; English.
XX
XX This is the amino acid sequence of wild-type human CCR5, which serves as
XX a co-receptor for infection by macrophage-tropic (M-tropic) strains of
XX HIV-1. The invention relates to the identification of a CCR5 variant (see
XX AAW8231), designated CCR5m303, comprising the first two transmembrane
XX domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
XX presence of the CCR5m303 variant with the wild type CCR5 allele shows a
XX positive correlation with resistance to infection with M-tropic HIV-1
XX strains, and may indicate slower progression of the disease. The
XX detection of CCR5 variants may be used to identify individuals at lower
XX risk of infection relative to the general population who, if infected,
XX may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
XX 36) are provided for use in diagnostic methods for detecting the presence
XX of such variants. A method is provided for inhibiting HIV-1 infection of
XX a cell expressing the CCR5 receptor. This involves introducing a nucleic
XX acid encoding a CCR5 variant into the cell, thereby reducing the number
XX of functional CCR5 molecules present on the cell surface
XX
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 YAFVGEKFRNLLVFFQK 18
XX |||||
XX 297 YAFVGEKFRNLLVFFQK 314
XX
XX Db
XX
XX RESULT 16
XX AAY80128
XX ID AAY80128 standard; protein; 352 AA.

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XX AC AAY80128;
XX DT 19-MAY-2000 (first entry)
XX DE Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
XX KW Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
XX KW diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
XX KW tumour; infection; leukaemia; psoriasis; allergy;
XX KW T-cell mediated autoimmune disease; atherosclerosis; anaphylaxis;
XX KW inflammation; allergic reaction; silicosis; sarcoidosis;
XX KW rheumatoid arthritis; hyper-eosinophilia syndrome.
XX OS Homo sapiens.
XX PN US6025154-A.
XX PD 15-FEB-2000.
XX PF 06-JUN-1995; 95US-00466343.
XX PR 06-JUN-1995; 95US-00466343.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Li Y, Ruben SM;
XX DR WPI; 2000-181807/16.
XX DR N-PSDB; AAZ91481.
XX PT Isolated nucleic acid encoding human G-protein chemokine receptor useful
XX PT for diagnostic assays, scientific research and screening for compounds
XX PT which bind to and activate or inhibit activation of the receptor
XX PT polypeptides.
XX PS Claim 1; Fig 1; 22pp; English.
XX CC The present sequence represents a human G-protein chemokine receptor
XX CC designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
XX CC screening for compounds which bind to and either: (1) activate the
XX CC HDGNR10 polypeptides causing stimulation of haematopoiesis, wound
XX CC healing, coagulation, and angiogenesis; treatment of solid tumours,
XX CC chronic infections, leukaemia, T-cell mediated autoimmune diseases,
XX CC parasitic infections, psoriasis, and to stimulate growth factor activity;
XX CC or (2) inhibit activation of the HDGNR10 polypeptides which is useful for
XX CC preventing and/or treating allergy, atherosclerosis, anaphylaxis,
XX CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
XX CC E-mediated allergic reactions, prostaglandin-independent fever, bone
XX CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
XX CC hyper-eosinophilia syndrome. The polynucleotides are also useful for
XX CC diagnostic assays for detecting diseases related to mutations in the
XX CC nucleic acid sequences encoding the polypeptides and for detecting an
XX CC altered level of the soluble form of the receptor polypeptides. The
XX CC polynucleotides are also useful for in vitro purposes related to
XX CC scientific research, synthesis of DNA and manufacture of DNA vectors
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314
RESULT 17
AAG79089
ID AAG79089 standard; protein; 352 AA.
XX AAG79089;
AC

XX DT 10-DEC-2001 (first entry)
XX DE Amino acid sequence of human CCR5 protein.
XX KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
XX OS Homo sapiens.
XX PN WO200164752-A2.
XX PD 07-SEP-2001.
XX PF 28-FEB-2001; 2001WO-US006322.
XX PR 02-MAR-2000; 2000US-00517605.
XX PA (UYNY) UNIV NEW YORK STATE.
XX PA (UYNI-) UNIV NIJMEGEN.
XX PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
XX DR WPI; 2001-602565/68.
XX PT An antibody for the treatment or prevention of HIV-infection comprises a
XX PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
XX PT DC-SIGN due to concomitant conformational change.
XX PS Disclosure; Page 118-119; 131pp; English.
XX CC The specification describes an antibody which is specific for an
XX CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
XX CC is exposed upon gp120 binding of DC-SIGN due to concomitant
XX CC conformational change. DC-SIGN is a receptor that is specifically
XX CC expressed on dendritic cells and facilitates infection of T lymphocytes
XX CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
XX CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
XX CC with high affinity. The antibody of the invention inhibits the trans
XX CC enhancement of HIV entry into a T cell or macrophage facilitated by
XX CC dendritic cells. The antibody is useful to treat or prevent HIV
XX CC infection. The present sequence represents a human CCR5 protein, which is
XX CC a translocation promoting agent that interacts with CD4. This receptor
XX CC functions in HIV-1 entry into cells
XX SQ Sequence 352 AA;
Query Match 100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314
RESULT 18
AAE07046
ID AAE07046 standard; protein; 352 AA.
XX AAE07046;
XX AAE07046;
XX DT 16-OCT-2001 (first entry)
XX DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
XX KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
KW cytosolic; immunosuppressive; neutropenic; neuroprotective; gene therapy;
KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
KW

KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT Domain 1..36
 FT /label= Extracellular_domain
 FT Domain 37..305
 FT /label= Transmembrane_domain
 FT Domain 37..58
 FT /label= Transmembrane_domain
 FT /note= "Segment 1"
 FT Domain 59..67
 FT /label= Intracellular_loop_1
 FT Domain 68..88
 FT /label= Transmembrane_domain
 FT /note= "Segment 2"
 FT Domain 89..102
 FT /label= Extracellular_loop_1
 FT Domain 103..124
 FT /label= Transmembrane_domain
 FT /note= "Segment 3"
 FT Domain 125..141
 FT /label= Intracellular_loop_2
 FT Domain 142..166
 FT /label= Transmembrane_domain
 FT /note= "Segment 4"
 FT Domain 167..195
 FT /label= Extracellular_loop_2
 FT Domain 196..223
 FT /label= Transmembrane_domain
 FT /note= "Segment 5"
 FT Domain 224..235
 FT /label= Intracellular_loop_3
 FT Domain 236..260
 FT /label= Transmembrane_domain
 FT /note= "Segment 6"
 FT Domain 261..274
 FT /label= Extracellular_loop_3
 FT Domain 287..305
 FT /label= Transmembrane_domain
 FT /note= "Segment 7"
 FT Domain 306..352
 FT /label= Intracellular_domain

PN WO200158916-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004153.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488966/53.

XX N-PSDB; AAD13282.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.

XX Claim 102; Fig 1; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)

CC HDGMR10 polypeptides and polynucleotides. CCR5 HDGMR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder

CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection; a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC disease or disorder may be associated with aberrant CCR5 expression, lack
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGMR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGMR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGMR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The
 CC present sequence is human CCR5 HDGMR10 protein

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.9e-07; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YAFVGEKFRNLLVFPQK 18

Db 297 YAFVGEKFRNLLVFPQK 314
 |||||

RESULT 19

AAE07048

ID AAE07048 standard; protein; 352 AA.

XX AAE07048;

XX 16-OCT-2001 (first entry)

XX Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; neutropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX WO200158916-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004153.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488966/53.

XX N-PSDB; AAD13299.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor

PT (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune

PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.

PS Example 40; Page 504-505; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)
 CC HDGMR10 polypeptides and polynucleotides. CCR5 HDGMR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC disease or disorder may be associated with aberrant CCR5 expression, lack
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGMR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGMR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGMR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The
 CC present sequence is human CCR5 HDGMR10 protein

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 20

AAAG80111
 ID AAG80111 standard; protein; 352 AA.

XX AAG80111;

DT 17-JAN-2002 (first entry)

XX Human CCR5 protein.

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.

XX Homo sapiens.

XX WO200172830-A2.

PD 04-OCT-2001.

PF 02-APR-2001; 2001WO-EP003708.

XX 31-MAR-2000; 2000DE-01016013.

XX (IPFP-) IPF PHARM GMEH.

XX (FORS/) FORSMANN U.

PI Forssmann W, Adermann K, Heitland A, Spodsborg N;

XX WPI; 2001-626256/72.

XX

PT Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.

PS Disclosure; Page 10; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 21

AAE04321
 ID AAE04321 standard; protein; 352 AA.

XX AAE04321;

DT 04-SEP-2001 (first entry)

XX Human chemokine receptor (CKR), CC-CKR-5 related protein #2.

XX Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CKR-5; envelope glycoprotein; anti-HIV.

XX Homo sapiens.

XX US6258527-B1.

XX 10-JUL-2001.

XX 21-MAY-1997; 97US-00861105.

XX 20-MAY-1996; 96US-0017157P.

XX 19-JUN-1996; 96US-0020043P.

XX 19-MAY-1997; 97US-00858660.

XX (AARO-) AARON DIAMOND AIDS RES CENT.

XX (UANY) UNIV NEW YORK STATE.

XX Littman DR, Deng H, Eilmeier W, Landau NR, Liu R;

XX WPI; 2001-417127/44.

XX N-PSDB; AAD08577.

XX

PT Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
 PT and HIV LTR for identification of drugs and antibodies for treatment of
 PT HIV.

XX

Db 297 YAFVGEKFRNYLLVFFQK 314
 |||
 297 YAFVGEKFRNYLLVFFQK 314

RESULT 23
 AAE07039
 ID AAE07039 standard; protein; 352 AA.
 XX AC AAE07039;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
 KW cytosolic; immunosuppressive; nontropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200158915-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004152.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 XX
 PR 09-MAR-2000; 2000US-0187999P.
 XX
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2001-488965/53.
 XX
 DR N-PSDB; AAD13198.
 XX
 PT Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX
 PS Example 40; Page 486-487; 495pp; English.
 XX
 CC The present sequence is human G-protein chemokine receptor (CCR5) HDGMR10
 CC protein. CCR5 HDGMR10 antibodies are useful for treating, preventing or
 CC ameliorating a disease or disorder associated with inflammation, such as
 CC defective or aberrant chemotaxis of immune cells, HIV infection, (such as
 CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
 CC aberrant T-cell antigen presenting cell interaction. The disease or
 CC disorder may also be an infectious disease (e.g. a viral infection such
 CC as an early stage HIV infection, a cytomegalovirus infection, or a
 CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
 CC neurodegenerative disorder. The disease or disorder may be associated
 CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
 CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGMR10 protein
 CC is used as a food additive or preservative to increase or decrease
 CC storage capabilities. CCR5 HDGMR10 DNA are useful for chromosome
 CC identification and in gene therapy. CCR5 HDGMR10 DNA, protein,
 CC antibodies, agonists and antagonists are also useful in the diagnosis,
 CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
 CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
 CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
 CC disorders (myocardial ischaemias) and wound healing

SQ Sequence 352 AA;
 Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||
 DB 297 YAFVGEKFRNYLLVFFQK 314
 |||

RESULT 24
 AAB46858
 ID AAB46858 standard; protein; 352 AA.
 XX AAB46858;
 XX
 DT 16-AUG-2001 (revised)
 XX
 DT 02-AUG-2001 (revised)
 XX
 DT 04-MAY-2001 (first entry)
 XX
 DE Human HDGMR10 protein.
 XX
 KW HDGMR10; human; G-protein chemokine receptor; antiinflammatory;
 KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
 KW cytosolic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;
 KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
 KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
 KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
 KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
 KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
 KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
 KW hyper-eosinophilic syndrome; vulnerary.
 XX
 OS Homo sapiens.
 XX
 PN US2001000241-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 29-NOV-2000; 2000US-00725285.
 XX
 PR 06-JUN-1995; 95US-00466343.
 XX
 PR 18-NOV-1998; 98US-00195662.
 XX
 PR 25-JUN-1999; 99US-00339912.
 XX
 PA (LIYY/) LI Y.
 PA (RUSE/) RUBEN S M.
 XX
 PI Li Y, Ruben SM;
 XX
 DR WPI; 2001-226317/23.
 XX
 DR N-PSDB; AAF26390.
 XX
 PT New human G-protein chemokine receptor polypeptides and polynucleotides,
 PT useful for identifying (antagonists to the G-protein chemokine receptor.
 XX
 PS Claim 1a; Page 15; 22pp; English.
 XX
 CC This invention describes a novel receptor polypeptide (I) selected from
 CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the
 CC specification; and (ii) a polypeptide encoded by the cDNA contained in a
 CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
 CC products of the invention have antiinflammatory, immunomodulatory,
 CC anticoagulant, antiallergic, immunosuppressive, vulnerary, cytostatic,
 CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic
 CC activity and can be used for gene therapy. The G-protein chemokine
 CC receptors, HDGMR10, (I) are useful for screening for compounds which
 CC activate or inhibit activation of (I). The products of the invention can
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,
 CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and
 CC stimulating growth factor activity. HDGMR10 is useful for treating

CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
 CC reactions, prostaglandin-independent fever, bone marrow failure,
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
 CC errors in the keyword formatting)

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 25
 ABB56342
 ID ABB56342 standard; protein; 352 AA.

XX AC ABB56342;

XX DT 18-FEB-2002 (first entry)

XX DE Non-endogenous human GPCR protein, SEQ ID NO: 477.

XX KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 constitutively activated GPCR; agonist; disease.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200177172-A2.

XX PD 18-OCT-2001.

XX PF 05-APR-2001; 2001WO-US011098.

XX PR 07-APR-2000; 2000US-0195747P.

XX PA (AREN-) ARENA PHARM INC.

XX PI Lehmann-Bruinsma K, Liaw CW, Lin I;

XX WPI; 2001-648759/74.

XX DR N-PSDB; ABI97978.

XX PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 disease treatment, comprises contacting candidate compounds with versions
 of GPCRs.

XX PS Claim 1; Page 277-278; 394pp; English.

XX CC The invention relates to G protein-coupled receptors (GPCRs) for which
 the endogenous ligand has been identified. Non-endogenous constitutively
 activated versions of known GPCRs are used in the invention for the
 direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence is a non-endogenous version of a known human GPCR.

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 26
 AAB83354
 ID AAB83354 standard; protein; 352 AA.

XX AC AAB83354;

XX DT 09-OCT-2001 (first entry)

XX DE Human CCR5 protein sequence.

XX KW Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
 human immunodeficiency virus; anti-inflammatory disease; human.

XX OS Homo sapiens.

XX PN BP1118858-A2.

XX PD 25-JUL-2001.

XX PF 03-JAN-2001; 2001EP-00300020.

XX PR 12-JAN-2000; 2000GB-00000659.

XX PR 12-JAN-2000; 2000GB-00000661.

XX PR 12-JAN-2000; 2000GB-00000663.

XX PA (PF12) PFIZER LTD.

XX PA (PF12) PFIZER INC.

XX PI Dobbs S, Perros M, Rickett GA;

XX WPI; 2001-477088/52.

XX DR N-PSDB; AAF87099.

XX PT Determining if an agent can modulate CCR5-gp120 interaction, comprises
 incubating the agent with CCR5 and gp120 and determining if the agent
 modulates the interaction.

XX PS Claim 1; Page 110; 113pp; English.

XX CC This sequence represents the human CCR5 protein sequence. The invention
 relates to a method for determining whether an agent is capable of
 CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and
 CC determining whether the agent modulates the interaction, where gp120 is
 CC associated with CD4, and where the interaction is a low affinity binding.
 CC The method is used to identify an agent capable of modulating the
 CC interaction of CCR5 with gp120. An agent identified by the method is used
 CC to prepare a pharmaceutical composition for the treatment of a disease or
 CC condition associated with CCR5 and gp120 interaction, to treat a subject
 CC with a disease or condition associated with CCR5 and gp120 interaction,
 CC and for preparing a pharmaceutical for treating human immunodeficiency
 CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
 CC is commercially useful, amenable to high throughput screening, and
 CC detects interaction of gp120 with cells expressing only CCR5

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 27
 AAB82948
 ID AAB82948 standard; protein; 352 AA.

XX AC AAB82948;

DT 21-DEC-2001 (first entry)
 XX Human HIV-1 co-receptor CCR5.
 XX CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
 XX infection; therapy; vaccine; anti-HIV-1.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX Binding-site 2..18
 XX /note="binds to HIV-1 gp120"
 XX W0200164710-A2.
 XX 07-SEP-2001.
 XX 28-FEB-2001; 2001WO-US006599.
 XX 29-FEB-2000; 2000US-0185657P.
 XX 19-MAY-2000; 2000US-0205939P.
 XX 07-FEB-2001; 2001US-0267231P.
 XX (PROG-) PROGENICS PHARM INC.
 XX (AARO-) AARON DIAMOND AIDS RES CENT.
 XX Dragic T, Olson WC;
 XX WPI; 2001-611273/70.
 XX N-PSDB; AAH26903.
 XX Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-
 XX receptor) amino terminal domain including negatively charged and two
 XX sulfated tyrosine residues is useful for treating HIV infection in
 XX humans.
 XX Claim 1; Page 30; 163pp; English.
 XX The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids
 XX 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding
 XX site that determines the specificity of the interaction between CCR5 and
 XX HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the
 XX CCR5 N-terminus is required for gp120 binding and may critically modulate
 XX the susceptibility of target cells to HIV-1 infection in vivo. The
 XX invention provides claimed sulfated peptides (see AAB82947) that are
 XX based on the CCR5 N-terminal region and which are effective for
 XX inhibiting HIV-1 binding to CCR5. These peptides are used in claimed
 XX methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+
 XX cells from becoming infected with HIV, of treating a subject whose CD4+
 XX cells are infected with HIV, and of identifying an agent which inhibits
 XX binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried
 XX out in a subject, especially a human, infected (therapeutic method), not
 XX infected with HIV (prophylactic method), or in a subject who is not
 XX infected with, but has been exposed to, HIV

XX Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
 XX immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 XX neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 XX hyperproliferative disease; neurological disease; receptor.
 XX Homo sapiens.
 XX US2002048786-A1.
 XX 25-APR-2002.
 XX 09-FEB-2001; 2001US-00779879.
 XX 09-FEB-2000; 2000US-0181258P.
 XX 09-MAR-2000; 2000US-0187999P.
 XX 22-SEP-2000; 2000US-0234336P.
 XX (ROSE/) ROSEN C A.
 XX (ROSC/) ROSCHKE V.
 XX (LIYY/) LI Y.
 XX (RUBE/) RUBEN S M.
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI: 2002-434754/46.
 XX N-PSDB; ABK51853.
 XX New nucleic acid encoding an antibody specific for the G-protein
 XX chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 XX inflammation.
 XX Claim 61; Fig 1; 180pp; English.
 XX The present invention relates to the isolation of a novel human G-protein
 XX chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
 XX sequences encoding it. The invention also describes antibodies that bind
 XX human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
 XX sequences encoding the antibodies. The antibodies are useful for treating
 XX or preventing inflammation, defective or aberrant chemotaxis of immune
 XX cells and T-cell/antigen-presenting cell interactions, infections and
 XX autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 XX infections (especially early-stage human immune deficiency virus (HIV),
 XX cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 XX associated with aberrant or deficient expression of the CCR5 receptor or
 XX its ligands. The antibodies are also useful to determine CCR5 expression,
 XX e.g. for diagnosis, prognosis and monitoring of cancer and other
 XX hyperproliferative diseases. The polynucleotide sequences encoding human
 XX G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
 XX recombinant receptor, and in the treatment of a wide range of diseases
 XX such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 XX Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 XX present sequence represents human G-protein chemokine receptor (CCR5)
 XX HDGNR10 #1

XX Sequence 352 AA;
 XX Query Match 100.0%; Score 95; DB 4; Length 352;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314
 |||||
 RESULT 28
 AAU97150
 ID AAU97150 standard; protein; 352 AA.
 XX AAU97150;
 XX 13-AUG-2002 (first entry)

XX Sequence 352 AA;
 XX Query Match 100.0%; Score 95; DB 5; Length 352;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314
 |||||
 RESULT 29
 AAU97152
 ID AAU97152 standard; protein; 352 AA.
 XX AAU97152;
 XX 13-AUG-2002 (first entry)

```

XX DT 13-AUG-2002 (first entry)
XX DE Human G-protein chemokine receptor (CCR5) HDGNR10 #2.
XX KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
XX KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
XX KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
XX KW hyperproliferative disease; neurological disease; receptor.
XX OS Homo sapiens.
XX PN US2002048786-A1.
XX PD 25-APR-2002.
XX PF 09-FEB-2001; 2001US-00779879.
XX PR 09-FEB-2000; 2000US-0181258P.
XX PR 09-MAR-2000; 2000US-0187999P.
XX PR 22-SEP-2000; 2000US-0234336P.
XX PA (ROSE/) ROSEN C A.
XX PA (ROSC/) ROSCHKE V.
XX PA (LIY/) LI Y.
XX PA (RUBE/) RUBEN S M.
XX PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX XX
XX DR WPI; 2002-434754/46.
XX DR N-PSDB; ABK51870.
XX PT New nucleic acid encoding an antibody specific for the G-protein
XX PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
XX PT inflammation.
XX PS Disclosure; Page 165-166; 180pp; English.
XX CC The present invention relates to the isolation of a novel human G-protein
XX CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
XX CC sequences encoding it. The invention also describes antibodies that bind
XX CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
XX CC sequences encoding the antibodies. The antibodies are useful for treating
XX CC or preventing inflammation, defective or aberrant chemotaxis of immune
XX CC cells and T-cell/antigen-presenting cell interactions, infections and
XX CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
XX CC infections (especially early-stage human immune deficiency virus (HIV),
XX CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
XX CC associated with aberrant or deficient expression of the CCR5 receptor or
XX CC its ligands. The antibodies are also useful to determine CCR5 expression,
XX CC e.g. for diagnosis, prognosis and monitoring of cancer and other
XX CC hyperproliferative diseases. The polynucleotide sequences encoding human
XX CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
XX CC recombinant receptor, and in the treatment of a wide range of diseases
XX CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
XX CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
XX CC present sequence represents human G-protein chemokine receptor (CCR5)
XX CC HDGNR10 #2
XX SQ Sequence 352 AA;
XX
Query Match 100.0%; Score 95; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314
RESULT 30
AAM52829
ID AAM52829 standard; protein; 352 AA.

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```

XX AC AAM52829;
XX DT 22-FEB-2002 (first entry)
XX DE Human CCR5 Gln 55 variant.
XX KW CCR5; CC chemokine receptor 5; human; HIV infection;
XX KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
XX KW drug screening; identification; variant.
XX OS Homo sapiens.
XX PN WO200171346-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009155.
XX PR 21-MAR-2000; 2000US-0190946P.
XX PR 21-MAR-2000; 2000US-0190996P.
XX PR 21-MAR-2000; 2000US-0191299P.
XX PR 20-MAR-2001; 2001US-00813448.
XX PR 20-MAR-2001; 2001US-00813651.
XX PR 20-MAR-2001; 2001US-00813653.
XX PA (CONS-) CONSENSUS PHARM INC.
XX PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX DR WPI; 2002-010610/01.
XX DR N-PSDB; ABA02318.
XX PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX PT comprises binding a molecule from library to a molecule having binding
XX PT property corresponding to CCR5 and identifying bound molecule.
XX PS Example 3; Fig 4B; 50pp; English.
XX CC The invention relates to a method for identifying a binding compound for
XX CC CC chemokine receptor 5 (CCR5). The method involves screening a library
XX CC of test molecules (particularly peptides) with immobilised CCR5, and then
XX CC identifying those molecules which bind. The invention also relates to
XX CC CCR5-binding molecules identified using the method of the invention,
XX CC methods for identifying consensus motifs for CCR5-binding peptides, a
XX CC transfer vector encoding tagged CCR5, a computer-aided methods for
XX CC determining the relative binding affinity of a test molecule to CCR5 and
XX CC a computer aided drug screening assay that utilises the three-dimensional
XX CC structure of CCR5. Compounds identified using the methods of the
XX CC invention are useful for treating or preventing HIV (human
XX CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
XX CC syndrome) in a patient. The methods of the invention may also be used to
XX CC identify agonists or antagonists of the interaction of CCR5 with its
XX CC natural ligand, and to determine a binding motif for CCR5. The present
XX CC sequence represents a naturally occurring variant of human CCR5 in which
XX CC there is a glutamine, rather than a leucine, at position 55
XX SQ Sequence 352 AA;
XX
Query Match 100.0%; Score 95; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314

```


RESULT 31

AAM52828
ID AAM52828 standard; protein; 352 AA.

XX AC AAM52828;

XX AC AAM52828;

XX DT 22-FEB-2002 (first entry)

XX DE Human CC chemokine receptor 5 (CCR5).

XX KW CCR5; CC chemokine receptor 5; human; HIV infection;
 XX KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
 KW drug screening; identification.

XX OS Homo sapiens.

XX PN WO200171346-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US009155.

XX PR 21-MAR-2000; 2000US-0190946P.

XX PR 21-MAR-2000; 2000US-0190996P.

XX PR 21-MAR-2000; 2000US-0191299P.

XX PR 20-MAR-2001; 2001US-00813448.

XX PR 20-MAR-2001; 2001US-00813651.

XX PR 20-MAR-2001; 2001US-00813653.

XX PA (CONS-) CONSENSUS PHARM INC.

XX PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;

XX DR WPI; 2002-010610/01.

XX DR N-PSDB; ABA02317.

XX PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
 PT comprises binding a molecule from library to a molecule having binding
 PT property corresponding to CCR5 and identifying bound molecule.

XX PS Example 3; Fig 4A; 50pp; English.

XX CC The invention relates to a method for identifying a binding compound for
 CC CC chemokine receptor 5 (CCR5). The method involves screening a library
 CC of test molecules (particularly peptides) with immobilised CCR5, and then
 CC identifying those molecules which bind. The invention also relates to
 CC CCR5-binding molecules identified using the method of the invention,
 CC methods for identifying consensus motifs for CCR5-binding peptides, a
 CC transfer vector encoding tagged CCR5, a computer-aided methods for
 CC determining the relative binding affinity of a test molecule to CCR5 and
 CC a computer aided drug screening assay that utilises the three-dimensional
 CC structure of CCR5. Compounds identified using the methods of the
 CC invention are useful for treating or preventing HIV (human
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
 CC syndrome) in a patient. The methods of the invention may also be used to
 CC identify agonists or antagonists of the interaction of CCR5 with its
 CC natural ligand, and to determine a binding motif for CCR5. The present
 CC sequence represents human CCR5

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 32

ABG70597

ID ABG70597 standard; protein; 352 AA.

XX AC ABG70597;

XX DT 03-DEC-2002 (first entry)

XX DE Human G-protein chemokine receptor, HDGNR10.

XX KW Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;
 KW haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;
 KW chronic infection; leukaemia; T-cell mediated autoimmune disease;
 KW parasitic infection; psoriasis; growth factor activity; allergy;
 KW atherogenesis; anaphylaxis; malignancy; inflammation; histamine;
 KW immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;
 KW prostaglandin-independent fever; bone marrow failure; shock;
 KW rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic;
 KW immunosuppressive; antiparasitic; antipsoriatic; antiallergic;
 KW antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;
 KW antipyretic; receptor.

XX OS Homo sapiens.

XX PN US2002099176-A1.

XX PD 25-JUL-2002.

XX PF 25-JUN-1999; 99US-00339912.

XX PR 06-JUN-1995; 95US-00466343.

XX PA (LIYY/) LI Y.

XX PA (RUBE/) RUBEN S M.

XX PI Li Y, Ruben SM;

XX DR WPI; 2002-690494/74.

XX DR N-PSDB; ABS54272.

XX PT Novel human G-protein chemokine receptor polypeptide useful for
 PT identifying modulators for stimulating hematopoiesis, wound healing,
 PT leukemia, for treating allergy, rheumatoid arthritis, shock and as
 PT research agents.

XX PS Claim 7; Fig 1; 22pp; English.

XX CC The present invention relates to the isolation of human G-protein
 CC chemokine receptor, HDGNR10 (CCR5 receptor), and the polynucleotide
 CC sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences
 CC are or useful for diagnosing a disease or a susceptibility to a disease
 CC related to underexpression of HDGNR10. They are useful for identifying
 CC modulators for stimulating haematopoiesis, wound healing, coagulation,
 CC angiogenesis, to treat solid tumours, chronic infections, leukaemia, T-
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, or
 CC for stimulating growth factor activity. The sequences are also useful for
 CC preventing and/or treating allergy, atherosclerosis, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 CC E (IgE)-mediated allergic reactions, prostaglandin-independent fever,
 CC bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. Polynucleotide sequences encoding HDGNR10 can be
 CC used in gene therapy to treat conditions related to underexpression of
 CC HDGNR10. The present sequence represents human G-protein chemokine
 CC receptor, HDGNR10

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

DB 297 YAFVGEKFRNLLVFFQK 314

XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 95; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQX 314
 |||||
 RESULT 34
 ABG92880
 ID ABG92880 standard; protein; 352 AA.
 XX AC ABG92880;
 XX AC ABG92880;
 DT 19-NOV-2002 (first entry)
 XX DE Human G-protein chemokine receptor (CCRS) HDGNR10 #1.
 XX KW Immunoglobulin; variable heavy chain; variable light chain; human;
 KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
 KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
 KW lymphocytopenia.
 OS Homo sapiens.
 XX OS Homo sapiens.
 XX WO200264612-A2.
 PD 22-AUG-2002.
 XX 08-FEB-2002; 2002WO-US003634.
 PR 09-FEB-2001; 2001US-00779880.
 PR 09-FEB-2001; 2001WO-US004153.
 PR 12-JUN-2001; 2001US-0297257P.
 PR 08-AUG-2001; 2001US-0310458P.
 PR 12-OCT-2001; 2001US-0328447P.
 PR 21-DEC-2001; 2001US-0341725P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Roschke V, Rosen CA, Ruben SM;
 WPI; 2002-643455/69.
 DR N-PSDB; ABS68606.
 XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for
 PT treating, preventing, ameliorating or monitoring diseases or disorders
 PT associated with aberrant expression of HDGNR10 e.g. cancer.
 XX Example 55; Fig 4; 562pp; English.
 XX The invention describes an isolated polynucleotide encoding a first
 CC antibody at least 95-100% identical to a second antibody consisting of an
 CC amino acid sequence comprising at least one, two or three CDR regions of
 CC a variable heavy (VH) or variable light (VL) domain of the antibody
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
 CC is useful treating, preventing, ameliorating, prognosing or monitoring
 CC cancers or other diseases or disorders e.g. immunologic deficiency
 CC syndromes such as blood protein disorders and ataxia telangiectasia,
 CC inflammation associated disorders such as endotoxin lethality, nephritis
 CC and inflammatory bowel disease, conditions associated with an increase in
 CC against HDGNR10

XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 95; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQX 314
 |||||
 RESULT 34
 ABG92880
 ID ABG92880 standard; protein; 352 AA.
 XX AC ABG92880;
 XX AC ABG92880;
 DT 19-NOV-2002 (first entry)
 XX DE Human G-protein chemokine receptor (CCRS) HDGNR10 #1.
 XX KW Immunoglobulin; variable heavy chain; variable light chain; human;
 KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
 KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
 KW lymphocytopenia.
 OS Homo sapiens.
 XX OS Homo sapiens.
 XX WO200264612-A2.
 PD 22-AUG-2002.
 XX 08-FEB-2002; 2002WO-US003634.
 PR 09-FEB-2001; 2001US-00779880.
 PR 09-FEB-2001; 2001WO-US004153.
 PR 12-JUN-2001; 2001US-0297257P.
 PR 08-AUG-2001; 2001US-0310458P.
 PR 12-OCT-2001; 2001US-0328447P.
 PR 21-DEC-2001; 2001US-0341725P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Roschke V, Rosen CA, Ruben SM;
 WPI; 2002-643455/69.
 DR N-PSDB; ABS68606.
 XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for
 PT treating, preventing, ameliorating or monitoring diseases or disorders
 PT associated with aberrant expression of HDGNR10 e.g. cancer.
 XX Example 55; Fig 4; 562pp; English.
 XX The invention describes an isolated polynucleotide encoding a first
 CC antibody at least 95-100% identical to a second antibody consisting of an
 CC amino acid sequence comprising at least one, two or three CDR regions of
 CC a variable heavy (VH) or variable light (VL) domain of the antibody
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
 CC is useful treating, preventing, ameliorating, prognosing or monitoring
 CC cancers or other diseases or disorders e.g. immunologic deficiency
 CC syndromes such as blood protein disorders and ataxia telangiectasia,
 CC inflammation associated disorders such as endotoxin lethality, nephritis
 CC and inflammatory bowel disease, conditions associated with an increase in
 CC against HDGNR10

CC certain haematopoietic cells such as histiocytosis, defective or aberrant
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
 CC an infectious disease, an autoimmune disease such as Addison's disease,
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
 CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
 CC disease or disorder associated with aberrant expression of novel human G-
 CC protein chemokine receptor (CCR5) HDGNR10. This is an amino acid sequence
 CC of Human G-protein chemokine receptor (CCR5) HDGNR10 #1
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLYLVFFQK 314

RESULT 35
 AAE25808
 ID AAE25808 standard; protein; 352 AA.
 XX
 AC AAE25808;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5), HDGNR10 #1.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
 KW inflammation; viral infection; autoimmune disease; neurodegeneration;
 KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
 KW hyperproliferative disease; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002061834-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 09-FEB-2001; 2001US-00779880.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 PA (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIY/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 XX
 DR WPI; 2002-499674/53.
 DR N-PSDB; AAD42409.
 XX
 PT New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
 PT useful for treatment, prevention and diagnosis of e.g. cancer, also
 PT related antibodies.
 XX
 PS Claim 61; Page 163-164; 186pp; English.
 XX
 CC The invention relates to human G-protein chemokine receptor (CCR5),
 CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
 CC antibodies are used for the treatment or prevention of inflammation,
 CC defective or aberrant chemotaxis of immune cells or T cell antigen-
 CC presenting cell interaction, viral infections (specifically human immune
 CC deficiency (including its early stages), cytomegalovirus or pox viruses),
 CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
 CC carinii infection, Kaposi's sarcoma or any condition associated with
 CC hyperproliferative diseases. The present sequence is human G-protein
 CC chemokine receptor (CCR5), HDGNR10 DNA

CC aberrant expression of CCR5 or their ligands. They are also used for the
 CC detection, diagnosis, prognosis and monitoring of cancers or other
 CC hyperproliferative diseases. The present sequence is human G-protein
 CC chemokine receptor (CCR5), HDGNR10 DNA
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLYLVFFQK 314

RESULT 36
 AAE25811
 ID AAE25811 standard; protein; 352 AA.
 XX
 AC AAE25811;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5), HDGNR10 #2.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
 KW inflammation; viral infection; autoimmune disease; neurodegeneration;
 KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
 KW hyperproliferative disease; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002061834-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 09-FEB-2001; 2001US-00779880.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 PA (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIY/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 XX
 DR WPI; 2002-499674/53.
 DR N-PSDB; AAD42426.
 XX
 PT New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
 PT useful for treatment, prevention and diagnosis of e.g. cancer, also
 PT related antibodies.
 XX
 PS Disclosure; Page 170; 186pp; English.
 XX
 CC The invention relates to human G-protein chemokine receptor (CCR5),
 CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
 CC antibodies are used for the treatment or prevention of inflammation,
 CC defective or aberrant chemotaxis of immune cells or T cell antigen-
 CC presenting cell interaction, viral infections (specifically human immune
 CC deficiency (including its early stages), cytomegalovirus or pox viruses),
 CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
 CC carinii infection, Kaposi's sarcoma or any condition associated with
 CC aberrant expression of CCR5 or their ligands. They are also used for the
 CC detection, diagnosis, prognosis and monitoring of cancers or other
 CC hyperproliferative diseases. The present sequence is human G-protein
 CC chemokine receptor (CCR5), HDGNR10 DNA
 XX
 SQ Sequence 352 AA;

```

Query Match      100.0%; Score 95; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314
|||||

RESULT 37
ABB81054
ID ABB81054 standard; protein; 352 AA.
XX
AC ABB81054;
XX
XX 05-NOV-2002 (first entry)
XX
DE G-protein chemokine receptor, HDGNR10.
XX
KW 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;
KW G-protein chemokine receptor; haematopoietic; immunosuppressant;
KW antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic;
KW antirheumatic; antiarthritic; gene therapy; human; receptor.
XX
OS Homo sapiens.
XX
XX US2002076745-A1.
XX
XX 20-JUN-2002.
XX
XX 18-NOV-1998; 98US-00195662.
XX
XX 06-JUN-1995; 95US-00466343.
XX
XX (LIYY/) LI Y.
XX (RUBE/) RUBEN S M.
XX
XX Li Y, Ruben SM;
XX
XX WPI; 2002-598724/64.
XX
XX N-PSDB; ABN86542.
XX
XX New polynucleotide encoding a human G protein chemokine receptor HDGNR10,
XX useful e.g. for treating tumors.
XX
XX Claim 7; Fig 1; 22pp; English.
XX
XX The invention relates to a novel human 7-transmembrane receptor, HDGNR10,
XX which has been identified as a G-protein chemokine receptor. The GPCR
XX HDGNR10 polypeptide can be expressed by standard recombinant methodology.
XX Compounds that activate or inhibit the receptor polypeptide, optionally
XX expressed from DNA in gene therapy vectors, are used to treat diseases
XX that require: (a) activation of the receptor (e.g. stimulation of
XX haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune
XX diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the
XX receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis
XX etc). The present sequence represents the human HDGNR10 receptor
XX polypeptide
XX
XX Sequence 352 AA;
XX
Query Match      100.0%; Score 95; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314
|||||

RESULT 38
ABB808343

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ID ABB08343 standard; protein; 352 AA.
XX
AC ABB08343;
XX
XX 18-JUN-2002 (first entry)
XX
DE Human chemokine (C-C motif) receptor 5 polypeptide.
XX
XX Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
XX single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
XX HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
XX genotype; polymorphic variant; transgenic; drug screening; gene therapy;
XX chromosome 3p21.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 55 /label= Leu, Gln
XX Misc-difference 182 /label= Phe, Leu
XX Misc-difference 223 /label= Arg, Gln
XX
XX WO200177125-A2.
XX
XX 18-OCT-2001.
XX
XX 04-APR-2001; 2001WO-US010708.
XX
XX 05-APR-2000; 2000US-0194361P.
XX
XX (GENA-) GENAISANCE PHARM INC.
XX
XX Choi JY, Kliehm SE, Koshy B;
XX WPI; 2002-041282/05.
XX N-PSDB; ABA97318, ABA97319.
XX
XX New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful
XX to diagnose and treat diseases associated with its abnormal expression or
XX function, including human immunodeficiency virus-1 infection.
XX
XX Claim 29; Fig 3; 61pp; English.
XX
XX The present sequence is that of a polypeptide encoded by the human
XX chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see
XX ABA97318, ABA97319). The specification describes haplotyping the CCR5
XX gene of an individual by determining if the individual has one of the
XX CCR5 haplotypes or haplotype pairs fully defined in the specification.
XX The specification also describes an isolated polynucleotide comprising a
XX nucleotide sequence which is a polymorphic variant of the reference CCR5
XX gene sequence and comprises an isogene defined by a haplotype described
XX in the specification and its encoded polypeptide. The methods of the
XX invention are useful to diagnose and develop treatment for diseases
XX associated with abnormal expression or function of the gene. The CCR5
XX isogene and the screened compounds are useful for treating human
XX immunodeficiency virus (HIV)-1 infection and the progression to acquired
XX immunodeficiency syndrome (AIDS). The invention has antiviral
XX applications. The specification describes genotyping the CCR5 gene of an
XX individual; predicting a haplotype pair for the CCR5 gene of an
XX haplotype pair of the CCR5 gene. The specification describes a
XX composition comprising a genotyping oligonucleotide for detecting a CCR5
XX polymorphism; a recombinant non-human organism transformed with CCR5
XX polynucleotide expressing a CCR5 protein encoded by the variant sequence;
XX an isolated antibody specific for the CCR5 polypeptide and a method for
XX screening drugs targeting the CCR5 polypeptide
XX
XX Sequence 352 AA;
XX
Query Match      100.0%; Score 95; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;

```

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 39
ABG75540
ID ABG75540 standard; protein; 352 AA.

XX AC ABG75540;
XX DT 16-APR-2003 (first entry)
XX DE Human G-protein chemokine receptor, HDGNR10, protein.
XX KW Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor;
KW HDGNR10; signal transduction; gene therapy; haematopoiesis;
KW wound healing; coagulation; angiogenesis; tumour; chronic infection;
KW leukaemia; T-cell mediated auto-immune disease; parasitic infection;
KW psoriasis; growth factor; allergy; atherogenesis; anaphylaxis;
KW malignancy; inflammation; histamine; IgE-mediated;
KW prostaglandin-independent fever; bone marrow failure; silicosis;
KW sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.
XX OS Homo sapiens.
XX PN US2002132269-A1.
XX PD 19-SEP-2002.
XX PF 11-FEB-2000; 2000US-00502783.
XX PR 06-JUN-1995; 95US-00466343.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Li Y, Ruben SM;
XX DR WPI; 2003-208944/20.
XX DR N-PSDB; ABX10635.
XX PT Novel human G-protein chemokine receptor polypeptide useful for
PT diagnostic purposes and for identifying modulators of the polypeptide
PT useful for treating leukemia, autoimmune diseases, psoriasis and allergic
PT reactions.
XX Claim 7; Fig 1; 22pp; English.

XX The invention discloses a G-protein chemokine receptor (sometimes
XX referred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the
XX polynucleotide encoding it. G-protein chemokine receptors are involved in
XX signal transduction pathways. The polynucleotide and polypeptide can be
XX used to identify compounds which activate or inhibit activation of the
XX protein and these compounds are useful for treating a patient having need
XX to activate or inhibit a G-protein chemokine receptor. The compound is
XX administered by providing to the patient DNA encoding the agonist or
XX antagonist and expressing them in vivo (gene therapy). The
XX polynucleotides and polypeptide are also useful for diagnosing a
XX disease or susceptibility to a disease related to an under-expression of
XX antibodies. Agonists are useful in stimulating haematopoiesis, wound
XX healing, coagulation, angiogenesis, to treat solid tumours, chronic
XX infections, leukaemia, T-cell mediated auto-immune diseases, parasitic
XX infections, psoriasis and to stimulate growth factor activity.
XX Antagonists are useful in the prevention and treatment of allergy.
XX atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation,
XX histamine and IgE-mediated allergic reactions, prostaglandin-independent
XX fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis,
XX shock and hyper-eosinophilic syndrome. The sequence presented is the
XX human HDGNR10 protein

SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. NO. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 40
ABR58602
ID ABR58602 standard; protein; 352 AA.
XX AC ABR58602;
XX DT 09-JUL-2003 (first entry)
XX DE Human cancer related protein SEQ ID NO:259.
XX KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX OS Homo sapiens.
XX PN WO2003025138-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-US029560.
XX PR 17-SEP-2001; 2001US-0323469P.
XX PR 20-SEP-2001; 2001US-0323887P.
XX PR 13-NOV-2001; 2001US-0350666P.
XX PR 08-FEB-2002; 2002US-0355145P.
XX PR 08-FEB-2002; 2002US-0355257P.
XX PR 12-APR-2002; 2002US-0372246P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnick A;
XX WPI; 2003-354600/33.
XX DR N-PSDB; ACC72740.
XX PT New genes that are up-regulated or down-regulated in cancers, useful as
XX markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX therapeutic targets for screening drugs for treating these diseases.
XX Claim 12; Page 745; 767pp; English.

XX The present invention describes an isolated nucleic acid molecule, which
XX comprises the sequence of any of the genes that are up-regulated or down-
XX regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX related gene nucleotide sequences which encode the proteins given in
XX ABR58521 to ABR58709. Also described: (1) determining the presence or
XX absence of a pathological cell in a patient; (2) an expression vector
XX comprising a nucleic acid molecule described above; (3) a host cell
XX comprising the vector; (4) an isolated polypeptide, which is encoded by
XX the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX of (4); (6) specifically targeting a compound to a pathological cell in a
XX patient by administering to the patient the antibody above; and (7) a
XX drug screening assay. The nucleic acid is useful as diagnostic markers or
XX therapeutic targets. In particular, the nucleic acid is useful for
XX diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
XX atherosclerosis and endometriosis. The nucleic acid is also useful in
XX drug screening, particularly for identifying agents for treating these
XX pathologies

XX
SQ Sequence 352 AA;
Query Match 100.0%; Score 95; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKPRNYLLVFFQK 18
| | | | | | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKPRNYLLVFFQK 314

Search completed: September 28, 2004, 09:03:39
Job time : 43.975 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:00:23 ; Search time 16.2 Seconds
(without alignments)
57.362 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95
Sequence: 1 YAFVGEKFRNYLLVFFQK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/prodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	352	3	US-08-466-343D-2
2	95	100.0	352	3	US-09-087-232A-13
3	95	100.0	352	3	US-08-861-105-14
4	95	100.0	352	3	US-08-575-967A-2
5	95	100.0	352	3	US-09-045-583-52
6	95	100.0	352	4	US-09-517-605-5
7	95	100.0	352	4	US-09-534-185-52
8	95	100.0	352	4	US-08-833-752-5
9	95	100.0	352	4	US-09-502-783A-2
10	95	100.0	352	4	US-09-796-202-1
11	80	84.2	354	4	US-08-724-984A-2
12	79	83.2	347	1	US-08-461-244-3
13	79	83.2	360	1	US-08-450-393A-4
14	79	83.2	360	3	US-08-446-669-4
15	79	83.2	360	3	US-09-045-583-50
16	79	83.2	360	4	US-09-534-185-50
17	79	83.2	360	4	US-09-131-827A-2
18	79	83.2	360	4	US-09-131-827A-20
19	79	83.2	360	5	PCT-US95-00476-4
20	77	81.1	360	4	US-08-833-752-7
21	76	80.0	360	3	US-09-045-583-51
22	76	80.0	360	4	US-09-534-185-51
23	65	68.4	355	3	US-08-575-967A-4
24	65	68.4	355	3	US-08-847-296B-1
25	65	68.4	355	3	US-09-045-583-54
26	65	68.4	355	4	US-09-534-185-54
27	65	68.4	355	4	US-08-720-565-2

28 65 68.4 355 4 US-08-720-565-4 Sequence 4, Appli
29 65 68.4 356 4 US-08-567-882-7 Sequence 7, Appli
30 63 66.3 355 1 US-08-461-244-2 Sequence 2, Appli
31 63 66.3 355 3 US-09-045-583-56 Sequence 56, Appli
32 63 66.3 355 4 US-09-534-185-56 Sequence 5, Appli
33 63 66.3 355 4 US-08-833-752-8 Sequence 8, Appli
34 61 64.2 365 4 US-09-503-219B-8 Sequence 8, Appli
35 61 64.2 374 3 US-09-045-583-48 Sequence 48, Appli
36 61 64.2 374 4 US-09-534-185-48 Sequence 48, Appli
37 60 63.2 355 1 US-08-012-988A-2 Sequence 2, Appli
38 60 63.2 355 1 US-08-450-393A-5 Sequence 5, Appli
39 60 63.2 355 3 US-08-446-669-5 Sequence 5, Appli
40 60 63.2 355 4 US-09-239-938-1 Sequence 1, Appli
41 60 63.2 355 4 US-09-886-319A-14 Sequence 14, Appli
42 60 63.2 355 5 PCT-US95-00476-5 Sequence 5, Appli
43 58 61.1 355 4 US-08-720-565-6 Sequence 6, Appli
44 57 60.0 355 1 US-08-153-848-28 Sequence 28, Appli
45 57 60.0 355 1 US-08-153-848-32 Sequence 32, Appli

ALIGNMENTS

RESULT 1
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-466-343D-2

Query Match 100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 297 YAFVGEKFRNYLLVFFQK 314

RESULT 2

US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillient et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-13
Query Match 100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YAFVGEKFRNLYLVFFQK 18
Db 297 YAFVGEKFRNLYLVFFQK 314
RESULT 3
US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-861-105-14
Query Match 100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YAFVGEKFRNLYLVFFQK 18
Db 297 YAFVGEKFRNLYLVFFQK 314
RESULT 4
US-08-575-967A-2
; Sequence 2, Application US/08575967A
; Patent No. 6265184
; GENERAL INFORMATION:
; APPLICANT: Gray et al.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,967A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6265184and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32918
; TELECOMMUNICATION INFORMATION:


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; TELEPHONE: 206-485-1900
; TELEFAX: 206-485-1662
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: /= "88c amino acid sequence"
US-08-575-967A-2

Query Match      100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. NO. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNYLLVFFQK 314
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RESULT 5
US-09-045-583-52
; Sequence 52, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-52

Query Match      100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. NO. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNYLLVFFQK 314
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RESULT 6
US-09-517-605-5
; Sequence 5, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeek, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-605-5

Query Match      100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. NO. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNYLLVFFQK 314
   |||||

RESULT 7
US-09-534-185-52
; Sequence 52, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; THEREFOR
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match          100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 8
US-08-833-752-5
; Sequence 5, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-752-5

Query Match          100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 9
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
; TITLE OF INVENTION: HDGMR10
; FILE REFERENCE: 1488.11150006
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; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match          100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 10
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JFW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match          100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
   |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 11
US-08-984A-2
; Sequence 2, Application US/08724984A
; Patent No. 6388055
; GENERAL INFORMATION:
; APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
; TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-
; TITLE OF INVENTION: CCR5 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,984A
; FILING DATE: October 3, 1996
```

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATGS0023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEFAX: 610 270 5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 354
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-724-384A-2

Query Match 84.2%; Score 80; DB 4; Length 354;
Best Local Similarity 83.3%; Pred. No. 3.5e-06;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||:|||||
DB 299 YAFVGEKFRSLSVFFRK 316

RESULT 12
US-08-461-244-3
Sequence 3, Application US/08461244
Patent No. 5778729
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Yi, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-244-3

Query Match 83.2%; Score 79; DB 1; Length 347;
Best Local Similarity 83.3%; Pred. No. 5.2e-06;

Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||:|||||
DB 292 YAFVGEKFRSLSVFFRK 309

RESULT 13
US-08-450-393A-4
Sequence 4, Application US/08450393A
Patent No. 5707815
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cserit, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-393A-4

Query Match 83.2%; Score 79; DB 1; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||:|||||
DB 305 YAFVGEKFRSLSVFFRK 322

RESULT 14
US-08-446-669-4
Sequence 4, Application US/08446669
Patent No. 6132987
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-045-583-50

Query Match      83.2%; Score 79; DB 3; Length 360;
Best Local Similarity 83.3%; Pred. NO. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 YAFVGEXFRNYLLVFFCK 18
        ||| ||||| ||| |||:|
Db      305 YAFVGEXFRRLSVFFRK 322

RESULT 16
US-09-534-185-50
; Sequence 50, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6407767el Molecules of the G Protein-Coupled
;                      Heptahelical Receptor Superfamily and Uses
;                      Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/534,185
  FILING DATE: 24-Mar-2000
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/045,583
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Mandragouras, Amy E.
  REGISTRATION NUMBER: 36,207
  REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (617)227-7400
  TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 50:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 360 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: peptide
    FRAGMENT TYPE: internal
    SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

Query Match      83.2%; Score 79; DB 4; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 YAFVGGEKFRNYLLVFFQK 18
        ||| ||| ||| ||| |||
Db      305 YAFVGGEKFRYLSVFFEK 322

RESULT 17
US-09-131-827A-2
Sequence 2, Application US/09131827A

```

```
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; FILE REFERENCE: 14014.0333
; CURRENT FILING DATE: 1998-08-10
; CURRENT APPLICATION NUMBER: US/09/131,827A
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: 60/055,659
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-2

Query Match      83.2%; Score 79; DB 4; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
Db      305 YAFVGEKFRNYLLVFFRK 322

RESULT 18
US-09-131-827A-20
; Sequence 20, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; FILE REFERENCE: 14014.0333
; CURRENT FILING DATE: 1998-08-10
; CURRENT APPLICATION NUMBER: US/09/131,827A
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: 60/055,659
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-20

Query Match      83.2%; Score 79; DB 4; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
Db      305 YAFVGEKFRNYLLVFFRK 322

RESULT 19
PCT-US95-00476-4
; Sequence 4, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
```

```
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-00476-4

Query Match      83.2%; Score 79; DB 5; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
Db      305 YAFVGEKFRNYLLVFFRK 322

RESULT 20
US-08-833-752-7
; Sequence 7, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6448375e
US-08-833-752-7

Query Match 81.1%; Score 77; DB 4; Length 360;
Best Local Similarity 77.8%; Pred. No. 1.2e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 305 YAFVGEKFRYISVFFRK 322

RESULT 21
US-09-045-583-51
Sequence 51, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-51

Query Match 80.0%; Score 76; DB 3; Length 360;
Best Local Similarity 77.8%; Pred. No. 1.8e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 305 YAFVGEKFRYISVFFRK 322

RESULT 22
US-09-534-185-51
Sequence 51, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51

Query Match 80.0%; Score 76; DB 4; Length 360;
Best Local Similarity 77.8%; Pred. No. 1.8e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 305 YAFVGEKFRYISVFFRK 322

RESULT 23
US-08-575-967A-4
Sequence 4, Application US/08575967A
Patent No. 6285184
GENERAL INFORMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:

```
;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6265184and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32918
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-485-1900
; TELEFAX: 206-485-1662
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88-2B amino acid sequence"
US-08-575-967A-4

Query Match 68.4%; Score 65; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
Db 301 YAFVGERFRKYLRRHFFHR 318

RESULT 24
US-08-847-296B-1
; Sequence 1, Application US/08847296B
; Patent No. 6271347
; GENERAL INFORMATION:
; APPLICANT: DAUGHERTY, BRUCE L.
; APPLICANT: DEMARTINO, JULIE A.
; APPLICANT: SICILIANO, SALVATORE J.
; APPLICANT: SPRINGER, MARTIN J.
; TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,296B
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/016,158
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 60/017,113
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Thies, J. Eric
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19634Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3904
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-847-296B-1

Query Match 68.4%; Score 65; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
Db 301 YAFVGERFRKYLRRHFFHR 318

RESULT 25
US-09-045-583-54
; Sequence 54, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MMI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-54

Query Match 68.4%; Score 65; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
Db 301 YAFVGERFRKYLRRHFFHR 318

RESULT 26
US-09-534-185-54
; Sequence 54, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
```

Therefor
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-09-534-185-54
Query Match 68.4%; Score 65; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 YAFVGEKERNYLLVFFQK 18
DB 301 YAFVGERFRKYLRRHFHR 318
RESULT 27
US-08-720-565-2
Sequence 2, Application US/08720565
Patent No. 6537764
GENERAL INFORMATION:
APPLICANT: Gerard, Craig J.
APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Mackay, Charles R.
APPLICANT: Ponath, Paul D.
APPLICANT: Post, Theodore W.
APPLICANT: Qin, Shixin
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
TITLE OF INVENTION: ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-565-2
Query Match 68.4%; Score 65; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 YAFVGEKERNYLLVFFQK 18
DB 301 YAFVGERFRKYLRRHFHR 318
RESULT 28
US-08-720-565-4
Sequence 4, Application US/08720565
Patent No. 6537764
GENERAL INFORMATION:
APPLICANT: Gerard, Craig J.
APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Mackay, Charles R.
APPLICANT: Ponath, Paul D.
APPLICANT: Post, Theodore W.
APPLICANT: Qin, Shixin
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
TITLE OF INVENTION: ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.

REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-565-4

Query Match 68.4%; Score 65; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 301 YAFVGERPKYLRHFFHR 318

RESULT 29
US-08-567-882-7
Sequence 7, Application US/08567882
Patent No. 6512103
GENERAL INFORMATION:
APPLICANT: Dairaghi, Daniel J.
APPLICANT: Hara, Takahiko
APPLICANT: Miyajima, Atsushi
APPLICANT: Schall, Thomas J.
APPLICANT: Wang, Wei
APPLICANT: Yoshimura, Akihiko
TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,882
FILING DATE: 08-DEC-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0506
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-567-882-7

Query Match 68.4%; Score 65; DB 4; Length 356;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 302 YAFVGERPKYLRHFFHR 319

RESULT 30
US-08-461-244-2
Sequence 2, Application US/08461244
Patent No. 5776729
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Yi, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELIA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESS: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-445
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-244-2

Query Match 66.3%; Score 63; DB 1; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0034;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 300 YAFVGEKPKHLSEIFQK 317

RESULT 31
US-09-045-583-56
Sequence 56, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-56

Query Match 66.3%; Score 63; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0034;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 300 YAFVGEKFKHLSEIFQK 317

RESULT 32
US-09-534-185-56
Sequence 56, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-534-185-56

Query Match 66.3%; Score 63; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0034;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 300 YAFVGEKFKHLSEIFQK 317

RESULT 33
US-08-833-752-8
Sequence 8, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92560
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6448375e
US-08-833-752-8

Query Match 66.3%; Score 63; DB 4; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.0034;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 301 YAFVGERFRKRIHFHR 318

RESULT 34
US-09-503-219B-8
Sequence 8, Application US/09503219B
Patent No. 6645491
GENERAL INFORMATION:
APPLICANT: Oldham, Elizabeth R.
APPLICANT: Horney, Bernhard
APPLICANT: Dieu-No. 6645491Jean, Marie C.

APPLICANT: Caux, Christophe
APPLICANT: Zlotnick, Albert
TITLE OF INVENTION: CHEMOKINE USES; COMPOSITIONS; METHODS
FILE REFERENCE: DX0934K1
CURRENT APPLICATION NUMBER: US/09/503,219B
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: US 60/118,335
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (579)..(579)
OTHER INFORMATION: unknown nucleotide
US-09-503-219B-8

Query Match 64.2%; Score 61; DB 4; Length 365;
Best Local Similarity 76.9%; Pred. No. 0.0079;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
Db 307 YAFIGQKFRNYFL 319
||||:|||||

RESULT 35
US-09-045-583-48
; Sequence 48, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-48

Query Match 64.2%; Score 61; DB 3; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0079;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
Db 307 YAFIGQKFRNYFL 319
||||:|||||

RESULT 36
US-09-534-185-48
; Sequence 48, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-534-185-48

Query Match 64.2%; Score 61; DB 4; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0081;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
Db 316 YAFIGQKFRNYFL 328
||||:|||||

RESULT 37
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; Macrophage Inflammatory Protein-1 alpha (MIP-1
; alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
US-09-534-185-48

Query Match 64.2%; Score 61; DB 4; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0081;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
Db 316 YAFIGQKFRNYFL 328
||||:|||||

RESULT 37
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; Macrophage Inflammatory Protein-1 alpha (MIP-1
; alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
US-09-534-185-48

Query Match 64.2%; Score 61; DB 3; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0081;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
Db 316 YAFIGQKFRNYFL 328
||||:|||||

RESULT 37
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; Macrophage Inflammatory Protein-1 alpha (MIP-1
; alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
US-09-534-185-48

Best Local Similarity 76.9%; Pred. No. 0.0081;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
Db 316 YAFIGQKFRNYFL 328
||||:|||||

RESULT 36
US-09-534-185-48
; Sequence 48, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-534-185-48

Query Match 64.2%; Score 61; DB 4; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0081;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
Db 316 YAFIGQKFRNYFL 328
||||:|||||

RESULT 37
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; Macrophage Inflammatory Protein-1 alpha (MIP-1
; alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
US-09-534-185-48

Query Match 64.2%; Score 61; DB 4; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0081;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
Db 316 YAFIGQKFRNYFL 328
||||:|||||

RESULT 37
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; Macrophage Inflammatory Protein-1 alpha (MIP-1
; alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
US-09-534-185-48

Query Match 64.2%; Score 61; DB 4; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0081;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
Db 316 YAFIGQKFRNYFL 328
||||:|||||

RESULT 37
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; Macrophage Inflammatory Protein-1 alpha (MIP-1
; alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
US-09-534-185-48

Query Match 64.2%; Score 61; DB 4; Length 374;
Best Local Similarity 76.9%; Pred. No. 0.0081;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLL 13
Db 316 YAFIGQKFRNYFL 328
||||:|||||

RESULT 37
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; Macrophage Inflammatory Protein-1 alpha (MIP-1
; alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
US-09-534-185-48

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Khourie and Crew
;; STREET: One Market Plaza, Steuart Tower, Suite 2000
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94610
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/012,988A
;; FILING DATE: 19930128
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weber, Kenneth A.
;; REGISTRATION NUMBER: 31,677
;; REFERENCE/DOCKET NUMBER: 15280-118
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-543-9600
;; TELEFAX: 415-543-5043
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 355 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-012-988A-2

Query Match 63.2%; Score 60; DB 1; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
|||:|:|:|:|:
Db 301 YAFVGERFRKYLRLQFHR 318

RESULT 38
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseerr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663

;; TELEX: 380816CooleyPA
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 355 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
;; US-08-450-393A-5

Query Match 63.2%; Score 60; DB 1; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
|||:|:|:|:|:
Db 301 YAFVGERFRKYLRLQFHR 318

RESULT 39
US-08-446-669-5
; Sequence 5, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816Cooleypa
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-446-669-5

Query Match 63.2%; Score 60; DB 3; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
|||:|:~|:|:|:~|:
Db 301 YAFVGERFRKYLRLQFHR 318

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RESULT 40
US-09-239-938-1
; Sequence 1, Application US/09239938
; Patent No. 6329510
; GENERAL INFORMATION:
; APPLICANT: Qin, Shixin
; APPLICANT: Newman, Walter
; APPLICANT: Kassam, Nasim
; APPLICANT: LeukoSite, Inc.
; TITLE OF INVENTION: ANTI-CCR1 ANTIBODIES AND METHODS OF USE
; FILE REFERENCE: LKS97-13
; CURRENT APPLICATION NUMBER: US/09/239,938
; CURRENT FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-239-938-1
Query Match      63.2%; Score 60; DB 4; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 YAFVGEKFRNYLLVFFOK 18
      |||||:|:|:|
Db      301 YAFVGERFRKYLROLFHR 318

Search completed: September 28, 2004, 09:21:33
Job time : 16.2 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 09:06:23 ; Search time 59.625 Seconds
(without alignments)
97.074 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95
Sequence: 1 YAFVGEKFRNLLVFFQK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
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 - 9: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
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 - 16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*
 - 19: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	95	100.0	18	14	US-10-084-813-105
3	95	100.0	332	14	US-10-095-876A-2
4	95	100.0	352	9	US-09-725-285-2
5	95	100.0	352	9	US-09-759-841-2
6	95	100.0	352	9	US-09-779-879A-2
7	95	100.0	352	9	US-09-779-879A-22
8	95	100.0	352	9	US-09-779-880A-2
9	95	100.0	352	9	US-09-779-880A-22
10	95	100.0	352	9	US-09-813-653-15
11	95	100.0	352	9	US-09-813-653-17
12	95	100.0	352	9	US-09-796-202-1
13	95	100.0	352	9	US-09-195-662A-2
14	95	100.0	352	9	US-09-339-912A-2
15	95	100.0	352	9	US-09-938-719-5

16	95	100.0	352	9	US-09-938-726-5	Sequence 5, Appli
17	95	100.0	352	9	US-09-938-703-5	Sequence 5, Appli
18	95	100.0	352	9	US-09-502-783A-2	Sequence 2, Appli
19	95	100.0	352	10	US-09-734-221A-14	Sequence 14, Appli
20	95	100.0	352	11	US-09-826-509-477	Sequence 477, App
21	95	100.0	352	12	US-10-151-274-5	Sequence 5, Appli
22	95	100.0	352	13	US-10-106-623-2	Sequence 2, Appli
23	95	100.0	352	13	US-10-106-623-20	Sequence 20, Appli
24	95	100.0	352	14	US-10-232-686-2	Sequence 2, Appli
25	95	100.0	352	14	US-10-086-814-1	Sequence 1, Appli
26	95	100.0	352	14	US-10-067-800-2	Sequence 2, Appli
27	95	100.0	352	14	US-10-067-800-22	Sequence 22, Appli
28	95	100.0	352	14	US-10-290-058A-6	Sequence 6, Appli
29	95	100.0	352	14	US-10-225-567A-352	Sequence 352, App
30	95	100.0	352	14	US-10-323-314-1	Sequence 1, Appli
31	95	100.0	352	14	US-10-072-301-1	Sequence 1, Appli
32	95	100.0	352	14	US-10-164-649-52	Sequence 52, Appli
33	95	100.0	352	14	US-10-071-866-1	Sequence 1, Appli
34	95	100.0	352	14	US-10-135-839-2	Sequence 2, Appli
35	95	100.0	352	14	US-10-135-839-22	Sequence 22, Appli
36	95	100.0	352	14	US-10-339-423-67	Sequence 67, Appli
37	95	100.0	352	14	US-10-439-845-2	Sequence 2, Appli
38	95	100.0	352	14	US-10-439-845-4	Sequence 4, Appli
39	95	100.0	352	15	US-10-360-828-1	Sequence 1, Appli
40	95	100.0	352	16	US-10-661-798-5	Sequence 5, Appli
41	95	100.0	352	16	US-10-791-905-2	Sequence 2, Appli
42	95	100.0	352	16	US-10-612-791-5	Sequence 5, Appli
43	79	83.2	347	9	US-09-104-792-3	Sequence 3, Appli
44	79	83.2	347	14	US-10-176-078-3	Sequence 3, Appli
45	79	83.2	360	9	US-09-131-827A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-084-813-15
; Sequence 15, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-15

Query Match	100.0%;	Score 95;	DB 14;	Length 18;
Best Local Similarity	100.0%;	Pred.No. 3.5e-08;		
Matches	18;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	YAFVGEKFRNLLVFFQK 18		
Db	1	YAFVGEKFRNLLVFFQK 18		
RESULT 2				
US-10-084-813-105				
; Sequence 105, Application US/10084813				
; Publication No. US20030068615A1				

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; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-105

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Query Match      100.0%; Score 95; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 YAFVGEKFRNLLVFFQK 18
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DB      1 YAFVGEKFRNLLVFFQK 18
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RESULT 3
US-10-095-876A-2
; Sequence 2, Application US/10095876A
; Publication No. US20030148294A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice; Bandman, Olga
; APPLICANT: Coleman, Roger; Wilde, Craig G.
; TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
; FILE REFERENCE: PP-0060-1 CON
; CURRENT APPLICATION NUMBER: US/10/095,876A
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 08/638,081
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2

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Query Match      100.0%; Score 95; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 YAFVGEKFRNLLVFFQK 18
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DB      277 YAFVGEKFRNLLVFFQK 294
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RESULT 4
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003

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; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

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Query Match      100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 YAFVGEKFRNLLVFFQK 18
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DB      297 YAFVGEKFRNLLVFFQK 314
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RESULT 5
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Perros, Manoussos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC10348ADME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-759-841-2

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Query Match      100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 YAFVGEKFRNLLVFFQK 18
      |||
DB      297 YAFVGEKFRNLLVFFQK 314
      |||

```

```

RESULT 6
US-09-779-879A-2
; Sequence 2, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A

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; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-2

Query Match      100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
Db      297 YAFVGEKFRNYLLVFFQK 314

RESULT 7
US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-22

Query Match      100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
Db      297 YAFVGEKFRNYLLVFFQK 314

RESULT 8
US-09-779-880A-2
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match      100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
Db      297 YAFVGEKFRNYLLVFFQK 314

RESULT 9
US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match      100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
Db      297 YAFVGEKFRNYLLVFFQK 314

RESULT 10
US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20

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; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 11
US-09-813-653-17
; Sequence 17, Application US/09813653
; Patent No. US20020084770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-17

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 12
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US2002008813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1

; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 13
US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGFR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 14
US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGFR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2

Query Match 100.0%; Score 95; DB 9; Length 352;

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Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
      |||||
Db      297 YAFVGEKFRNLLVFFQK 314
      |||||

RESULT 15
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
;
US-09-938-719-5

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
      |||||
Db      297 YAFVGEKFRNLLVFFQK 314
      |||||

RESULT 16
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17

```

NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 18

US-09-502-783A-2
Sequence 2, Application US/09502783A
Patent No. US20020132269A1

GENERAL INFORMATION:

APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
FILE REFERENCE: 1498.1150006
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 19

US-09-734-221A-14
Sequence 14, Application US/09734221A
Publication No. US20030096221A1
GENERAL INFORMATION:
APPLICANT: LITWAN, DAN R.
ELMEIER, WILFRIED
LANDAU, NATHANIEL R.
LIU, RONG

TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,221A
FILING DATE: 11-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 N2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14

Query Match 100.0%; Score 95; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 20

US-09-826-509-477
Sequence 477, Application US/09826509
Publication No. US20030204073A1
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
Protein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 477
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-509-477

Query Match 100.0%; Score 95; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YAFVGEKFRNYLLVFFQK 18
      |||||
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 21
US-10-151-274-5
; Sequence 5, Application US/10151274
; Publication No. US2003064071A1
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
; TITLE OF INVENTION: INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/10/151,274
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/09/517,605
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-274-5

Query Match 100.0%; Score 95; DB 12; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
      |||||
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 22
US-10-106-623-2
; Sequence 2, Application US/10106623
; Publication No. US2002015088A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US2002015088A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-106-623-2

Query Match 100.0%; Score 95; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
      |||||
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 23
US-10-106-623-20
; Sequence 20, Application US/10106623
; Publication No. US2002015088A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US2002015088A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-106-623-20

Query Match 100.0%; Score 95; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
      |||||
Db 297 YAFVGEKFRNYLLVFFQK 314
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Db      297 YAFVGEKFRNYLLVFFQK 314
|||||
RESULT 24
US-10-232-686-2
; Sequence 2, Application US/103232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
|||||
Db      297 YAFVGEKFRNYLLVFFQK 314

RESULT 25
US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana C.
; APPLICANT: Olson, William A.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
|||||
Db      297 YAFVGEKFRNYLLVFFQK 314

RESULT 26
US-10-067-800-2
; Sequence 2, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000I
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-2

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
|||||
Db      297 YAFVGEKFRNYLLVFFQK 314

RESULT 27
US-10-067-800-22
; Sequence 22, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000I
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-22

Query Match      100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
|||||
Db      297 YAFVGEKFRNYLLVFFQK 314
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; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
; US-10-323-314-1

Query Match          100.0%; Score 95;
Best Local Similarity 100.0%; Pred. No.
Matches 18; Conservative 0; Mismatch

Qy 1 YAFVGEKFRNLLVFFQK 18
    |||||
Db 297 YAFVGEKFRNLLVFFQK 314
    |||||

RESULT 31
US-10-072-301-1
; Sequence 1, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIB
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-072-301-1

Query Match          100.0%; Score 95;
Best Local Similarity 100.0%; Pred. No.
Matches 18; Conservative 0; Mismatch

Qy 1 YAFVGEKFRNLLVFFQK 18
    |||||
Db 297 YAFVGEKFRNLLVFFQK 314
    |||||

RESULT 32
US-10-164-649-52
; Sequence 52, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. US200301629
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD,
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/164
; FILING DATE: 07-Jun-2002
; CLASSIFICATION: <Unknown>

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-164-649-52

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 33
US-10-071-866-1
; Sequence 1, Application US/10071866
; Publication No. US20030165988A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST
; TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
; FILE REFERENCE: 25636-717
; CURRENT APPLICATION NUMBER: US/10/071,866
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-866-1

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 34
US-10-135-839-2
; Sequence 2, Application US/10135839
; Publication No. US20030166024A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammatory Diseases;
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
; FILE REFERENCE: 022217us
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-09-23

```



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; PRIOR APPLICATION NUMBER: DEL0016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-67
Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 37
US-10-439-845-2
; Sequence 2, Application US/10439845
; Publication No. US20030195348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-439-845-2

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 38
US-10-439-845-4
; Sequence 4, Application US/10439845
; Publication No. US20030195348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-439-845-4

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 39
US-10-360-828-1
; Sequence 1, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
;
QY 1 YAFVGEKFRNLLVFFQK 18
```

```

| | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 38
US-10-439-845-4
; Sequence 4, Application US/10439845
; Publication No. US20030195348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-439-845-4

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 39
US-10-360-828-1
; Sequence 1, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
;
QY 1 YAFVGEKFRNLLVFFQK 18
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; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-360-828-1

Query Match 100.0%; Score 95; DB 15; Length 352;
Best Local Similarity 100.0%; Pred.No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
|||
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 40

US-10-661-798-5
; Sequence 5, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
; APPLICANT: Samson, Michael
; APPLICANT: Parmentier, Marc
; APPLICANT: Vassart, Gilbert
; APPLICANT: Frederic, Libert
; TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV En
; TITLE OF INVENTION: a Cell
; FILE REFERENCE: 9409/2023F
; CURRENT APPLICATION NUMBER: US/10/661,798
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: 09/938,703
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: 08/810,028
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: EP 96870021.1
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: EP 96870102.9
; PRIOR FILING DATE: 1996-08-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-798-5

Query Match 100.0%; Score 95; DB 16; Length 352;
Best Local Similarity 100.0%; Pred.No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
|||
Db 297 YAFVGEKFRNYLLVFFQK 314

Search completed: September 28, 2004, 09:44:42
Job time : 59.625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:57:36 ; Search time 9.675 Seconds
(without alignments)
178.961 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGEKFRNLLVFFQK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.78.*

2: PIR1.*

3: PIR2.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	352	2 A43113	chemokine (C-C) re
2	79	83.2	360	2 J02443	chemokine (C-C) re
3	65	68.4	355	2 G02436	chemokine (C-C) re
4	64	67.4	359	2 I49341	MIP-1 alpha recept
5	63	66.3	355	2 J05067	G protein-coupled
6	62	65.3	383	2 S55594	G protein-coupled
7	61	64.2	369	2 J05068	G protein-coupled
8	60	63.2	355	2 A45177	chemokine (C-C) re
9	58	61.1	354	2 I58186	probable G protein
10	57	60.0	355	2 J04304	orphan G protein-c
11	57	60.0	360	2 A57160	chemokine (C-C) re
12	53	55.8	355	2 I49339	macrophage inflam
13	53	55.8	356	2 I49340	MIP-1 alpha recept
14	52	54.7	360	2 J04587	chemokine (C-C) re
15	52	54.7	378	2 B55735	lymphocyte-specifi
16	50	52.6	356	2 S42096	interleukin-8 rece
17	50	52.6	359	2 A48921	interleukin-8 rece
18	50	52.6	360	2 A53611	interleukin-8 rece
19	50	52.6	378	2 A45680	G protein-coupled
20	49	51.6	76	2 B95247	hypothetical prote
21	49	51.6	76	2 B98112	hypothetical prote
22	49	51.6	374	2 I38450	chemokine (C-C) re
23	48	50.5	367	2 J50349	interleukin-8 rece
24	47	49.5	358	2 A53752	interleukin-8 rece
25	47	49.5	378	2 A55735	G protein-coupled
26	46	48.4	354	2 A23669	interleukin-8 rece
27	46	48.4	355	2 J01211	interleukin-8 rece
28	45.5	47.9	377	2 B57185	Glycosyltransferas
29	45	47.4	350	2 JN0621	G protein-coupled

ALIGNMENTS

RESULT 1

A43113

chemokine (C-C) receptor 5 - human

N/Alternate names: C-C CKR-5; CCR5

C/Species: Homo sapiens (man)

C/Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text_change 20-Jun-2000

C/Accession: A43113; S71808; A58834; A58832; G02653; A58833

R/Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochemistry 35, 3362-3367, 1996

A/Title: Molecular cloning and functional expression of a new human CC-chemokine receptor:

A/Reference number: A43113; MUID:962411590; PMID:8639485

A/Accession: A43113

A/Molecule type: mRNA

A/Residues: 1-352 <SAMI>

A/Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811

R/Samson, M.; Libert, P.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti

M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa

Nature 382, 722-725, 1996

A/Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of

A/Reference number: S71808; MUID:96345670; PMID:8751444

A/Accession: S71808

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 182-206;207-230 <SAM2>

A/Accession: A58834

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-184,'IKDHLGAGPAACHGHLILGNPKNSASVSK' <SAM3>

A/Cross-references: GB:X93393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063

A/Note: this frameshift mutation results in a non-functional receptor but confers a degree

nd may have had a selective advantage by conferring resistance to Yersinia plague infecti

R/Combiadere, C.; Anuja, S.K.; Tiffany, H.L.; Murphy, P.M.

J. Leukoc. Biol. 60, 147-152, 1996

A/Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rece

A/Reference number: A58832; MUID:96295970; PMID:8699119

A/Accession: A58832

A/Molecule type: mRNA

A/Residues: 1-352 <COM1>

A/Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409

A/Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes

R/Combiadere, C.

submitted to the EMBL Data Library, May 1996

A/Reference number: H01541

A/Accession: G02653

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-89,'L',91-352 <COM2>

A/Cross-references: EMBL:U57840

R/Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.

J. Biol. Chem. 271, 17161-17166, 1996

A/Title: Molecular cloning and functional characterization of a novel human CC chemokine

A/Reference number: A58833; MUID:96291862; PMID:8663314

A;Accession: A59833
 A;Molecule type: mRNA
 A;Residues: 1-352 <RAP>
 A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
 C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30575), and dual-tropic strains of HIV-1 bind to a complex of chemokine receptors.
 C;Genetics:
 A;Gene: GDB:CMKBR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
 A;Cross-references: GDB:1230510; OMIM:601373
 A;Map position: 3p21-3p21
 C;Function:
 A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES.
 A;Note: Probably acts to control granulocyte proliferation and differentiation
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;32-56/Domain: transmembrane #status predicted <TM1>
 F;67-87/Domain: transmembrane #status predicted <TM2>
 F;103-124/Domain: transmembrane #status predicted <TM3>
 F;142-166/Domain: transmembrane #status predicted <TM4>
 F;193-218/Domain: transmembrane #status predicted <TM5>
 F;236-257/Domain: transmembrane #status predicted <TM6>
 F;285-300/Domain: transmembrane #status predicted <TM7>
 F;20-269,101-178/Disulfide bonds: #status predicted
 F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
 F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted
 Query Match 100.0%; Score 95; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNYLLVFPQK 18
 DB 297 YAFVGEKFRNYLLVFPQK 314

RESULT 2
 J02443
 Chemokine (C-C) receptor 2, splice form B - human
 N;Alternate names: C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1
 C;Species: Homo sapiens (man)
 C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
 C;Accession: J02443; J38463
 R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
 A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 2
 A;Reference number: J02443; MUID:94324942; PMID:8048929
 A;Accession: J02443
 A;Molecule type: mRNA
 A;Residues: 1-360 <YAM>
 A;Cross-references: DBJ:U29884; NID:G531246; PIDN:BA06253.1; PID:G531247
 R;Charo, I.F.; Myers, S.J.; Herman, A.; Frangi, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A;Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2
 A;Reference number: A53477; MUID:94195821; PMID:8146186
 A;Accession: I38463
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-360 <RES>
 A;Cross-references: EMBL:U03905; NID:G472557; PIDN:AAA19120.1; PID:G472558
 C;Genetics:
 A;Gene: GDB:CMKBR2
 A;Cross-references: GDB:337364; OMIM:601267
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
 F;43-70/Domain: transmembrane #status predicted <TM1>
 F;81-100/Domain: transmembrane #status predicted <TM2>
 F;115-136/Domain: transmembrane #status predicted <TM3>
 F;154-178/Domain: transmembrane #status predicted <TM4>
 F;207-226/Domain: transmembrane #status predicted <TM5>
 F;244-268/Domain: transmembrane #status predicted <TM6>
 F;287-309/Domain: transmembrane #status predicted <TM7>

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;113-190/Disulfide bonds: #status predicted

Query Match 83.2%; Score 79; DB 2; Length 360;
 Best Local Similarity 83.3%; Pred. No. 1.6e-05;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFPQK 18
 DB 305 YAFVGEKFRNYLLVFPQK 322

RESULT 3

G02436

Chemokine (C-C) receptor 3 - human

N;Alternate names: C-C CR-3

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000

C;Accession: G02436; A57237

R;Ponath, P.D.

Submitted to the EMBL Data Library, February 1996

A;Reference number: H01272

A;Accession: G02436

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-355 <PON>

A;Cross-references: EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561

R;Combadere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.

A;Reference number: A57237; MUID:95348056; PMID:7622448

A;Accession: A57237

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-106, N', 108-275, S', 277-280, R', 282-355 <COM>

A;Cross-references: GB:U28694; NID:g1195579; PIDN:AAC50469.1; PID:g1195580

A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.1

C;Genetics:

A;Gene: GDB:CMKBR3

A;Cross-references: GDB:579624; OMIM:601268

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

F;36-60/Domain: transmembrane #status predicted <TM1>

F;71-91/Domain: transmembrane #status predicted <TM2>

F;108-129/Domain: transmembrane #status predicted <TM3>

F;147-171/Domain: transmembrane #status predicted <TM4>

F;205-223/Domain: transmembrane #status predicted <TM5>

F;240-261/Domain: transmembrane #status predicted <TM6>

F;288-305/Domain: transmembrane #status predicted <TM7>

F;24-273,106-183/Disulfide bonds: #status predicted

F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 68.4%; Score 65; DB 2; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.0035;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFPQK 18
 DB 301 YAFVGEKFRNYLLVFPQK 318

RESULT 4

I49341

MIP-1 alpha receptor like-2 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998

C;Accession: I49341

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptors

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Accession: I49341

Cell 72, 415-425, 1993
A;Title: Molecular cloning, functional expression, and signaling character-
A;Reference number: A45177; MUID:93161416; PMID:7679328

```

A:Accession: A45177
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-355 <NEO>
A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A:Experimental source: Hu60 cells
A:Note: sequence extracted from NCBI backbone (NCBIP:124876)
R:Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A:Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
A:Reference number: 155671; MUID:9240122; PMID:7683036
A:Accession: I58671
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-355 <RES>
A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C:Genetics:
A:Gene: GDB:CMKBR1; CMKR-1
A:Cross-references: GDB:I38446; OMIM:601159
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tm
F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-264/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:24-273.106-183/disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 63.2%; Score 60; DB 2; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.024;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
DB 301 YAFVGEKFRNVLVFFQK 318

RESULT 9
I58196
Probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: I58186
R:Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A:Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and
A:Reference number: I58186; MUID:94323113; PMID:8047298
A:Accession: I58186
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>
A:Cross-references: EMBL:U04808; NID:g2558635; PIDN:AA87093.1; PID:g439861
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 61.1%; Score 58; DB 2; Length 354;
Best Local Similarity 61.1%; Pred. No. 0.053;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
DB 294 YAFVGEKFRNVLVFFQK 311

RESULT 10
JC4304
Orphan G protein-coupled receptor - human
N:Alternate names: V28 protein

C:Species: Homo sapiens (man)
C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C:Accession: JC4304
R:Rapport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to ge
A:Reference number: JC4304; MUID:96011651; PMID:7590284
A:Accession: JC4304
A:Molecule type: mRNA
A:Residues: 1-355 <RAP>
A:Cross-references: GB:U03050; NID:g665580; PIDN:AAA91783.1; PID:g665581
A:Experimental source: peripheral blood mononuclear cell
C:Comment: This protein is a cell-surface receptor which recognizes extracellular signals;
C:Comment: This protein is a key regulator of many immune and homeostatic responses, and
C:Genetics:
A:Gene: v28
A:Map position: 3pter-p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F:35-57/Domain: transmembrane #status predicted <TM1>
F:66-88/Domain: transmembrane #status predicted <TM2>
F:104-125/Domain: transmembrane #status predicted <TM3>
F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>
F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>

Query Match 60.0%; Score 57; DB 2; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.078;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
DB 293 YAFVGEKFRNVLVFFQK 310

RESULT 11
A57160
Chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: A57160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogwerf, A.J.; Proudfoot, A.E.I.; We
J. Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor cbr
A:Reference number: A57160; MUID:95370289; PMID:7642634
A:Accession: A57160
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POW>
A:Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A:Note: source clone K5-5
C:Genetics:
A:Gene: GDB:CMKBR4
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F:40-55/Domain: transmembrane #status predicted <TM1>
F:76-97/Domain: transmembrane #status predicted <TM2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:243-264/Domain: transmembrane #status predicted <TM6>
F:291-308/Domain: transmembrane #status predicted <TM7>
F:29-276,110-187/disulfide bonds: #status predicted
F:72.350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 60.0%; Score 57; DB 2; Length 360;

```

```

A;Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAG62372.1; PID:g1167852
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
F;Keywords: Glycoprotein; phosphoprotein; receptor; thymus
F;2_183_194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72_202_350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match          54.7%; Score 52; DB 2; Length 360;
Best Local Similarity 52.9%; Pred. No. 0.55;
Matches      9; Conservative      3; Mismatches      5; Indels      0; Gaps      0;

Qy      1 YAFVGEKFRNYLLVFFQ 17
| : ||||| | :
Db      304 YFFLGKFRKYITQLFR 320

RESULT 15
B55735
Lymphocyte-specific G protein-coupled receptor EB11 - human
N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: B55735; S52443
R;Schwackart V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B., et al. Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835; PMID:7851899
A;Accession: B55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:I31591; NID:g468319; PIDN:AAI74231.1; PID:g468320
R;Burgstahler, R.; Kempkes, B.; Staebue, K.; Lipp, M. Submitted to the EMBL Data Library, February 1995
A;Description: The expression of the chemokine receptor BLR2/EB11 is specifically transcribed in human thymocytes.
A;Reference number: S52443
A;Accession: S52443
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 21-378 <BUR>
A;Cross-references: EMBL:X84702
C;Genetics:
A;Gene: GDB:CMKB7; EB11; BLR2; CCR7
A;Cross-references: GDB:342065; OMIM:600242
A;Map position: 17q12-17q21.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match          54.7%; Score 52; DB 2; Length 378;
Best Local Similarity 58.8%; Pred. No. 0.57;
Matches     10; Conservative      2; Mismatches      5; Indels      0; Gaps      0;

Qy      1 YAFVGEKFRNYLLVFFQ 17
| : ||||| | :
Db      326 YAFIVGKFRNDLFKLFX 342

RESULT 16
S42096
Interleukin-8 receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C;Accession: S42096
R;Gohl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K. submitted to the EMBL Data Library, February 1994
A;Description: Molecular cloning of the rat IL8 receptor.
A;Reference number: S42096
A;Accession: S42096
A;Status: preliminary

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A:Molecule type: mRNA
A:Residues: 1-359 <RE3>
A:Cross-references: GB:D17630; NID:G493671; PIDN:BA04536.1; PID:G493672
C:Genetics:
A:Gene: IL8RB
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:49-74/Domain: transmembrane #status predicted <TM1>
F:84-106/Domain: transmembrane #status predicted <TM2>
F:120-141/Domain: transmembrane #status predicted <TM3>
F:163-182/Domain: transmembrane #status predicted <TM4>
F:213-234/Domain: transmembrane #status predicted <TM5>
F:251-271/Domain: transmembrane #status predicted <TM6>
F:308-328/Domain: transmembrane #status predicted <TM7>

Query Match 52.6%; Score 50; DB 2; Length 359;
Best Local Similarity 69.2%; Pred. No. 1.2;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
DB 313 YAFIQKFRHGILL 325

RESULT 18
A53611
interleukin-8 receptor type B - human
C:Species: Homo sapiens (man)
C>Date: 07-Oct-1994 #sequence revision 12-Apr-1996 #text_change 05-Nov-1999
C:Accession: I37898; I38712; A53611; A39446
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human interleukin-8
A:Reference number: I37898; MUID:95014476; PMID:7929358
A:Accession: I37898
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U11869; NID:G511801; PIDN:AAB60656.1; PID:G511803
A:Accession: I38712
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <RE2>
A:Cross-references: EMBL:U11872; NID:G511808; PIDN:AAA4380.1; PID:G511809; EMBL:U11873; I1876; NID:G511816; PID:G511817; EMBL:U11877; NID:G511818; PID:G511819; EMBL:U11878; NID:R:Sprengrer, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A:Title: Structure, genomic organization, and expression of the human interleukin-8 receptor
A:Reference number: A53611; MUID:94209273; PMID:7512557
A:Accession: A53611
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 6-360 <SPR>
A:Cross-references: GB:M99412; GB:L19593
R:Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor.
A:Reference number: A39446; MUID:91368200; PMID:1891716
A:Accession: A39446
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 6-360 <MUR>
A:Cross-references: GB:M73969
C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, inc
C:Genetics:
A:Gene: GDB:IL8RB; IL8RA
A:Cross-references: GDS:127868; OMIM:146928
A:Map position: 2q35-2q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 52.6%; Score 50; DB 2; Length 360;

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A:Molecule type: mRNA
A:Residues: 1-356 <GOB>
A:Cross-references: EMBL:X77797
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 52.6%; Score 50; DB 2; Length 356;
Best Local Similarity 69.2%; Pred. No. 1.2;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
DB 310 YAFIQKFRHGILL 322

RESULT 17
A48921
interleukin-8 receptor type B - mouse
N:Alternate names: G-protein coupled receptor Gpcr16
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text change 05-Nov-1999
C:Accession: A48921; A53677; I49348; I55421; H48909; I53774
R:Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert,
Genomics 18, 410-413, 1993
A:Title: The murine homologue of the human interleukin-8 receptor type B maps near the
A:Reference number: A48921; MUID:94117014; PMID:8288247
A:Accession: A48921
A:Molecule type: DNA
A:Residues: 1-359 <CEB>
A:Cross-references: GB:L23637; NID:G435093; PIDN:AAA39305.1; PID:G435094
R:Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
J. Biol. Chem. 269, 18263-18266, 1994
A:Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding
A:Reference number: A53677; MUID:94308043; PMID:7518426
A:Accession: A53677
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-359 <SUZ>
A:Cross-references: GB:L26549
A:Note: sequence extracted from NCBI backbone (NCBIP:149812)
R:Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
J. Immunol. 155, 2158-2164, 1995
A:Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
A:Reference number: I49348; MUID:95363183; PMID:7636264
A:Accession: I49348
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <RES>
A:Cross-references: EMBL:U31207; NID:G950174; PIDN:AAC52239.1; PID:G950175
R:Bozic, C.R.; Gerard, N.P.; von Uexkull-Guidenband, C.; Kolakowski, L.F.
J. Biol. Chem. 269, 23355-23358, 1994
A:Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression
A:Reference number: I55421; MUID:95050766; PMID:7961909
A:Accession: I55421
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <REZ>
A:Cross-references: GB:L13239; NID:G293665; PIDN:AAA62109.1; PID:G293666
R:Wilkie, T.M.; Chen, Y.; Gilbert, D.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.
Genomics 18, 175-184, 1993
A:Title: Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptor
A:Reference number: A48909; MUID:94116980; PMID:8288218
A:Accession: A48909
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 145-258 <MIL>
A:Cross-references: GB:L20337; NID:G438800; PIDN:AAA16853.1; PID:G438801
R:Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
Gene 142, 297-300, 1994
A:Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
A:Reference number: I53774; MUID:94252584; PMID:8194768
A:Accession: I53774
A>Status: preliminary; translated from GB/EMBL/DBJ

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Best Local Similarity 59.2%; Pred. No. 1.2; Mismatches 3; Gaps 0;
Matches 9; Conservative 1; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFF 13
|||:||||:
Db 314 YAFVGEKFRHGLL 326

RESULT 19

A:Accession: A45680
G protein-coupled peptide receptor EBI 1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R:Birkenbach, M.; Josefsen, K.; Valananchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled R
A:Reference number: A45680; MUID:93188173; PMID:8383238
A:Accession: A45680
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-378 <BIR>
A:Cross-references: GB:108176; NID:G183484; PID:G183485
A:Experimental source: B-lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIP:127095)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 52.6%; Score 50; DB 2; Length 378;
Best Local Similarity 52.9%; Pred. No. 1.2; Mismatches 3; Gaps 0;
Matches 9; Conservative 1; Indels 5; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQ 17
|||:||||:
Db 326 YAFVGEKFRNDIFKLFK 342

RESULT 20

E95247
hypothetical protein SP2115 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: E95247
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-76 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK76174.1; PID:G14973627; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2115

Query Match 51.6%; Score 49; DB 2; Length 76;
Best Local Similarity 62.5%; Pred. No. 0.37; Mismatches 1; Gaps 0;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFF 16
|||:||||:
Db 24 YAFKGDFFNYLAVVF 39

RESULT 21

E98112
Hypothetical protein spr1925 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001

C:Accession: B98112
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Es
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B98112
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-76 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAL00727.1; PID:G15459622; GSPDB:GN00174
C:Genetics:
A:Gene: spr1925

Query Match 51.6%; Score 49; DB 2; Length 76;
Best Local Similarity 62.5%; Pred. No. 0.37; Mismatches 1; Gaps 0;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFF 16
|||:||||:
Db 24 YAFKGDFFNYLAVVF 39

RESULT 22

I38450
chemokine (C-C) receptor 2, splice form A - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C:Accession: I38450
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant prot
A:Reference number: A53477; MUID:94195821; PMID:8146186
A:Accession: I38450
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: EMBL:U03882; NID:G472555; PIDN:AAA19119.1; PID:G472556
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
F:44-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:244-265/Domain: transmembrane #status predicted <TM6>
F:292-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:32-277,113-190/Disulfide bonds: #status predicted

Query Match 51.6%; Score 49; DB 2; Length 374;
Best Local Similarity 90.0%; Pred. No. 1.8; Mismatches 1; Gaps 0;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRN 10
|||:||||:
Db 305 YAFVGEKFRS 314

RESULT 23

JF0349
interferon-inducible protein 10 (IP-10) receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C:Accession: JF0349
R:Tamaru, M.; Tominaga, Y.; Yatsunami, K.; Narumi, S.

Biochem. Biophys. Res. Commun. 251, 41-48, 1998
 A;Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its
 A;Reference number: JE0349; MUID:99009219; PMID:9790904
 A;Accession: JE0349
 A;Molecule type: mRNA
 A;Residues: 1-367 <TAN>
 A;Cross-references: DBJ:AB003174; NID:G3798731; PIDN:AAA34045.1; PID:G3798732
 C;Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
 C;Superfamily: vertebrate rhodopsin

Query Match 50.5%; Score 48; DB 2; Length 367;
 Best Local Similarity 50.0%; Pred. No. 2.6;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVPFQK 18
 ||||| : : :
 DB 317 YAFVGVKFRQWMLFTR 334

RESULT 24
 A53752
 interleukin-8 receptor (clone 5B1a) - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C;Accession: A53752
 R;Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navar-
 J. Biol. Chem. 269, 12391-12394, 1994
 A;Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
 A;Reference number: A53752; MUID:94230294; PMID:8175642
 A;Accession: A53752
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-358 <PRA>
 A;Cross-references: GB:L24445; NID:G437661; PIDN:AAA31378.1; PID:G437662
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 49.5%; Score 47; DB 2; Length 358;
 Best Local Similarity 69.2%; Pred. No. 3.8;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYL 13
 ||||| : : :
 DB 312 YAFICQKFRYGLL 324

RESULT 25
 A55735
 G protein-coupled receptor EB11 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
 C;Accession: A55735
 R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
 Genomics 23, 643-650, 1994
 A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
 A;Reference number: A55735; MUID:95154835; PMID:7851893
 A;Accession: A55735
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-378 <SCH>
 A;Cross-references: GB:L31580; NID:G468340; PIDN:AAA74232.1; PID:G468341
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor

Query Match 49.5%; Score 47; DB 2; Length 378;
 Best Local Similarity 52.9%; Pred. No. 4;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVPFQK 17
 ||||| : : :
 DB 326 YAFVGVKFRSLFKLFK 342

RESULT 26

A23669
 interleukin-8 receptor, high affinity - rabbit
 N;Alternate names: fMLP receptor
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
 C;Accession: A23669
 R;Thomas, K.M.; Pyun, H.Y.; Navarro, J.
 J. Biol. Chem. 265, 20061-20064, 1990
 A;Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
 A;Reference number: A23669; MUID:91056034; PMID:1700779
 A;Accession: A23669
 A;Molecule type: mRNA
 A;Residues: 1-354 <THO>
 A;Cross-references: GB:M58021; GB:J05705; NID:G165442; PIDN:AAA31377.1; PID:G165443
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 48.4%; Score 46; DB 2; Length 354;
 Best Local Similarity 61.5%; Pred. No. 5.5;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYL 13
 ||||| : : :
 DB 309 YAFIQGNFRNGFL 321

RESULT 27

JQ1231
 interleukin-8 receptor - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
 C;Accession: JQ1231; A46483
 R;Reckmann, M.P.; Mungar, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerar-
 Biochem. Biophys. Res. Commun. 179, 784-789, 1991
 A;Title: Molecular characterization of the interleukin-8 receptor.
 A;Reference number: JQ1231; MUID:91378994; PMID:1898400

A;Accession: JQ1231
 A;Molecule type: DNA
 A;Residues: 1-355 <BEC>
 A;Cross-references: GB:M74240; NID:G165438; PIDN:AAA31375.1; PID:G165439

R;Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
 J. Immunol. 148, 1261-1264, 1992

A;Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
 A;Reference number: A46483; MUID:92148149; PMID:1737938

A;Accession: A46483
 A;Status: preliminary
 A;Molecule type: mRNA

A;Residues: 1-355 <LEE>
 A;Cross-references: GB:M82873; NID:G165440; PIDN:AAA31376.1; PID:G165441

A;Experimental source: neutrophils
 A;Note: Sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)

C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 48.4%; Score 46; DB 2; Length 355;
 Best Local Similarity 61.5%; Pred. No. 5.5;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYL 13
 ||||| : : :
 DB 310 YAFIQGNFRNGFL 322

RESULT 28

B97185
 glycosyltransferase [imported] - Clostridium acetobutylicum
 C;Species: Clostridium acetobutylicum
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C;Accession: B97185

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001

A48857
angiotensin II receptor type 1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A48857
R:Burns, K.D.; Inagami, T.; Harris, R.C.
Am. J. Physiol. 264, F645-F654, 1993
A:Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is present i
A:Reference number: A48857; MUID:93236091; PMID:7916579
A:Accession: A48857
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-359

A:Cross-references: GB:S59041; NID:9299614; PIDN:AAB26239.1; PID:9299615
A:Experimental source: proximal tubule cells
A>Note: sequence extracted from NCBI backbone (NCBIN:129600, NCBIIP:129601)

Db 302 YGFLGKKFRYFL 314

RESULT 33

A48857

angiotensin II receptor type 1 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999

C:Accession: A48857

R:Burns, K.D.; Inagami, T.; Harris, R.C.

Am. J. Physiol. 264, F645-F654, 1993

A:Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is present i

A:Reference number: A48857; MUID:93236091; PMID:7916579

A:Accession: A48857

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-359 <BU>

A:Cross-references: GB:S59041; NID:Q299614; PIDN:AAB26229.1; PID:Q299615

A:Experimental source: proximal tubule cells

A>Note: sequence extracted from NCBI backbone (NCBIN:129600, NCBIIP:129601)

A:Accession: JQ1516
A:Molecule type: DNA
A:Residues: 1-359 <ELT>
A>Note: the authors translated the codon AGC for residue 120 as Thr, GTC for residue 225
R:Kakar, S.S.; Sellers, J.C.; Devor, D.C.; Musgrove, L.C.; Neill, J.D.
Biochem. Biophys. Res. Commun. 183, 1090-1096, 1992
A:Title: Angiotensin II type-1 receptor subtype cDNAs: differential tissue expression and
A:Reference number: JH0578; MUID:92231868; PMID:1567388
A:Accession: JH0578
A:Molecule type: mRNA
A:Residues: 1-74, '1', '76'-119, 'T', '121-224, 'A', '226-359 <KAK>
A:Cross-references: GB:M87003; NID:g202920; PIDN:AAA40739.1; PID:g202921

A;Experimental source: anterior pituitary
 R;Ye, M.Q.; Healy, D.P. Commun. 185, 204-210, 1992
 Biochem. Biophys. Res. Commun. 185, 204-210, 1992
 A;Title: Characterization of an angiotensin type-1 receptor partial cDNA from rat kidney
 A;Reference number: PH0850; MUID:92287094; PMID:1599457
 A;Accession: PH0850
 A;Molecule type: mRNA
 A;Residues: 84-119, 'T', 121-224, 'A', 226-259 <YEW>
 A;Cross-references: GB:S37461; NID:G249938; PIDN:AAB22267.1; PID:G249939
 A;Experimental source: kidney
 C;Genetics:
 A;Gene: AT1B
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;27-53/Domain: transmembrane #status predicted <TM1>
 F;65-90/Domain: transmembrane #status predicted <TM2>
 F;103-125/Domain: transmembrane #status predicted <TM3>
 F;145-166/Domain: transmembrane #status predicted <TM4>
 F;194-216/Domain: transmembrane #status predicted <TM5>
 F;240-264/Domain: transmembrane #status predicted <TM6>
 F;274-304/Domain: transmembrane #status predicted <TM7>
 F;4, 176, 188, 344/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;232, 323/Binding site: phosphate (Thr) (covalent) #status predicted
 F;331, 338, 348/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 47.4%; Score 45; DB 2; Length 359;
 Best Local Similarity 53.8%; Pred. No. 8.2;
 Matches 7; Conservative 3; Mismatches 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
 | | : | : | : |
 Db 302 YGFLGKFKKYFL 314

RESULT 36
 S15403
 angiotensin II receptor type 1 - bovine
 C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 C;Accession: S15403
 R;Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.
 Nature 351, 230-233, 1991
 A;Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiotensin II receptor
 A;Reference number: S15403; MUID:91251900; PMID:2041569
 A;Accession: S15403
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-359 <SAS>
 A;Cross-references: GB:X62294; NID:G43; PIDN:CAA44182.1; PID:G44
 C;Superfamily: vertebrate rhodopsin

Query Match 47.4%; Score 45; DB 2; Length 359;
 Best Local Similarity 53.8%; Pred. No. 8.2;
 Matches 7; Conservative 3; Mismatches 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
 | | : | : | : |
 Db 302 YGFLGKFKKYFL 314

RESULT 37
 JH0621
 angiotensin II receptor 1A - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Nov-1999
 C;Accession: JH0621; JCI193
 R;Sasamura, H.; Heine, L.; Krieger, J.E.; Pratt, R.E.; Kobilka, B.K.; Dzau, V.J.
 Biochem. Biophys. Res. Commun. 185, 253-259, 1992
 A;Title: Cloning, characterization, and expression of two angiotensin receptor (AT-1) is
 A;Reference number: JH0621; MUID:92287102; PMID:1599461
 A;Accession: JH0621
 A;Molecule type: DNA
 A;Residues: 1-359 <SAS>

A;Cross-references: GB:S37484; NID:G249945; PIDN:AAB22269.1; PID:G249946
 A;Experimental source: strain Balb/C
 R;Ooshima, H.; Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.; van der Meer-de Jong, R.; Ii
 Biochem. Biophys. Res. Commun. 186, 1042-1049, 1992
 A;Title: Analysis of the evolution of angiotensin II type 1 receptor gene in mammals (mouse)
 A;Reference number: JCI193; MUID:92359981; PMID:1497638
 A;Accession: JCI193
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-6, 'I', 8-19, 'IS', 22-37, 'M', 39-133, 'K', 135-359 <YOS>
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;37-57/Domain: transmembrane #status predicted <TM1>
 F;65-85/Domain: transmembrane #status predicted <TM2>
 F;103-123/Domain: transmembrane #status predicted <TM3>
 F;145-165/Domain: transmembrane #status predicted <TM4>
 F;201-220/Domain: transmembrane #status predicted <TM5>
 F;241-261/Domain: transmembrane #status predicted <TM6>
 F;286-306/Domain: transmembrane #status predicted <TM7>
 F;4, 176, 188/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;331, 338/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 47.4%; Score 45; DB 2; Length 359;
 Best Local Similarity 53.8%; Pred. No. 8.2;
 Matches 7; Conservative 3; Mismatches 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
 | | : | : | : |
 Db 302 YGFLGKFKKYFL 314

RESULT 38
 JC2134
 angiotensin II receptor type 1A - rat
 N;Alternate names: AT1a receptor; AT3 receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
 C;Accession: JC2134; S15404; S20424; JQ1055
 R;Conchon, S.; Monnot, C.; Sirrieix, M.E.; Bihoreau, C.; Corvol, P.; Clauser, E.
 Biochem. Biophys. Res. Commun. 199, 1347-1354, 1994
 A;Title: Synthetic cDNA encoding the rat AT1a receptor: a useful tool for structure-function
 A;Reference number: JC2134; MUID:94197726; PMID:8147879
 A;Accession: JC2134
 A;Molecule type: mRNA
 A;Residues: 1-359 <CON>
 A;Note: the amino acid sequence of this protein is not given
 R;Murphy, T.J.; Alexander, R.W.; Griendling, K.K.; Runge, M.S.; Bernstein, K.E.
 Nature 351, 233-236, 1991
 A;Title: Isolation of a cDNA encoding the vascular type-1 angiotensin II receptor.
 A;Reference number: S15404; MUID:91251901; PMID:2041570
 A;Accession: S15404
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-359 <MUR>
 A;Cross-references: GB:X62295; NID:G57773; PIDN:CAA44183.1; PID:G57774
 R;Iwai, N.; Inagami, T.
 FEBS Lett. 298, 257-260, 1992
 A;Title: Identification of two subtypes in the rat type I angiotensin II receptor.
 A;Reference number: S20423; MUID:92183879; PMID:1544458
 A;Accession: S20424
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-359 <IWA>
 R;Iwai, N.; Yamano, Y.; Chaki, S.; Konishi, F.; Bardhan, S.; Tibbette, C.; Sasaki, K.; He
 Biochem. Biophys. Res. Commun. 177, 299-304, 1991
 A;Title: Rat angiotensin II receptor: cDNA sequence and regulation of the gene expression
 A;Reference number: JQ1055; MUID:91254291; PMID:2043116
 A;Accession: JQ1055
 A;Molecule type: mRNA
 A;Residues: 1-80, 'C', 82-108, 'T', 110-359 <IWA>
 A;Cross-references: GB:M74054; NID:G202918; PIDN:AAA40738.1; PID:G202919
 A;Experimental source: kidney
 C;Comment: AT1 receptor consists of two closely related AT1 isoforms of angiotensin II re

A;Title: Cloning of a novel member of the G protein-coupled receptor family related to p
A:Reference number: JC5294; MUID:97224403; PMID:9070864
A:Accession: JC5294
A:Molecule type: DNA
A:Residues: 1-311,'T',313-375 <P>
A:Cross-references: GB:U7827; NID:g1906591; PIDN:AAC51173.1; PID:g1906592
C:Comment: This protein plays a role in B-cell functions and is involved in endothelial c
C:Genetics:
A:Gene: GDB:CMKRL2; CEPR
A:Cross-references: GDB:3929190
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:64-83/Domain: transmembrane #status predicted <TM1>
F:96-114/Domain: transmembrane #status predicted <TM2>
F:126-148/Domain: transmembrane #status predicted <TM3>
F:180-198/Domain: transmembrane #status predicted <TM4>
F:221-238/Domain: transmembrane #status predicted <TM5>
F:260-283/Domain: transmembrane #status predicted <TM6>
F:308-321/Domain: transmembrane #status predicted <TM7>
F:25,32,44/Binding site: carbohydrate (Asn) #status predicted

Query Match 46.3%; Score 44; DB 2; Length 375;
Best Local Similarity 38.9%; Pred. No. 13;
Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKERNYLLVFQK 18
| : | | | | : | : | :
Db 324 YSFLGETFRDLRYIEQ 341

Search completed: September 28, 2004, 09:07:11
Job time : 10.925 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:55:11 ; Search time 5.625 Seconds
(without alignments)
166.624 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGKFRNYLLVFFQK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	95	100.0	352	1	CKR5_CERAE
2	95	100.0	352	1	CKR5_CERP
3	95	100.0	352	1	CKR5_CERG
4	95	100.0	352	1	CKR5_GORGO
5	95	100.0	352	1	CKR5_HUMAN
6	95	100.0	352	1	CKR5_HYLL
7	95	100.0	352	1	CKR5_HYLM
8	95	100.0	352	1	CKR5_HYLS
9	95	100.0	352	1	CKR5_MACMU
10	95	100.0	352	1	CKR5_PANTR
11	95	100.0	352	1	CKR5_PAPHA
12	95	100.0	352	1	CKR5_PONPY
13	95	100.0	352	1	CKR5_PYGIB
14	95	100.0	352	1	CKR5_PYGNE
15	95	100.0	352	1	CKR5_TRAPR
16	95	100.0	352	1	CKR5_TRAPH
17	85	89.5	354	1	CKR5_RAT
18	80	84.2	354	1	CKR5_MOUSE
19	78	82.1	373	1	CKR2_MOUSE
20	78	82.1	373	1	CKR2_RAT
21	76	80.0	360	1	CKR2_MACMU
22	65	68.4	355	1	CKR3_CERAE
23	65	68.4	355	1	CKR3_HUMAN
24	65	68.4	355	1	CKR3_MACMU
25	64	67.4	353	1	CKR8_MOUSE
26	64	67.4	359	1	CKR3_MOUSE
27	64	67.4	359	1	CKR3_RAT
28	63	66.3	355	1	CKR8_HUMAN
29	63	66.3	356	1	CKR8_MACMU
30	61	64.2	374	1	CKR6_HUMAN
31	60	63.2	355	1	CKR1_HUMAN
32	59	62.1	367	1	CKR6_MOUSE
33	58	61.1	354	1	C3X1_RAT

ALIGNMENTS

```

RESULT 1
CKR5_CERAE
ID CKR5_CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CCR5R5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
RT gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U83324; AAC51795.1; -
CC EMBL; U83325; AAC51796.1; -
CC EMBL; AB015944; BAA1328.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHOODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
CC Polymorphism.
CC
CC -----
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

```

```

34 57 60.0 354 1 C3X1_MOUSE Q920d9 mus musculus
35 57 60.0 355 1 C3X1_HUMAN P49238 homo sapien
36 57 60.0 360 1 CKR4_HUMAN P51679 homo sapien
37 56 58.9 355 1 CKR1_MACMU P56482 macaca mula
38 55 57.9 358 1 CKR3_CAVPO Q922i3 cavia porce
39 53 55.8 355 1 CKR1_MOUSE P51675 mus musculus
40 53 55.8 356 1 CKR1_MOUSE P51676 mus musculus
41 52 54.7 360 1 CKR4_MOUSE P51680 mus musculus
42 52 54.7 378 1 CKR7_HUMAN P32480 homo sapien
43 50 52.6 353 1 IL8B_MACMU Q28519 macaca mula
44 50 52.6 353 1 IL8B_PANTR Q28807 pan troglod
45 50 52.6 356 1 IL8B_CANFA O97571 canis famil

```

FT TRANSMEM 31 58 1 (POTENTIAL).

FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 69 89 2 (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).

FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 142 166 4 (POTENTIAL).

FT DOMAIN 167 198 5 (POTENTIAL).

FT TRANSMEM 199 218 6 (POTENTIAL).

FT DOMAIN 219 235 7 (POTENTIAL).

FT TRANSMEM 236 260 8 (POTENTIAL).

FT DOMAIN 261 277 9 (POTENTIAL).

FT TRANSMEM 278 301 10 (POTENTIAL).

FT DOMAIN 302 325 11 (POTENTIAL).

FT TRANSMEM 326 352 12 (POTENTIAL).

FT DISULFID 101 178 BY SIMILARITY.

FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

FT VARIANT 14 14 N -> Y.

FT VARIANT 352 352 F -> L.

SQ SEQUENCE 352 AA; 40561 MW; 7852E690C72EC29A CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 2

ID CKR5_CERP STANDARD; PRT; 352 AA.

AC Q9TV42.

DT 15-VAR-2004 (Rel. 43, Created)

DT 15-VAR-2004 (Rel. 43, Last sequence update)

DT 15-VAR-2004 (Rel. 43, Last annotation update)

DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCRS-5) (CCRS).

GN CCR5 OR CMKR5.

OS Cercopithecus pygerythrus (Vervet monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Cercopithecus.

OX NCBI_TaxID=60710;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=100;

RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,

RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;

RT "Mutations in CCR5-coding sequences are not associated with SIV

RT carrier status in African nonhuman primates."

RL AIDS Res. Hum. Retroviruses 15:931-939 (1999).

CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC MIP-1-beta and RANTES and subsequently transduces a signal by

CC increasing the intracellular calcium ions level. May play a role

CC in the control of granulocytic lineage proliferation or

CC differentiation.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC or send an email to license@isb-sib.ch).

CC EMBL; AF035222; AAD44015.1; -

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PRO0237; GPCRHOOPS.

DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.

DR PROSITE; PS00262; G-PROTEIN RECEPTOR; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 31 58 1 (POTENTIAL).

FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 69 89 2 (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).

FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 142 166 4 (POTENTIAL).

FT DOMAIN 167 198 5 (POTENTIAL).

FT TRANSMEM 199 218 6 (POTENTIAL).

FT TRANSMEM 219 235 7 (POTENTIAL).

FT DOMAIN 236 260 8 (POTENTIAL).

FT TRANSMEM 261 277 9 (POTENTIAL).

FT DOMAIN 278 301 10 (POTENTIAL).

FT TRANSMEM 302 352 11 (POTENTIAL).

FT DISULFID 101 178 BY SIMILARITY.

FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 3

ID CKR5_CERTO STANDARD; PRT; 352 AA.

AC Q62743; Q62744; Q62745; Q62746;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCRS).

GN CCR5 OR CMKR5.

OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Cercopithecus.

OX NCBI_TaxID=9531;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Isolate 079, 085, 087, and 089;

RA MEDLINE=98321155; PubMed=9656999;

RA Chen Z., Gettler A., Ho D.D., Marx P.A.;

RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys

RT naturally infected in west Africa: a comparison of coreceptor usage

RT of primary SIVsm, HIV-2, and SIVmac."

RL Virology 246:113-124 (1998).

CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC MIP-1-beta and RANTES and subsequently transduces a signal by

CC increasing the intracellular calcium ions level. May play a role

CC in the control of granulocytic lineage proliferation or

CC differentiation.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC or send an email to license@isb-sib.ch).

CC EMBL; AF035222; AAD44015.1; -

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.


```

DR EMBL; AF051902; AAC39830.1; -.
DR EMBL; AF051903; AAC39831.1; -.
DR EMBL; AF051904; AAC39832.1; -.
DR EMBL; AF051905; AAC39833.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECF Fl_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECF Fl_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT VARIANT 1 2
FT VARIANT 2 3
FT VARIANT 25 25
FT VARIANT 100 100
FT VARIANT 107 107
FT VARIANT 134 134
FT VARIANT 146 146
FT VARIANT 340 340
FT VARIANT 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
Db 297 YAFVGEKFRNVLVFFQK 314
|||||
RESULT 4
CKR5 GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amadee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CKR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
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EMBL; AF005659; AAB62553.1; -.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PROSITE; PS00237; G-PROTEIN RECF Fl_1; 1.
PROSITE; PS0262; G-PROTEIN RECF Fl_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT VARIANT 1 2
FT VARIANT 2 3
FT VARIANT 25 25
FT VARIANT 100 100
FT VARIANT 107 107
FT VARIANT 134 134
FT VARIANT 146 146
FT VARIANT 340 340
FT VARIANT 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
Db 297 YAFVGEKFRNVLVFFQK 314
|||||
RESULT 5
CKR5 HUMAN STANDARD; PRT; 352 AA.
ID CKR5 HUMAN STANDARD; PRT; 352 AA.
AC P51881; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708; O15538; G9UPA4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
GN CKR5 OR CMKR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241590; PubMed=8639485;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RA "Molecular cloning and functional expression of a new human

```


Genetically divergent strains of simian immunodeficiency virus use CCR5 as a coreceptor for entry." J. Virol. 71:2705-2714(1997).

SEQUENCE FROM N.A. SPECIES=M.mulatta; PubMed=11461684; MEDLINE=21354176; Hauer B.J., Clements J.E.; "Identification and comparison of eleven rhesus macaque chemokine receptors." Hum. Retroviruses 17:981-986(2001).

SEQUENCE FROM N.A. SPECIES=M.mulatta, M.fascicularis, and M.nemestrina; MEDLINE=97268687; PubMed=9108095; Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M., Peiper S.C., Parmentier M., Broder C.C., Doms R.W.; "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains." Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).

MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; U77672; AAC51109.1; --
DR EMBL; U73739; AAC51158.1; --
DR EMBL; U96762; AAC34132.1; --
DR EMBL; AF005660; AAB62554.1; --
DR EMBL; AF005661; AAB62555.1; --
DR EMBL; AF005662; AAB62556.1; --
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7cm_1; 1.
DR PRINTS; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD RES 3 3
FT MOD RES 10 10
FT MOD RES 14 14
FT MOD RES 15 15
FT CARBOHYD 268 268
FT CONFLICT 241 241
FT CONFLICT 252 252
FT SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. NO. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
DB 297 YAFVGEKFRNLYLVFFQK 314

RESULT 10
CKR5_PANTR STANDARD; PRT; 352 AA.
AC PS6440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CC-CKR-5) (CCR-5) (CCRS).
GN CCR5 OR CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M., Peiper S.C., Parmentier M., Broder C.C., Doms R.W.; "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains." Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Zimmerman P.A., Buckler-White A., Alkhatib G.; Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B., Ho D.D.; "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism." AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97426118; PubMed=9282822;
RA Zacharova V., Zachar V., Goustin A.S.; "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural HIV type 1 host." AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.; "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1." AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RN [6]
RP SEQUENCE FROM N.A.
RX Zhang Y., Ryder O.A., Zhang Y.; "Sequence comparison of the CCR5 gene in primates and primate phylogeny." Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 DR EMBL; AF005663; AAB62557.1; -
 DR EMBL; U94329; AAB58446.1; -
 DR EMBL; AF011542; AAB65742.1; -
 DR EMBL; U97666; AAC51670.1; -
 DR EMBL; AF011540; AAB65740.1; -
 DR EMBL; U89797; AAC03717.1; -
 DR EMBL; AF177894; AAK43377.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 FT CARBOHYD 268 268
 FT CONFLICT 123 123
 FT CONFLICT T -> S (IN REF. 1.) (POTENTIAL).
 SQ SEQUENCE 352 AA; 40539 MW; 44338698B80FE34C CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 11
 ID_CK5_PAPHA STANDARD; PRT; 352 AA.
 AC P5641;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-CR-5) (CC-CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CWKBR5.
 OS Papio hamadryas (Hamadryas baboon), and
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OC NCBI_TaxID=9557, 9555;
 [1]

SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas;
 RX MEDLINE=9726868; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharpton M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;

RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas;
 RX MEDLINE=99210133; PubMed=10195758;
 RA Sakkena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
 RT "Species-specific changes in the CCR5 gene from African and Asian
 RT nonhuman primates";
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
 [3]
 RN SEQUENCE FROM N.A.
 RP SPECIES=P.anubis;
 RC Bontton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
 RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 DR EMBL; AF005658; AAB62552.1; -
 DR EMBL; AF105287; AAD20556.1; -
 DR EMBL; AF105288; AAD20557.1; -
 DR EMBL; AF105289; AAD20558.1; -
 DR EMBL; AF105290; AAD20559.1; -
 DR EMBL; AF023452; AAC63830.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 FT CARBOHYD 268 268
 FT CONFLICT 123 123
 FT CONFLICT T -> S (IN REF. 1.) (POTENTIAL).
 SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1FE8B2 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 DB 297 YAFVGEKFRNLLVFFQK 314

```

Db      297 YAFVGEKFRNLLVFFQK 314
RESULT 12
CKRS_PONPY STANDARD; PRT; 352 AA.
AC O97881;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: AF075446; AAD19858.1; -
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD RES 3 3
FT MOD RES 10 10
FT MOD RES 14 14
FT MOD RES 15 15
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;
Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      297 YAFVGEKFRNLLVFFQK 314
RESULT 13
CKRS_PYGBI STANDARD; PRT; 352 AA.
AC O97880;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKCR5.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF075445; AAD19857.1; -
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD RES 3 3
FT MOD RES 10 10
FT MOD RES 14 14
FT MOD RES 15 15
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;
Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
|||||

```

Db 297 YAFVGEKFRNLLVFFQK 314
|||||

RESULT 14

CKR5_PYGNE STANDARD; PRT; 352 AA.
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075448; AAD19860.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsin.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58
FT DOMAIN 1 (POTENTIAL).
FT TRANSMEM 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT TRANSMEM 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT TRANSMEM 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT TRANSMEM 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT TRANSMEM 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40532 MW; FE4FD9D98D3E861 CRC64;
Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||
Db 297 YAFVGEKFRNLLVFFQK 314
|||||

RESULT 15

CKR5_TRAFR STANDARD; PRT; 352 AA.
AC O97878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075442; AAD19854.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsin.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT TRANSMEM 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT TRANSMEM 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT TRANSMEM 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT TRANSMEM 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT TRANSMEM 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;
Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY 1 YAFVGEKFRNLLVFFQK 18
    |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 16
CKR5 TRAPH
ID CKR5 TRAPH STANDARD; PRT; 352 AA.
AC Q87879;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
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-----
EMBL: AF075443; AAD19855.1; -.
InterPro: IPR00276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHOPOPSN.
PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
TRANSMEM 31 58 1 (POTENTIAL).
DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
TRANSMEM 69 89 2 (POTENTIAL).
DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
TRANSMEM 103 124 3 (POTENTIAL).
DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
TRANSMEM 142 166 4 (POTENTIAL).
DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
TRANSMEM 199 218 5 (POTENTIAL).
DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
TRANSMEM 236 260 6 (POTENTIAL).
DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
TRANSMEM 278 301 7 (POTENTIAL).
DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
DISULFID 101 178
MOD RES 3 3 SULFATION (BY SIMILARITY).
MOD RES 10 10 SULFATION (BY SIMILARITY).
MOD RES 14 14 SULFATION (BY SIMILARITY).
MOD RES 15 15 SULFATION (BY SIMILARITY).
SEQUENCE 352 AA; 4366F148D3A5938F CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
    |||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 17
CKR5 RAT
ID CKR5 RAT STANDARD; PRT; 354 AA.
AC O08556;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
DE alpha receptor).
GN CKR5 OR CMKBR5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Wistar; TISSUE=Brain;
MEDLINE=98334064; PubMed=9670389;
RA Speiss C., Gourmal N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
RA Berger M., Gebicke-Haerter P.J.;
RT "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
RT upregulation of its mRNA in ischemic and endotoxemic rat brain.";
J. Neurosci. Res. 53:16-28(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis".
J. Neuroimmunol. 86:1-12(1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
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-----
EMBL: Y12009; CAA72737.1; -.
EMBL: U77350; AAC03243.1; -.
InterPro: IPR00276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHOPOPSN.
PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
TRANSMEM 33 60 1 (POTENTIAL).
DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
TRANSMEM 71 91 2 (POTENTIAL).
DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
TRANSMEM 105 126 3 (POTENTIAL).
DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
TRANSMEM 144 168 4 (POTENTIAL).
DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
TRANSMEM 201 220 5 (POTENTIAL).
DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
TRANSMEM 238 262 6 (POTENTIAL).
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FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 280 303 7 (POTENTIAL).
FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
FT DISULFID 103 180 BY SIMILARITY.
FT CARBOHYD 270 270 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 89.5%; Score 85; DB 1; Length 354;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKERNYLVFFQK 18
| | | | | | | | | | | | | | | | | |
DB 299 YAFVGEKERNYLVFFRK 316

RESULT 18
ID CKR5 MOUSE STANDARD; PRT: 354 AA.
AC P51682; O35313; O35891; P97308; P97405; Q61867;
DI 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (MIP-1
alpha receptor).
DE alpha receptor).
GN CKR5 OR CMKBR5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Spleen;
RX MEDLINE=96205938; PubMed=86311787;
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT 1alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9";
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96278910; PubMed=8662890;
RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Cloning and characterization of a novel murine macrophage
RT inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 271:14445-14451(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=123/Ola;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CKR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=97404635; PubMed=92611347;
RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
RT "Two distinct CCR5 domains can mediate coreceptor usage by human
RT immunodeficiency virus type 1.";
RL J. Virol. 71:6305-6314(1997).
RN [6]

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Query Match 84.2%; Score 80; DB 1; Length 354;
 Best Local Similarity 83.3%; Pred. No. 2.7e-06;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 299 YAFVGEKFRNYLLVFFQK 316

RESULT 19
CKR2_MOUSE
ID CKR2_MOUSE STANDARD; PRT; 373 AA.
AC PS1683; Q61172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (JE/ETC receptor) (MCP-1 receptor).
GN CCR2 OR CMK3B2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9."
RL J. Biol. Chem. 271:7551-7558 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RX MEDLINE=96216064; PubMed=8662823;
RA Kurihara T., Bravo R.;
RT "Cloning and functional expression of mCCR2, a murine receptor for
RT the C-C chemokines JE and PIC."
RL J. Biol. Chem. 271:11603-11606 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97026720; PubMed=8872898;
RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
RA Post T.W., Gerard C., Dorf M.E.;
RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
RT transcriptase-polymerase chain reaction does not detect mRNA for the
RT KC or new MCP-1 receptor."
RL J. Neurosci. Res. 45:382-391 (1996).
CC -1- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U47035; AAC52453.1; -;
CC EMBL; U51717; AAC52557.1; -;
CC EMBL; U56819; AAC52784.1; -;
CC GDB; MGI:106185; Ccr2.
CC GO; GO:0016493; P:C-C chemokine receptor activity; IDA.
CC GO; GO:0019955; P:cytokine binding; IPI.
CC GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
CC GO; GO:0030097; P:hemoipoiesis; IMP.
CC GO; GO:0006959; P:humoral immune response; IMP.
CC GO; GO:0006954; P:inflammatory response; IMP.

GO; GO:0030334; P:regulation of cell migration; IMP.
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
DR PRINIS; PR00337; GPCRHOPOPSN
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 55
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 56 83
FT DOMAIN 84 93
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 94 114
FT DOMAIN 115 127
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 128 149
FT DOMAIN 150 166
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 191
FT DOMAIN 192 219
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 239
FT DOMAIN 240 256
FT TRANSMEM 257 281
FT DOMAIN 282 298
FT TRANSMEM 299 322
FT DOMAIN 323 373
FT CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 203
FT BY SIMILARITY.
FT CONFLICT 39 39 Y -> H (IN REF. 1).
FT CONFLICT 184 184 A -> G (IN REF. 1).
FT CONFLICT 264 264 V -> G (IN REF. 1).
SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;
Query Match 82.1%; Score 78; DB 1; Length 373;
Best Local Similarity 77.8%; Pred. No. 6.4e-06;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 318 YAFVGEKFRNYLLVFFQK 335

RESULT 20
CKR2_RAT
ID CKR2_RAT STANDARD; PRT; 373 AA.
AC O55193;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2).
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=9818173; PubMed=9655467;
RA Jiang Y., Salafraza M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA deFiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis".
RL J. Neuroimmunol. 86:1-12 (1998).
CC -1- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level (by similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
CC macrophages.
CC -1- INDUCTION: In animals in which experimental allergic
CC encephalomyelitis (EAE) has been induced.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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 CC -----
 DR EMBL; U77349; AAC03242.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 61 81 POTENTIAL.
 FT TRANSMEM 82 91 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 92 112 POTENTIAL.
 FT TRANSMEM 113 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149 POTENTIAL.
 FT TRANSMEM 150 170 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 171 191 POTENTIAL.
 FT TRANSMEM 192 220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 241 POTENTIAL.
 FT TRANSMEM 242 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 257 277 POTENTIAL.
 FT TRANSMEM 278 301 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 302 322 POTENTIAL.
 FT TRANSMEM 323 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 126 203 BY SIMILARITY.
 SQ SEQUENCE 373 AA; 42763 MW; 287BB012F5D6FD09 CRC64;
 Query Match 82.1%; Score 78; DB 1; Length 373;
 Best Local Similarity 77.8%; Pred. No. 6.4e-06;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNVLVFFQK 18
 |||||
 Db 318 YAFVGEKFRNVLVFFQK 335
 |||||
 RESULT 21
 CKR2_MACMU
 ID CKR2_MACMU STANDARD; PRT; 360 AA.
 AC O18793;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 26-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
 GN CKR2 OR CMKBR2.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.F.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=B;
 CC IsoId=O18793-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=O18793-2; Sequence=Not described;
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC -----
 DR EMBL; AF013958; AAD11572.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
 Alternative splicing.
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 43 70 1 (POTENTIAL).
 FT TRANSMEM 71 80 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 81 100 2 (POTENTIAL).
 FT TRANSMEM 101 114 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 115 136 3 (POTENTIAL).
 FT TRANSMEM 137 153 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 154 178 4 (POTENTIAL).
 FT TRANSMEM 179 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 226 5 (POTENTIAL).
 FT TRANSMEM 227 243 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 244 268 6 (POTENTIAL).
 FT TRANSMEM 269 285 7 (POTENTIAL).
 FT TRANSMEM 286 309 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 310 360 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 14 14 N-LINKED (GLCNAC...) (POTENTIAL).
 FT MOD RES 26 26 SULFATION (BY SIMILARITY).
 FT DISULFID 113 190 BY SIMILARITY.
 SQ SEQUENCE 360 AA; 41139 MW; 4B2552BC913FE9F CRC64;
 Query Match 80.0%; Score 76; DB 1; Length 360;
 Best Local Similarity 77.8%; Pred. No. 1.4e-05;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNVLVFFQK 18
 |||||
 Db 305 YAFVGEKFRNVLVFFQK 322
 |||||
 RESULT 22
 CKR3_CERAE
 ID CKR3_CERAE STANDARD; PRT; 355 AA.
 AC P56492;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
 DE (CCR3).
 GN CCR3 OR CMKBR3.
 OS Cercopithecoidea aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercopithecoidea.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sol N., Treboute C., Gomas E., Ferchal F., Alison M.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
 CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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DR ENBL: Y13775; CAA74106.1; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR PRINTS: PR00237; GPCR_Rhodopsin.
 DR PROSITE: PS00237; G PROTEIN RECP F1.1; 1.
 DR PROSITE: PS00262; G PROTEIN RECP F1.2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 35 62 1 (POTENTIAL).
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 73 93 2 (POTENTIAL).
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 204 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 SQ SEQUENCE 355 AA; 44F7ASEFE978FF CRC64;

Query Match 68.4%; Score 65; DB 1; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.0011;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
 Db 301 YAFVGEKFRNLLVFFQK 318

RESULT 23

CC CR3_HUMAN STANDARD; PRT; 355 AA.
 AC P51677; Q15748; Q86WD2; Q9ULY8;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3) (CCR3)
 DE (CCR3) (Eosinophil eotaxin receptor).
 GN CCR3 OR CCR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Monocytes;
 RX MEDLINE=95348056; PubMed=7622448;
 RA Combadiere C., Ahuja S.K., Murphy P.M.;
 RT "Cloning and functional expression of a human eosinophil CC chemokine
 RT receptor";
 RL J. Biol. Chem. 270:16491-16494(1995).
 RN [2]
 RP ERRATUM.
 RA Combadiere C., Ahuja S.K., Murphy P.M.;
 RL J. Biol. Chem. 270:30235-30235(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96235044; PubMed=9642344;
 RA Daugherty B.B., Siciliano S.J., Demartino J.A., Malkowitz L.,
 RA Sirotnin A., Springer M.S.;
 RT "Cloning, expression, and characterization of the human eosinophil
 RT eotaxin receptor";
 RL J. Exp. Med. 183:2349-2354(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RX MEDLINE=96281895; PubMed=8676064;
 RA Ponath P.D., Qin S., Post T.W., Wang J., Wu L., Gerard N.P.,
 RA Newman W., Gerard C., Mackay C.R.;
 RT "Molecular cloning and characterization of a human eotaxin receptor
 RT expressed selectively on eosinophils";
 RL J. Exp. Med. 183:2737-2748(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;
 RT "Partial resistance to infection by syncytium-inducing primary HIV-1
 RT in exposed uninfected individuals homozygous for CCR5 32bp deletion";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A., AND VARIANT SER-218.
 RX MEDLINE=21040311; PubMed=11196669;
 RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
 RA Hirai K., Tokunaga K.;
 RT "New variations of human CC-chemokine receptors CCR3 and CCR4";
 RL Genes Immun. 1:97-104(1999).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22074933; PubMed=12079287;
 RA Vijh S., Dayhoff D.E., Wang C.E., Imam Z., Ehrenberg P.K.,
 RA Michael N.L.;
 RT "Transcription regulation of human chemokine receptor CCR3: evidence
 RT for a rare TATA-less promoter structure conserved between Drosophila
 RT and humans";
 RL Genomics 50:86-95(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronson R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org)";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Lung, and Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
 CC eotaxin-3, MCP-3, MCP-4, RANTES and MIP-1 delta. Subsequently
 CC transduces a signal by increasing the intracellular calcium ions
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: In eosinophils as well as trace amounts in
 CC neutrophils and monocytes.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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15-JUL-1998 (Rel. 36, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 C-C chemokine receptor type 8 (C-C CKR-8) (CC-CKR-8) (CCR-8).
 CCR8 OR CMKBR8 OR TER1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zaballos A., Goya I.I., Gutierrez J., Varona R., Marquez G.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=98334001; PubMed=9670926;
 RA Zingoni A., Soto H., Hedrick J.A., Stoppacciaro A., Storlazzi C.T.,
 RA Sinigaglia F., D'Ambrosio D., O'Garra A., Robinson D., Rocchi M.,
 RA Santoni A., Zlotnik A., Napolitano M.;
 RT "The chemokine receptor CCR8 is preferentially expressed in Th2 but
 not Th1 cells";
 RL J. Immunol. 161:547-551(1998).
 CC -1- FUNCTION: Receptor for the TCA-3 chemokine.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; Z98206; CAB10896.1; -;
 CC EMBL; Z98205; CAB10895.1; -;
 CC EXBL; AF001277; AAC97598.1; -;
 CC MGD; MGI:1201402; Ccr8.
 CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC GO; GO:0006935; P:chemotaxis; IDA.
 CC InterPro; IPR004068; CC 8 receptor.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR01530; CHEMOKINER8.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PROSITE; PS00237; G PROTEIN RECEPTOR F1 1; 1.
 CC PROSITE; PS0262; G PROTEIN RECEPTOR F1 2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 CC DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 34 61 1 (POTENTIAL).
 CC DOMAIN 62 71 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 72 91 2 (POTENTIAL).
 CC DOMAIN 92 105 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 106 127 3 (POTENTIAL).
 CC DOMAIN 128 144 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 145 169 4 (POTENTIAL).
 CC DOMAIN 170 200 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 201 220 5 (POTENTIAL).
 CC DOMAIN 221 236 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 237 261 6 (POTENTIAL).
 CC DOMAIN 262 278 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 279 302 7 (POTENTIAL).
 CC DOMAIN 303 353 CYTOPLASMIC (POTENTIAL).
 CC DISULFID 104 181 BY SIMILARITY.
 CC CARBOHYD 8 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 353 AA; 40045 MW; 31EC4B642CDB9A5 CRC64;
 Query Match 67.4%; Score 64; DB 1; Length 353;
 Best Local Similarity 61.1%; Pred. No. 0.0016;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 298 YAFIGKEFKKHLMDVFOK 315
 |||||:|:|
 RESULT 26
 CCR3 MOUSE
 ID CCR3 MOUSE STANDARD; PRT; 359 AA.
 AC P51678;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3)
 DE (CCR3) (CCR3) (Macrophage inflammatory protein-1 alpha receptor-like
 DE 2) (MIP-1 alpha RL2).
 GN CCR3 OR CMKBR3 OR CMKBR1L2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=96072806; PubMed=7594543;
 RA Post T.W., Bosic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
 RA Gerard C.;
 RT "Molecular characterization of two murine eosinophil beta chemokine
 RT receptors";
 RL J. Immunol. 155:5299-5305(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=95340546; PubMed=7542241;
 RA Gao J.-L., Murphy P.M.;
 RT "Cloning and differential tissue-specific expression of three mouse
 RT beta chemokine receptor-like genes, including the gene for a
 RT functional macrophage inflammatory protein-1 alpha receptor.";
 RL J. Biol. Chem. 270:17494-17501(1995).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
 CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
 CC amounts in Leukocytes.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U29677; AAA86118.1; -;
 CC EMBL; U28406; AAA89155.1; -;
 CC MGD; MGI:104616; Ccr3.
 CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC GO; GO:0006935; P:chemotaxis; IDA.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PROSITE; PS00237; G PROTEIN RECEPTOR F1 1; 1.
 CC PROSITE; PS0262; G PROTEIN RECEPTOR F1 2; 1.
 CC G-protein coupled receptor; Transmembrane.
 CC DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 39 64 1 (POTENTIAL).
 CC DOMAIN 65 68 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 69 95 2 (POTENTIAL).
 CC DOMAIN 96 111 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 112 133 3 (POTENTIAL).
 CC DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 151 175 4 (POTENTIAL).

QY 1 YAFVGKPRNLLVFFOK 18

[5] SEQUENCE FROM N.A.
 RP Nakajima T., Yoshida R., Harada S.;
 RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RP LIGAND BINDING.
 RX MEDLINE=98180363; PubMed=9521068;
 RA Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;
 RT "Identification of the CC chemokines TARC and macrophage inflammatory
 protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 CC -!- FUNCTION: Receptor for the chemokines SCY1/I-309, SCY44/MIP-1-
 CC beta and SCY1/TARC. May regulate monocyte chemotaxis and thymic
 CC cell line apoptosis. Alternative coreceptor with CD4 for HIV-1
 CC infection.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U45983; AB61962.1; -;
 CC DR EMBL: U62556; AB05542.1; -;
 CC DR EMBL: Z79782; CAB02142.1; -;
 CC DR EMBL: Y08456; CAA69712.1; -;
 CC DR EMBL: D49919; BAA23387.1; -;
 CC DR EMBL: AF005210; AAB62547.1; -;
 CC DR PIR: JC5067; JC5067.
 CC DR GENE: HGNC:1609; CCR8.
 CC DR MIN: 601834; -;
 CC DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 CC DR GO: GO:0004950; F: chemokine receptor activity; TAS.
 CC DR GO: GO:001026; F: coreceptor activity; TAS.
 CC DR GO: GO:0001155; P: cell adhesion; TAS.
 CC DR GO: GO:0006935; P: chemotaxis; TAS.
 CC DR GO: GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
 CC DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. .; TAS.
 CC DR GO: GO:0006955; P: immune response; TAS.
 CC DR InterPro: IPR004068; CC 8 receptor.
 CC DR InterPro: IPR002276; GPCR_Rhodpsn.
 CC DR Pfam: PF00001; 7tm.1; 1.
 CC DR PRINTS: PR01530; CHEMOKINER8.
 CC DR PRINTS: PR00237; GPCRHOPOFSN.
 CC DR PROSITE: PS00237; G-PROTEIN RECP F1.1; 1.
 CC DR PROSITE: PS0262; G-PROTEIN RECP F1.2; 1.
 CC DR G-protein coupled receptor; Transmembrane; Glycoprotein.
 CC KW DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 36 63 1 (POTENTIAL).
 CC FT DOMAIN 64 73 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 74 93 2 (POTENTIAL).
 CC FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 108 129 3 (POTENTIAL).
 CC FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 147 171 4 (POTENTIAL).
 CC FT DOMAIN 172 202 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 203 222 5 (POTENTIAL).
 CC FT DOMAIN 223 238 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 239 263 6 (POTENTIAL).
 CC FT DOMAIN 264 280 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 281 304 7 (POTENTIAL).
 CC FT DOMAIN 305 355 CYTOPLASMIC (POTENTIAL).
 CC FT DISULFID 106 183 BY SIMILARITY.
 CC SQ SEQUENCE 355 AA; 40844 MW; BC14A153CF695361 CRC64;

Query Match 66.3%; Score 63; DB 1; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.0024;

Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLYLVFFQK 18
 |||||:|
 Db 300 YAFVGEKPKHLSEIFQK 317
 RESULT 29
 CCR8_MACMU
 ID CCR8 MACMU STANDARD; PRT; 356 AA.
 AC O97655;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 8 (C-C CCR-8) (CC-CCR-8) (CCR-8).
 GN CCR8.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Spleen;
 RC MEDLINE=21354176; PubMed=11461684;
 RX Margulies B.J., Hauer D.A., Clements J.E.;
 RA "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 CC -!- FUNCTION: Receptor for the chemokines SCY1/I-309, SCY44/MIP-1-
 CC beta and SCY1/TARC. May regulate monocyte chemotaxis and thymic
 CC cell line apoptosis (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF100205; AAC72403.1; -;
 CC DR InterPro: IPR004068; CC 8 receptor.
 CC DR InterPro: IPR002276; GPCR_Rhodpsn.
 CC DR Pfam: PF00001; 7tm.1; 1.
 CC DR PRINTS: PR01530; CHEMOKINER8.
 CC DR PRINTS: PR00237; GPCRHOPOFSN.
 CC DR PROSITE: PS00237; G-PROTEIN RECP F1.1; 1.
 CC DR PROSITE: PS0262; G-PROTEIN RECP F1.2; 1.
 CC DR G-protein coupled receptor; Transmembrane; Glycoprotein.
 CC KW DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 36 63 1 (POTENTIAL).
 CC FT DOMAIN 64 73 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 74 93 2 (POTENTIAL).
 CC FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 108 129 3 (POTENTIAL).
 CC FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 147 172 4 (POTENTIAL).
 CC FT DOMAIN 173 203 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 204 223 5 (POTENTIAL).
 CC FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 240 264 6 (POTENTIAL).
 CC FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 282 305 7 (POTENTIAL).
 CC FT DOMAIN 306 356 CYTOPLASMIC (POTENTIAL).
 CC FT DISULFID 106 184 BY SIMILARITY.
 CC SQ SEQUENCE 356 AA; 41210 MW; 1979628DEE44845B CRC64;

Query Match 66.3%; Score 63; DB 1; Length 356;
 Best Local Similarity 66.7%; Pred. No. 0.0024;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVCEKERNVLLVFFQK 18
 DB 301 YAFVCEKERNVLLVFFQK 318

RESULT 30
 CCR6 HUMAN
 ID CCR6 HUMAN STANDARD; PRT; 374 AA.
 AC P51684; P78553; Q92846;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 6 (C-C CKR-6) (CCR-6) (IARC
 DE receptor) (GPR-CY4) (GPCY4) (Chemokine receptor-like 3) (CCR-L3)
 DE (DRY6)
 GN CCR6 OR CCR6B OR STRL22 OR GPR29 OR CXCR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RX MEDLINE=97313465; PubMed=9169459;
 RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
 RA Nomiya H., Yoshie O.;
 RT "Identification of CCR6, the specific receptor for a novel
 RT lymphocyte-directed CC chemokine LARC.";
 RL J. Biol. Chem. 272:14893-14898 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lautens L.B., Modi W., Bonner T.I.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97040707; PubMed=8886020;
 RA Zaballero A., Varona R., Guierrez J., Lind P., Marquez G.;
 RT "Molecular cloning and RNA expression of two new human chemokine
 RT receptor-like genes";
 RL Biochem. Biophys. Res. Commun. 227:846-853 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA McCoy R., Perlmutter D.H.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224503; PubMed=9070937;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27";
 RL Genomics 40:175-180 (1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Warren C.N., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22935763; PubMed=14574404;
 RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
 RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
 RA Babbage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
 RA Blakey S., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
 RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
 RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
 RA Cullley K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,

Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
 Gilby L.M., Gillson C.J., Griffiths R.J., Grafham D.V., Grant M.,
 Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Hall K.S.,
 Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
 Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
 Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
 Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
 Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
 Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
 Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
 McMurray A., Moore M.J.E., Mullikin J.C., Niblett D., Nickerson T.,
 Novik K.L., Oliver K., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
 Pearce A.V., Peck A.I., Phillips S.A., Rice C.M., Ross M.T., Searle S.M.,
 Porter K.M., Sheridan E., Skuce C.B., Smith S., Smith M., Spraggon L.,
 Sehra H.K., Sheridan E., Skuce C.B., Smith S., Smith M., Spraggon L.,
 Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
 Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
 Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
 Whitaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
 Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
 Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
 RT "The DNA sequence and analysis of human chromosome 6";
 RL Nature 425:805-811 (2003).
 RN [8]
 RP SEQUENCE FROM N.A.
 TISSUE=Pancreas;
 MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3-
 CC alpha/LARC and subsequently transduces a signal by increasing the
 CC intracellular calcium ions level.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Spleen, lymph nodes, appendix, and fetal
 CC liver. Expressed in lymphocytes, T cells and B cells but not in
 CC natural killer cells, monocytes or granulocytes.
 CC -1- INDUCTION: By interleukin-2.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-6 is the initiator.
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 CC -----
 CC EMBL; U45984; AAB62714.1; -
 CC EMBL; U79784; CAB02144.1; ALT_INIT.
 CC EMBL; U60000; AAB06949.1; -
 CC EMBL; U68030; AAC51124.1; -
 CC EMBL; U68032; AAC51125.1; -
 CC EMBL; AY242126; AAC92293.1; -
 CC EMBL; AL121935; CAB99328.1; -

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DR EMBL; BC037960; AAH37960.1; -.
DR HSSP; P34996; 1DDD.
DR Genew; HGNC:1607; CCR6.
DR MIM; 601835; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004950; F:chemokine receptor activity; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0006959; P:humoral immune response; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR004067; CC 6 receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01529; CHEMOKINER6.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 47
FT TRANSMEM 48 74
FT DOMAIN 75 83
FT TRANSMEM 84 104
FT DOMAIN 105 119
FT TRANSMEM 120 141
FT DOMAIN 142 159
FT TRANSMEM 160 180
FT DOMAIN 181 211
FT TRANSMEM 212 238
FT DOMAIN 239 254
FT TRANSMEM 255 279
FT DOMAIN 280 303
FT TRANSMEM 304 321
FT DOMAIN 322 374
FT DISULFID 118 197
FT CARBOHYD 7 7
FT CARBOHYD 23 23
FT CONFLICT 60 60
FT CONFLICT 74 74
FT CONFLICT 86 86
FT CONFLICT 164 164
FT CONFLICT 182 182
FT CONFLICT 192 192
FT CONFLICT 206 206
FT CONFLICT 225 225
FT CONFLICT 370 374
SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 64.28; Score 61; DB 1; Length 374;
Best Local Similarity 75.98; Pred. No. 0.0056;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YAFVGEFRNYLL 13
|||:|||||
Db 316 YAFIQKFRNVL 328

RESULT 31
CKR1 HUMAN STANDARD; PRT; 355 AA.
AC P32246;
AT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DI 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)
DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
DE (RANTES-R) (HM145) (LD78 receptor).
GN CKR1 OR CWKBR1 OR CWKRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=93161416; PubMed=7679328;
RA Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
RT "Molecular cloning, functional expression, and signaling
characteristics of a C-C chemokine receptor.";
RL Cell 72:415-425(1993).
RN [2]_SEQUENCE FROM N.A.
RP MEDLINE=93240122; PubMed=7683036;
RA Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
Murphy P.M.;
RT "Structure and functional expression of the human macrophage
inflammatory protein 1 alpha/RANTES receptor.";
RL J. Exp. Med. 177:1421-1427(1993).
RN [3]_SEQUENCE FROM N.A.
RP TISSUE=Monocytes;
RX MEDLINE=94092629; PubMed=7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
leukocyte chemotactic peptide receptors.";
RL Int. Immunol. 5:1239-1249(1993).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-
beta or MCP-1 and subsequently transduces a signal by increasing
the intracellular calcium ions level. Responsible for affecting
stem cell proliferation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed in different hematopoietic
cells.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL; L09230; AAA58408.1; -.
CC EMBL; L10918; AAA36543.1; -.
CC EMBL; D10925; BAA01723.1; -.
CC PIR; A45177; A45177.
CC Genew; HGNC:1602; CCR1.
CC MIM; 601159; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004950; F:chemokine receptor activity; TAS.
CC GO; GO:0007155; P:cell adhesion; TAS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0006935; P:chemotaxis; TAS.
CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
CC GO; GO:0006955; P:immune response; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC GO; GO:0007125; P:invasive growth; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_REC_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34
FT TRANSMEM 35 60
FT DOMAIN 61 64
FT TRANSMEM 65 91
FT DOMAIN 92 107
FT TRANSMEM 108 129
FT DOMAIN 130 146
FT CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 5 (EXTRACELLULAR (POTENTIAL)).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 6 (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 7 (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 7 (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFLICT 337 337 E -> D (IN REF. 3).
FT CONFLICT 337 337 E -> D (IN REF. 3).
SQ SEQUENCE 355 AA; 41172 MW; B3C100FFED275985 CRC64;

Query Match 63.2%; Score 60; DB 1; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.0079;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKERNVLLVFFQK 18
    |||||:|||||:
Db 301 YAFVGERFKYLRQLFHR 318

RESULT 32
CKR6 MOUSE
ID CKR6 MOUSE STANDARD; PRT; 367 AA.
AC O54689;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 6 (C-CR-6) (CCR-6) (KY411).
DE CCR6 OR CMKBR6.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077268; PubMed=9862452;
RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
RA Albar J.P., Ardavin C., Marquez G.;
RT "Molecular cloning, functional characterization and mRNA expression
RT analysis of the murine chemokine receptor CCR6 and its specific ligand
RT MIP-3alpha.";
RT FEBS Lett. 440:188-194 (1998).
RL CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3-
RL alpha/LARC and subsequently transduces a signal by increasing the
RL intracellular calcium ions level.
CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC CC
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CC or send an email to license@isb-sib.ch).
CC CC
CC EMBL; AB009369; BAA23776.1; -.
CC EMBL; AJ222714; CAA10956.1; -.
DR MGD; MGI:1333797; Cr6.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR004067; CC-6_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR01529; CHEMOKINR6.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

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DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 66 1 (POTENTIAL).
FT DOMAIN 67 75 2 (POTENTIAL).
FT TRANSMEM 76 96 2 (POTENTIAL).
FT DOMAIN 97 111 3 (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 151 4 (POTENTIAL).
FT TRANSMEM 152 172 4 (POTENTIAL).
FT DOMAIN 173 203 5 (POTENTIAL).
FT TRANSMEM 204 230 5 (POTENTIAL).
FT DOMAIN 231 246 6 (POTENTIAL).
FT TRANSMEM 247 271 6 (POTENTIAL).
FT DOMAIN 272 295 7 (POTENTIAL).
FT TRANSMEM 296 313 7 (POTENTIAL).
FT DOMAIN 314 367 7 (POTENTIAL).
FT DISULFID 110 189 BY SIMILARITY.
FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 367 AA; 42102 MW; 6A309AF83B1117E CRC64;

Query Match 62.1%; Score 59; DB 1; Length 367;
Best Local Similarity 69.2%; Pred. No. 0.012;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKERNVLL 13
    |||||:|||||:
Db 308 YAFIQGKFRNPFM 320

RESULT 33
C3X1 RAT
ID C3X1 RAT STANDARD; PRT; 354 AA.
AC F35411;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CX3C chemokine receptor 1 (C-X3-C CR-1) (CX3CR1) (Fractalkine
DE receptor) (GPR13) (RBS11).
GN CX3CR1 OR GPR13.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Spinal cord;
RX MEDLINE=94323113; PubMed=8047298;
RA Harrison J.K., Barber C.M., Lynch K.R.;
RT "cDNA cloning of a G-protein-coupled receptor expressed in rat spinal
RT cord and brain related to chemokine receptors.";
RL Neurosci. Lett. 169:85-89 (1994).
CC CC -!- FUNCTION: Receptor for the CX3C chemokine fractalkine and mediates
CC both its adhesive and migratory functions.
CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC CC -!- TISSUE SPECIFICITY: Most abundant in adult spinal cord, brain,
CC kidney, gut, uterus and testes.
CC CC -!- FTM: This protein is not N-glycosylated which is unusual for G-
CC protein-coupled receptors.
CC CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC CC
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CC or send an email to license@isb-sib.ch).
CC CC
CC EMBL; U04808; AAB87093.1; -.
DR PIR; I58186; I58186.
DR InterPro; IPR005387; Fractalkiner.

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DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR01562; GPCRALKINER.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
DR G-protein coupled receptor; Transmembrane.
KW DOMAIN 1 32
FT DOMAIN 1 32
FT TRANSMEM 33 60
FT DOMAIN 61 70
FT TRANSMEM 71 91
FT DOMAIN 92 104
FT TRANSMEM 105 126
FT DOMAIN 127 143
FT TRANSMEM 144 168
FT DOMAIN 169 196
FT TRANSMEM 197 216
FT DOMAIN 217 232
FT TRANSMEM 233 257
FT DOMAIN 258 274
FT TRANSMEM 275 298
FT DOMAIN 299 354
FT DISULFID 103 176
SQ SEQUENCE 354 AA; 40327 MW; CFC4578095E77376 CRC64;

Query Match 61.1%; Score 58; DB 1; Length 354;
Best Local Similarity 61.1%; Pred. No. 0.017;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 YAFVGEKFRNYLVFFQK 18
DB 294 YAFAGEKFRNYLVHLYNK 311

RESULT 34
C3X1_MOUSE STANDARD; PRT; 354 AA.
ID C3X1_MOUSE
AC Q920D9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C3X3 chemokine receptor 1 (C-X3-C CKR-1) (C3XCR1) (Fractalkine
DE receptor).
DE C3XCR1.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=99119076; PubMed=9918795;
RA Combadiere C., Gao J.-L., Tiffany H.L., Murphy P.M.;
RT "Gene cloning, RNA distribution, and functional expression of mCX3CR1,
RT a mouse chemotactic receptor for the CX3C chemokine fractalkine.";
RL Biochem. Biophys. Res. Commun. 253:728-732(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX Coultas L., McCall S.R.;
RT "Cloning and characterization of murine CX3CR1, a receptor for murine
RT fractalkine/neurotactin.";
RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary gland;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., Kernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for the CX3C chemokine fractalkine and mediates
CC both its adhesive and migratory functions.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: This protein is not N-glycosylated which is unusual for
CC G-protein-coupled receptors.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
DR EMBL; AF074912; AAD08665.1; -
DR EMBL; AF102269; AAC72408.1; -
DR EMBL; BC012653; AAH12653.1; -
DR MGD; MGI:133815; Cx3cr1.
DR InterPro; IPR005387; Fractalkiner.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR01562; GPCRALKINER.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
DR G-protein coupled receptor; Transmembrane.
KW DOMAIN 1 32
FT DOMAIN 1 32
FT TRANSMEM 33 60
FT DOMAIN 61 70
FT TRANSMEM 71 91
FT DOMAIN 92 104
FT TRANSMEM 105 126
FT DOMAIN 127 143
FT TRANSMEM 144 168
FT DOMAIN 169 196
FT TRANSMEM 197 216
FT DOMAIN 217 232
FT TRANSMEM 233 257
FT DOMAIN 258 274
FT TRANSMEM 275 298
FT DOMAIN 299 354
FT DISULFID 103 176
SQ SEQUENCE 354 AA; 40266 MW; 12C745E8E3755CA9 CRC64;

Query Match 60.0%; Score 57; DB 1; Length 354;
Best Local Similarity 61.1%; Pred. No. 0.026;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 YAFVGEKFRNYLVFFQK 18
DB 294 YAFAGEKFRNYLVHLYNK 311

RESULT 35
C3X1_HUMAN STANDARD; PRT; 355 AA.
ID C3X1_HUMAN
AC P49238;
DT 01-FEB-1996 (Rel. 33, Created)

```

DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE CX3C chemokine receptor 1 (C-X3-C CRF-1) (CX3CR1) (Fractalkine
 DE receptor) (GPR13) (V28) (Beta chemokine receptor-like 1) (CMK-BRL-1)
 DE (CMKBLR1).
 GN CX3CR1 OR GPR13.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=96011651; PubMed=7590284;
 RA Raport C.J., Schweickart V.L., Eddy R.L. Jr., Shows T.B., Gray P.W.;
 RT "The orphan G-protein-coupled receptor-encoding gene V28 is closely
 RT related to genes for chemokine receptors and is expressed in lymphoid
 RT and neural tissues.";
 RL Gene 163:295-299 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=95374679; PubMed=7646814;
 RA Combadiere C., Ahuja S.K., Murphy P.M.;
 RT "Cloning, chromosomal localization, and RNA expression of a human
 RT beta chemokine receptor-like gene.";
 RL DNA Cell Biol. 14:673-680 (1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Blood;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscin T.B., Toshyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP CHARACTERIZATION.
 RP MEDLINE=98050927; PubMed=9390561;
 RA Imai T., Hieshima K., Haskell C., Baba M., Nagira M., Nishimura M.,
 RA Kakizaki M., Takagi S., Nomiya H., Schall T.J., Yoshie O.;
 RT "Identification and molecular characterization of fractalkine receptor
 RT CX3CR1, which mediates both leukocyte migration and adhesion.";
 RL Cell 91:521-530 (1997).
 RN [5]
 RP CHARACTERIZATION.
 RP MEDLINE=98395093; PubMed=9726990;
 RA Combadiere C., Salzwedel K., Smith E.D., Tiffany H.L., Berger E.A.,
 RA Murphy P.M.;
 RT "Identification of CX3CR1, A chemotactic receptor for the human CX3C
 RT chemokine fractalkine and a fusion coreceptor for HIV-1.";
 RL J. Biol. Chem. 273:23799-23804 (1998).
 RN [6]
 RP VARIANTS ALA-57; ILE-122; ILE-249 AND MET-280.
 RX MEDLINE=20196025; PubMed=10731151;
 RA Faure S., Meyer L., Costagliola D., Vaneensberghe C., Genin E.,
 RA Autran B., Delfraissy J.-F., McDermott D.H., Murphy P.M., Debre P.,
 RA Theodorou I., Combadiere C.;
 RT "Rapid progression to AIDS in HIV+ individuals with a structural
 RT variant of the chemokine receptor CX3CR1."

RL Science 287:2274-2277 (2000).
 CC -!- FUNCTION: Receptor for the CX3C chemokine fractalkine and mediates
 CC both its adhesive and migratory functions. Acts as co-receptor
 CC with CD4 for HIV-1 virus envelope protein (in vitro).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in lymphoid and neural tissues.
 CC -!- DISEASE: Increased susceptibility to HIV infection and rapid
 CC progression to AIDS are associated with the Ile-249/Met-280
 CC haplotype.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC EMBL; U20350; AAA91783.1; -;
 CC DR EMBL; U28934; AAA87032.1; -;
 CC DR EMBL; BC028078; AAH28078.1; -;
 CC DR PIR; J4304; J4304;
 CC DR Genew; HGNC:2558; CX3CR1.
 CC MIM; 601470; -;
 CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC DR GO; GO:0004950; F:chemokine receptor activity; TAS.
 CC DR GO; GO:0007155; P:cell adhesion; TAS.
 CC DR GO; GO:0006968; P:cellular defense response; TAS.
 CC DR GO; GO:0006935; P:chemotaxis; TAS.
 CC DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
 CC DR InterPro; IPR005387; Fractalkiner.
 CC DR InterPro; IPR00276; GPCR_Rhodopsn.
 CC DR Pfam; PF00001; 7tm1; 1.
 CC DR PRINTS; PR01562; FRCTALKINER.
 CC DR PRINTS; PR0237; GPCR_RHODOPSN.
 CC DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC DR PROSITE; PS02662; G_PROTEIN_RECEP_F1_2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Polymorphism.
 CC FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 32 59 1 (POTENTIAL).
 CC FT DOMAIN 60 69 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 70 90 2 (POTENTIAL).
 CC FT DOMAIN 91 103 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 104 125 3 (POTENTIAL).
 CC FT DOMAIN 126 142 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 143 167 4 (POTENTIAL).
 CC FT DOMAIN 168 195 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 196 215 5 (POTENTIAL).
 CC FT DOMAIN 216 231 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 232 256 6 (POTENTIAL).
 CC FT DOMAIN 257 273 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 274 297 7 (POTENTIAL).
 CC FT DOMAIN 298 355 CYTOPLASMIC (POTENTIAL).
 CC FT DISULFID 102 175 BY SIMILARITY.
 CC FT VARIANT 57 57 T -> A.
 CC FT VARIANT 122 122 V -> I.
 CC FT VARIANT 249 249 V -> I (common polymorphism in Caucasian
 CC population).
 CC FT VARIANT 280 280 /FTid=VAR_010043.
 CC FT VARIANT 280 280 T -> M (common polymorphism in Caucasian
 CC population).
 CC FT /FTid=VAR_010044.
 CC FT /FTid=VAR_010045.
 CC SQ SEQUENCE 355 AA; 40396 MW; C59DC5F4C312F22 CRC64;
 Query Match 60.0%; Score 57; DB 1; Length 355;
 Best Local Similarity 61.1%; Pred. No. 0.026;
 Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 YAFVGEKERNYLLVFFQK 18
 ||| ||||| ||| |

Db 293 YAFAGEKFRRLYHLYGK 310

RESULT 36

CKR4_HUMAN STANDARD; PRT; 360 AA.

AC P51679; Q9ULY6; Q9ULY7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 4 (C-C CKR-4) (CCR-4) (CCR4)
 DE (X5-5).
 GN CCR4 OR CMKBR4.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spine;
 RX MEDLINE=95370289; PubMed=7642634;
 RA Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,
 RA Proudfoot A.E.I., Wells T.N.C.;
 RT "Molecular cloning and functional expression of a novel CC chemokine
 receptor cDNA from a human basophilic cell line.";
 RL J. Biol. Chem. 270:19495-19500(1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.
 RX MEDLINE=21040311; PubMed=11196669;
 RA Kato H., Tsuchiya N., Izumi S., Miyama M., Nakajima T., Kawasaki H.,
 RA Hirai K., Tokunaga K.;
 RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
 RL Genes Immun. 1:97-104(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=97313486; PubMed=9169480;
 RA Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
 RT "The T cell-directed CC chemokine TARC is a highly specific
 biological ligand for CC chemokine receptor 4.";
 RL J. Biol. Chem. 272:15036-15042(1997).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=98104169; PubMed=9430724;
 RA Imai T., Chantray D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,
 RA Yoshie O., Gray P.W.;
 RT "Macrophage-derived chemokine is a functional ligand for the CC
 chemokine receptor 4.";
 RL J. Biol. Chem. 273:1764-1768(1998).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=99394604; PubMed=10466728;
 RA Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P.,
 RA Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher E.C.;
 RT "The chemokine receptor CCR4 in vascular recognition by cutaneous but
 not intestinal memory T cells.";
 RL Nature 400:776-780(1999).
 RN [7]
 RP FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.
 RX MEDLINE=20219238; PubMed=10754297;
 RA Ingjerdengen M., Damaj B., Maghazachi A.A.;
 RT "Human NK cells express CC chemokine receptors 4 and 8 and respond to
 thymus and activation-regulated chemokine, macrophage-derived
 chemokine, and I-309.";
 RL J. Immunol. 164:4048-4054(2000).
 CC -!- FUNCTION: High affinity receptor for the C-C type chemokines
 TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is
 mediated by G(i) proteins which activate a phosphatidylinositol-

CC calcium second messenger system. Can function as a chemoattractant
 homing receptor on circulating memory lymphocytes and as a
 coreceptor for some primary HIV-2 isolates. In the CNS, could
 mediate hippocampal-neuron survival.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in the thymus, in
 peripheral blood leukocytes, including T cells, mostly cd4+ cells,
 and in monocytes. Detected also in macrophages, ifn-2-activated
 natural killer cells and skin-homing memory T cells, mostly the
 ones expressing the cutaneous lymphocyte antigen (CLA). Expressed
 in brain microvascular and coronary artery endothelial cells.
 CC -!- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
 PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
 BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X85740; CAA59743.1; -;
 DR EMBL; AB023888; BAA86965.1; -;
 DR EMBL; AB023889; BAA86966.1; -;
 DR EMBL; AB023890; BAA86967.1; -;
 DR EMBL; AB023891; BAA86968.1; -;
 DR EMBL; AB023892; BAA86969.1; -;
 DR EMBL; AY322539; AAP84352.1; -;
 DR PIR; A57160; A57160.
 DR Genew; HGNC:1605; CCR4.
 DR MIM; 604836; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0004950; F: chemokine receptor activity; TAS.
 DR GO; GO:0006935; P: chemotaxis; TAS.
 DR GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0006955; P: immune response; TAS.
 DR GO; GO:0006954; P: inflammatory response; TAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO0237; GPCRHHODOPSN.
 DR PROSITE; PS0237; G-PROTEIN RECF_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECF_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Polymorphism.
 FT DOMAIN 1 39
 FT TRANSMEM 40 67 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 68 77 1 (POTENTIAL).
 FT TRANSMEM 78 98 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 99 111 2 (POTENTIAL).
 FT TRANSMEM 112 133 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 134 150 3 (POTENTIAL).
 FT TRANSMEM 151 175 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 176 206 4 (POTENTIAL).
 FT TRANSMEM 207 226 5 (POTENTIAL).
 FT DOMAIN 227 242 6 (POTENTIAL).
 FT TRANSMEM 243 267 7 (POTENTIAL).
 FT DOMAIN 268 284 8 (POTENTIAL).
 FT TRANSMEM 285 308 9 (POTENTIAL).
 FT DOMAIN 309 360 10 (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 110 187 BY SIMILARITY.
 FT VARIANT 130 130 L -> V.
 FT VARIANT 178 178 /FTID=VAR_010669.
 FT VARIANT 360 360 /FTID=VAR_010670.
 SQ SEQUENCE 360 AA; 41402 MW; 51EBE2AD1FAFBF CRC64;
 Query Match 60.0%; Score 57; DB 1; Length 360;

Best Local Similarity 58.8%; Pred. No. 0.026;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 17
DB 304 YFGLGKFRKYLQLFK 320

RESULT 37
CKR1_MACMU STANDARD; PRT; 355 AA.
AC P56482;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1).
GN CKR1 OR CMKBR1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine receptors";
RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, RANTES, MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-BETA AND MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL PROLIFERATION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL; AF017282; AAB70526.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 5 (POTENTIAL).
FT TRANSMEM 198 223 6 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 7 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 8 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 106 183 N-LINKED (GLCNAC...) (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
SQ SEQUENCE 355 AA; 41198 MW; 41CAEA7CC19D23D4 CRC64;
Query Match 58.9%; Score 56; DB 1; Length 355;
Best Local Similarity 55.6%; Pred. No. 0.039;

Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 301 YAFAGERFRKYLQLFHR 318

RESULT 38
CKR3_CAVPO STANDARD; PRT; 358 AA.
AC Q92213;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
GN CCR3 OR CMKBR3.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99049845; PubMed=9834099;
RA Sabroe I., Conroy D.M., Gerard N.P., Li Y., Collins P.D., Post T.W., Jose P.J., Williams T.J., Gerard C.J., Ponath P.D.;
RT "Cloning and characterization of the guinea pig eosinophil ectaxon receptor, C-C chemokine receptor-3: blockade using a monoclonal antibody in vivo";
RL J. Immunol. 161:6139-6147 (1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin, MCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL; AF060698; AAC80428.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 64 1 (POTENTIAL).
FT DOMAIN 65 74 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 75 95 2 (POTENTIAL).
FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 113 133 3 (POTENTIAL).
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 4 (POTENTIAL).
FT DOMAIN 176 206 5 (POTENTIAL).
FT TRANSMEM 207 227 6 (POTENTIAL).
FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 264 7 (POTENTIAL).
FT DOMAIN 265 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 308 8 (POTENTIAL).
FT DOMAIN 309 358 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 106 183 BY SIMILARITY.
SQ SEQUENCE 358 AA; 41623 MW; 7B73FAB7A3BC3670 CRC64;
Query Match 57.9%; Score 55; DB 1; Length 358;
Best Local Similarity 55.6%; Pred. No. 0.058;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:56:16 ; Search time 28.8 Seconds
(without alignments)
197.199 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95
Sequence: 1 YAFVGEKFRNLLVFFQK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp Vertebrate: *
14: sp Unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	333	4	O14694
2	95	100.0	334	6	Q9TU07
3	95	100.0	339	4	Q3UN24
4	95	100.0	339	4	Q3UN26
5	95	100.0	339	4	Q3UN23
6	95	100.0	339	4	Q9UBJ7
7	95	100.0	339	4	Q3UN25
8	95	100.0	339	4	Q3UN27
9	95	100.0	339	4	Q3UBT9
10	95	100.0	339	4	Q3UN28
11	95	100.0	339	6	Q3TQW0
12	95	100.0	339	6	Q9TUX1
13	95	100.0	339	6	Q9TU09
14	95	100.0	339	6	Q9TUW8
15	95	100.0	339	6	Q9TUT4
16	95	100.0	339	6	Q9TUW9

17 95 100.0 339 6 Q9TSQ1
18 95 100.0 339 6 Q9TU08
19 95 100.0 339 6 Q9TQW4
20 95 100.0 339 6 Q9TUW4
21 95 100.0 339 6 Q9TQW7
22 95 100.0 339 6 Q9TUQ5
23 95 100.0 339 6 Q9TUW3
24 95 100.0 339 6 Q9TUS9
25 95 100.0 339 6 Q9TQW0
26 95 100.0 339 6 Q9TSN2
27 95 100.0 339 6 Q9TUR6
28 95 100.0 339 6 Q9TQV6
29 95 100.0 339 6 Q9TUW6
30 95 100.0 339 6 Q9TUQ9
31 95 100.0 339 6 Q9TSN3
32 95 100.0 339 6 Q9TSK3
33 95 100.0 339 6 Q9TUT7
34 95 100.0 339 6 Q9TUR2
35 95 100.0 339 6 Q9TQV0
36 95 100.0 339 6 Q9TUW6
37 95 100.0 339 6 Q9TQW5
38 95 100.0 339 6 Q9TUS7
39 95 100.0 339 6 Q9TUW7
40 95 100.0 339 6 Q9TUW3
41 95 100.0 339 6 Q9TUS5
42 95 100.0 339 6 Q9TUW0
43 95 100.0 339 6 Q9TQW2
44 95 100.0 339 6 Q9TQV3
45 95 100.0 339 6 Q9TUQ8

ALIGNMENTS

RESULT 1

O14694 PRELIMINARY; PRT; 333 AA.
AC O14694
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011504; AAB65704.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PFC0001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS02622; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 333 333
AEFA07A67893AEB CRC64;

Query Match 100.0%; Score 95; DB 4; Length 333;

Best Local Similarity 100.0%; Pred. No. 1.1e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

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Db      278 YAFVGEKFRNYLLVFFQK 295

RESULT 2
Q9TUQ7 PRELIMINARY; PRT; 334 AA.
AC Q9TUQ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
CCR5.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Erythrocybus.
OX NCBI_TaxID=95338;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162049; AAD47804.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 334
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 38460 MW; B19DOCEC667B69F0 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 285 YAFVGEKFRNYLLVFFQK 302

RESULT 3
Q9UN24 PRELIMINARY; PRT; 339 AA.
AC Q9UN24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161919; AAD47676.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4B CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 5
Q9UN23 PRELIMINARY; PRT; 339 AA.
AC Q9UN23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
CCR5.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F932C91AA7 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307
[1]

RESULT 6
Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR EMBL; AF161917; AAD47674.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FF1F2F27A CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307
[1]

RESULT 7
Q9UN25 PRELIMINARY; PRT; 339 AA.
AC Q9UN25;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161919; AAD47675.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307
[1]

RESULT 8
Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.

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DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B4E2CB4EC2 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||
DB 290 YAFVGEKFRNLLVFFQK 307
|||

RESULT 9
Q9UBT9
ID Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||
DB 290 YAFVGEKFRNLLVFFQK 307
|||

RESULT 10
Q9UN28
ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||
DB 290 YAFVGEKFRNLLVFFQK 307
|||

RESULT 11
Q9TQW0
ID Q9TQW0 PRELIMINARY; PRT; 339 AA.
AC Q9TQW0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (created gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1

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FT NON TER      339      339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
      |||||
DB      290 YAFVGEKFRNLLVFFQK 307

RESULT 12
Q9TUX1
ID Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (Crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER      1      1
FT NON TER      339      339
SQ SEQUENCE 339 AA; 39075 MW; 09257FBFB834C4AE CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
      |||||
DB      290 YAFVGEKFRNLLVFFQK 307

RESULT 13
Q9TUU9
ID Q9TUU9 PRELIMINARY; PRT; 339 AA.
AC Q9TUU9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,

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RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47704.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER      1      1
FT NON TER      339      339
SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
      |||||
DB      290 YAFVGEKFRNLLVFFQK 307

RESULT 14
Q9TUN8
ID Q9TUN8 PRELIMINARY; PRT; 339 AA.
AC Q9TUN8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER      1      1
FT NON TER      339      339
SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNLLVFFQK 18
      |||||
DB      290 YAFVGEKFRNLLVFFQK 307

RESULT 15

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Q9TUT4      PRELIMINARY;      PRT;      339 AA.
ID Q9TUT4;
AC Q9TUT4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161979; AAD47734.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00037; GPCR_RHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER      1      339
FT          1
SQ SEQUENCE      339 AA; 39032 MW; 84B51B9548E0703C CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||||
DB      290 YAFVGEKFRNYLLVFFQK 307
      |||||

RESULT 16
Q9TUT9      PRELIMINARY;      PRT;      339 AA.
ID Q9TUT9;
AC Q9TUT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER      1      339
FT          1
SQ SEQUENCE      339 AA; 39032 MW; 84B51B9548E0703C CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||||
DB      290 YAFVGEKFRNYLLVFFQK 307
      |||||

RESULT 16
Q9TUT9      PRELIMINARY;      PRT;      339 AA.
ID Q9TUT9;
AC Q9TUT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER      1      339
FT          1
SQ SEQUENCE      339 AA; 39032 MW; 84B51B9548E0703C CRC64;

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DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER      1      339
FT          1
SQ SEQUENCE      339 AA; 39032 MW; EC4CE48DEEF107E CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||||
DB      290 YAFVGEKFRNYLLVFFQK 307
      |||||

RESULT 17
Q9TSQ1      PRELIMINARY;      PRT;      339 AA.
ID Q9TSQ1;
AC Q9TSQ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162023; AAD47778.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER      1      339
FT          1
SQ SEQUENCE      339 AA; 39216 MW; 847E935FA403E52D CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||||
DB      290 YAFVGEKFRNYLLVFFQK 307
      |||||

RESULT 18
Q9TUU8      PRELIMINARY;      PRT;      339 AA.
ID Q9TUU8;
AC Q9TUU8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.

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OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161949; AAD47705.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39049 MW; 6D1A93F66270F3ED CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307
|||||
RESULT 19
Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39159 MW; 8E699B892EAC0E84 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307
|||||
RESULT 20
Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39159 MW; 8E699B892EAC0E84 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307
|||||
RESULT 21
Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.

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DR EMBL; AF162044; AAD47799.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39150 MW; 847D5F92BB03E6E2 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 22
Q9TU05 PRELIMINARY; PRT; 339 AA.
AC Q9TU05;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5
OS Erythrocybus, patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161961; AAD47716.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39121 MW; AFB6E3EE4D6D3484 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 24
Q9TUR9 PRELIMINARY; PRT; 339 AA.
AC Q9TUR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Saguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162015; AAD47770.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39048 MW; 1A2E19E3A6A5A52A CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 23
Q9TU03 PRELIMINARY; PRT; 339 AA.
AC Q9TU03;

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FT NON TER 339 339
SQ SEQUENCE 339 AA; 39063 MW; 78BC37A84B877085 CRC64;

Query Match
Best Local Similarity 100.0%; Score 95; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307

RESULT 25
Q9TQT0 PRELIMINARY; PRT; 339 AA.
AC Q9TQT0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161954; AAD47710.1; -.
DR EMBL; AF161950; AAD47706.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39067 MW; 5BFCBC5BA96C2F9E CRC64;

Query Match
Best Local Similarity 100.0%; Score 95; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307

RESULT 27
Q9TSN2 PRELIMINARY; PRT; 339 AA.
AC Q9TSN2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161953; AAD47709.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 339 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match
Best Local Similarity 100.0%; Score 95; DB 6; Length 339;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
Db 290 YAFVGEKFRNLLVFFQK 307

RESULT 26
Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;

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Db      290 YAFVGEKFRNLLVFFQK 307

RESULT 28
Q9TUQ6 PRELIMINARY; PRT; 339 AA.
AC
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
CCRS.
GN Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162002; AAD47751.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39178 MW; 9DF2A6F446C55AED CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db      290 YAFVGEKFRNLLVFFQK 307

RESULT 29
Q9TUQ6 PRELIMINARY; PRT; 339 AA.
AC
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
CCRS.
GN Colobus guereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162005; AAD47760.1; -.
DR EMBL; AF162000; AAD47755.1; -.
DR EMBL; AF162001; AAD47756.1; -.
DR EMBL; AF162002; AAD47757.1; -.

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DR EMBL; AF162003; AAD47758.1; -.
DR EMBL; AF162004; AAD47759.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39168 MW; 6A4BF72FEBFF566F CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db      290 YAFVGEKFRNLLVFFQK 307

RESULT 30
Q9TUW6 PRELIMINARY; PRT; 339 AA.
AC
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
CCRS.
GN Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161900; AAD47657.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39103 MW; 4038C132D024C5A4 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
Db      290 YAFVGEKFRNLLVFFQK 307

RESULT 31
Q9TUQ9 PRELIMINARY; PRT; 339 AA.
AC
Q9TUQ9

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus mona.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36226;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162041; AAD47796.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39019 MW; 7176P940AF11F3ED CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
Db 290 YAFVGEKFRNVLVFFQK 307

RESULT 32
Q9TSN3
ID Q9TSN3 PRELIMINARY; PRT; 339 AA.
AC Q9TSN3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161951; AAD47707.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39019 MW; 7176P940AF11F3ED CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
Db 290 YAFVGEKFRNVLVFFQK 307

RESULT 33
Q9TUU7
ID Q9TUU7 PRELIMINARY; PRT; 339 AA.
AC Q9TUU7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161953; AAD47711.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39037 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
Db 290 YAFVGEKFRNVLVFFQK 307

RESULT 34
Q9TUR2
ID Q9TUR2 PRELIMINARY; PRT; 339 AA.
AC Q9TUR2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Erythrocebus patas (Red guenon) (Husar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]

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RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162034; AAD47789.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39138 MW; AD31455EBBC69499 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 35
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161989; AAD47744.1; -.
DR EMBL; AF161988; AAD47743.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39113 MW; 7F9803EA0E0AF9ED CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 36
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161956; AAD47712.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39080 MW; 4DCA9C72B093216D CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 37
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162046; AAD47801.1; -.
DR EMBL; AF162043; AAD47798.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.

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DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39178 MW; 847F8F936B00E6E2 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
   |||||
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 38
Q9TUS7
ID Q9TUS7 PRELIMINARY; PRT; 339 AA.
AC Q9TUS7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161995; AAD47750.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39068 MW; 84EB018085DC0A62 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
   |||||
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 39
Q9TUW7
ID Q9TUW7 PRELIMINARY; PRT; 339 AA.
AC Q9TUW7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).

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GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161899; AAD47656.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39157 MW; 4A9EBAD183E8E72D CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
   |||||
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 40
Q9TUW3
ID Q9TUW3 PRELIMINARY; PRT; 339 AA.
AC Q9TUW3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161908; AAD47665.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 4350C4625FB0657C CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
| | | | | | | | | | | | | | | |
Db 290 YAFVGEKFRNYLLVFFQK 307

Search completed: September 28, 2004, 09:06:20
Job time : 28.8 secs